



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 94941

TO: Phillip Gambel
Location: 8b03 / 9e12
Saturday, May 24, 2003
Au: 1644
Serial Number: 919408

From: Jan Delaval
Location: Biotech-Chem Library
CM1-1E07
Phone: 308-4498

jan.delaval@uspto.gov

Search Notes

NOTE :

Nucleic acid search results will be forwarded to you when they are available.

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

94941
Delaval, Jan

From: Gambel, Phillip
Sent: Saturday, May 24, 2003 8:34 AM
To: Delaval, Jan
Subject: 09/919,408 lemischka amd

jan

please perform a sequence and a sequence interference search for

ussn 09/919,408 (lemischka amd)

SEQ ID NO: 1

SEQ ID NO: 2

SEQ ID NO: 3

SEQ ID NO: 4

thanx

phillip gambel
art unit 1644
308--3997

if there is going to be a delay with the nucleic acid sequences,
then searching the amino acid sequences would be sufficient
thanx

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

Set Name Query

side by side

Hit Count Set Name

result set

*DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ*L4 L3 same (antibod\$ or immunoglobulin\$ or hybridoma\$)36 L4L3 'flk-2'86 L3*DB=USPT,PGPB; PLUR=YES; OP=ADJ*L2 L1 and 'flk-2'10 L2L1 lemischka-ihor\$11 L1

END OF SEARCH HISTORY

WEST[Help](#)[Logout](#)[Interrupt](#)[Main Menu](#)[Search Form](#)[Posting Counts](#)[Show S Numbers](#)[Edit S Numbers](#)[Preferences](#)[Cases](#)**Search Results -**

Term	Documents
ANTIBOD\$	0
ANTIBOD.DWPI,EPAB,JPAB,USPT,PGPB.	731
ANTIBODANTIBODA.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODAY.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODEES.DWPI,EPAB,JPAB,USPT,PGPB.	2
ANTIBODEIES.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODEIS.DWPI,EPAB,JPAB,USPT,PGPB.	2
ANTIBODES.DWPI,EPAB,JPAB,USPT,PGPB.	213
ANTIBODEY.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODFIES.DWPI,EPAB,JPAB,USPT,PGPB.	2
ANTIBODHYBRIDOMAS.DWPI,EPAB,JPAB,USPT,PGPB.	1
(L3 SAME (ANTIBOD\$ OR IMMUNOGLOBULIN\$ OR HYBRIDOMAS\$)).USPT,PGPB,JPAB,EPAB,DWPI.	36

[There are more results than shown above. Click here to view the entire set.](#)

Database:

US Patents Full-Text Database
US Pre-Grant Publication Full-Text Database
JPO Abstracts Database
EPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search:

L4

[Refine Search](#)[Recall Text](#)[Clear](#)**Search History**

DATE: Saturday, May 24, 2003 [Printable Copy](#) [Create Case](#)

Set Name Query
side by side**Hit Count Set Name**
result set*DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ*L4 L3 same (antibod\$ or immunoglobulin\$ or hybridoma\$)36 L4L3 'flk-2'86 L3*DB=USPT,PGPB; PLUR=YES; OP=ADJ*L2 L1 and 'flk-2'10 L2L1 lemischka-ihor\$11 L1

END OF SEARCH HISTORY

U.S. DEPARTMENT OF COMMERCE
PATENT AND TRADEMARK OFFICE

EXAMINER'S CASE ACTION WORKSHEET

Application No. <div style="text-align: center;">09/919,408</div>		Legal Instrument Examiner
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CHECK TYPE OF ACTION		DATE OF COUNT
<input checked="" type="checkbox"/> Non-Final Rejection	<input type="checkbox"/> Restriction/Election Only	<input type="checkbox"/> Final Rejection
<input type="checkbox"/> Ex Parte Quayle	<input type="checkbox"/> Allowance	<input type="checkbox"/> Advisory Action
<input type="checkbox"/> Examiner's Answer	<input type="checkbox"/> Reply Brief Noted	<input type="checkbox"/> Non-Entry of Late Paper
<input type="checkbox"/> Defective Notice of Appeal or Defective Appeal Brief	<input type="checkbox"/> Interference SPE <small>(Approval for Disposal)</small>	<input type="checkbox"/> Suspension SPE <small>(Initial)</small>
<input type="checkbox"/> Allowance After Examiner's Answer	<input type="checkbox"/> SIR Disposal <small>(use only after FAOM)</small>	<input type="checkbox"/> Post-Allowance Communication
<input type="checkbox"/> Miscellaneous Office Letter <small>(With Shortened Statutory Period Set)</small>	<input type="checkbox"/> Notice of Non-Responsive Amendment <small>(With One Month Time Period Set)</small>	<input type="checkbox"/> Miscellaneous Office Letter <small>(No Response Period Set)</small>
<input type="checkbox"/> Letter Requiring Formal Drawings	<input type="checkbox"/> Supplemental Action <small>(Excluding Examiner's Answer)</small>	<input type="checkbox"/> Response to a Rule 312 Amendment
<input type="checkbox"/> Restart Time Period <small>(e.g., Missing References)</small>	<input type="checkbox"/> Interview Summary	<input type="checkbox"/> Authorization to Change Previous Office Action SPE: <small>(Initial)</small>
<input type="checkbox"/> Abandonment	<input type="checkbox"/> Express Abandonment <small>Date: _____</small>	<input type="checkbox"/> Abandonment After Examiner's Answer

Examiner's Name : _____ First Last AU: _____ 1234

[Generate Collection](#)[Print](#)**Search Results - Record(s) 21 through 30 of 36 returned.**

-
- ☐ 21. 5747651. 15 Feb 96; 05 May 98. Antibodies against tyrosine kinase receptor flk-1. Lemischka; Ihor R.. 530/387.9; 530/388.22 530/388.7 530/389.1 530/389.6. C07K016/28 C12P021/08.
-
- ☐ 22. 5710134. 19 May 95; 20 Jan 98. Combination of necrosis-inducing substances with substances which are activated by necroses for the selective therapy of tumors and inflammatory disorders. Bosslet; Klaus, et al. 514/34; 536/6.4. A61K031/70.
-
- ☐ 23. 5635388. 04 Apr 94; 03 Jun 97. Agonist antibodies against the flk2/flt3 receptor and uses thereof. Bennett; Brian D., et al. 435/334; 424/85.1 424/85.2 424/85.5 435/320.1 435/328 435/70.21 530/351 530/387.3 530/388.22 530/389.1 536/23.53. C12N005/20 C07K016/28 C07H015/12.
-
- ☐ 24. 5621090. 26 Jun 92; 15 Apr 97. Nucleic acids encoding soluble human FLK-2 extracellular domain. Lemischka; Ihor R.. 536/23.5; 435/69.1. C07H021/00.
-
- ☐ 25. 5548065. 31 Oct 94; 20 Aug 96. Tyrosine kinase receptor human flk-2-specific antibodies. Lemischka; Ihor R.. 530/388.22; 530/387.9 530/388.23 530/388.7 530/389.2 530/389.6. C07K016/18 C07K016/28.
-
- ☐ 26. 5367057. 30 Apr 93; 22 Nov 94. Tyrosine kinase receptor flk-2 and fragments thereof. Lemischka; Ihor R.. 530/350; 530/403. C07K013/00.
-
- ☐ 27. 5283354. 17 Sep 92; 01 Feb 94. Nucleic acids encoding hematopoietic stem cells receptors flk-1. Lemischka; Ihor R.. 536/23.5; 435/69.1 530/350 530/403. C07H021/00.
-
- ☐ 28. 5270458. 19 Nov 92; 14 Dec 93. Nucleic acids encoding fragments of hematopoietic stem cell receptor flk-2. Lemischka; Ihor R.. 536/23.5; 435/320.1 435/69.1 530/350 530/403. C07H021/00.
-
- ☐ 29. 5185438. 24 Dec 91; 09 Feb 93. Nucleic acids encoding hencatoporetic stem cell receptor flk-2. Lemischka; Ihor R.. 536/23.2; 435/320.1 435/69.1 530/350 530/403. C07H021/00.
-
- ☒ 30. EP 1186301 A2. 07 Sep 94. 13 Mar 02. Monoclonal antibodies that recognize flk-2 receptors and the isolation of primitive hematopoietic stem cell populations. GOLDSTEIN, NEIL I, et al. A61K039/395; A61P035/02.
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Term	Documents
ANTIBOD\$	0
ANTIBOD.DWPI,EPAB,JPAB,USPT,PGPB.	731
ANTIBODANTIBODA.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODAY.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODEES.DWPI,EPAB,JPAB,USPT,PGPB.	.2
ANTIBODEIES.DWPI,EPAB,JPAB,USPT,PGPB.	1
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ANTIBODHYBRIDOMAS.DWPI,EPAB,JPAB,USPT,PGPB.	1
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ANTIBOD.DWPI,EPAB,JPAB,USPT,PGPB.	731
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ANTIBODEIES.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODEIS.DWPI,EPAB,JPAB,USPT,PGPB.	2
ANTIBODES.DWPI,EPAB,JPAB,USPT,PGPB.	213
ANTIBODEY.DWPI,EPAB,JPAB,USPT,PGPB.	1
ANTIBODFIES.DWPI,EPAB,JPAB,USPT,PGPB.	2
ANTIBODHYBRIDOMAS.DWPI,EPAB,JPAB,USPT,PGPB.	1
(L3 SAME (ANTIBOD\$ OR IMMUNOGLOBULIN\$ OR HYBRIDOMAS\$)).USPT,PGPB,JPAB,EPAB,DWPI.	36

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US Pre-Grant Publication Full-Text Database
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Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search:

L4

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DATE: Saturday, May 24, 2003 [Printable Copy](#) [Create Case](#)

WEST[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 10 of 10 returned.**☐ 1. Document ID: US 20020119545 A1

L2: Entry 1 of 10

File: PGPB

Aug 29, 2002

PGPUB-DOCUMENT-NUMBER: 20020119545

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020119545 A1

TITLE: Soluble human flk-2 protein

PUBLICATION-DATE: August 29, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
<u>Lemischka, Ihor R.</u>	Princeton	NJ	US	

US-CL-CURRENT: 435/194; 435/320.1, 435/325, 435/69.1, 536/23.2

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	RWC	Draw Desc	Image
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☐ 2. Document ID: US 20020072077 A1

L2: Entry 2 of 10

File: PGPB

Jun 13, 2002

PGPUB-DOCUMENT-NUMBER: 20020072077

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020072077 A1

TITLE: Method for isolating cells expressing FLk-2 receptors and isolated populations of cells that express FLk-2 receptors

PUBLICATION-DATE: June 13, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
<u>Lemischka, Ihor R.</u>	Princeton	NJ	US	

US-CL-CURRENT: 435/7.21; 435/320.1, 435/325, 435/69.1, 536/23.5

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	RWC	Draw Desc	Image
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☐ 3. Document ID: US 5912133 A

L2: Entry 3 of 10

File: USPT

Jun 15, 1999

US-PAT-NO: 5912133

DOCUMENT-IDENTIFIER: US 5912133 A

**** See image for Certificate of Correction ****

TITLE: Method for isolating stem cells expressing flk-1 receptors

DATE-ISSUED: June 15, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 435/7.21; 435/971, 530/388.7, 530/389.6

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KIMC	Draw Desc	Image
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☐ 4. Document ID: US 5747651 A

L2: Entry 4 of 10

File: USPT

May 5, 1998

US-PAT-NO: 5747651

DOCUMENT-IDENTIFIER: US 5747651 A

TITLE: Antibodies against tyrosine kinase receptor flk-1

DATE-ISSUED: May 5, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 530/387.9; 530/388.22, 530/388.7, 530/389.1, 530/389.6

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KIMC	Draw Desc	Image
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☐ 5. Document ID: US 5621090 A

L2: Entry 5 of 10

File: USPT

Apr 15, 1997

US-PAT-NO: 5621090

DOCUMENT-IDENTIFIER: US 5621090 A

TITLE: Nucleic acids encoding soluble human FLK-2 extracellular domain

DATE-ISSUED: April 15, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 536/23.5; 435/69.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KIMC	Draw Desc	Image
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☐ 6. Document ID: US 5548065 A

L2: Entry 6 of 10

File: USPT

Aug 20, 1996

US-PAT-NO: 5548065

DOCUMENT-IDENTIFIER: US 5548065 A

TITLE: Tyrosine kinase receptor human flk-2-specific antibodies

DATE-ISSUED: August 20, 1996

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 530/388.22; 530/387.9, 530/388.23, 530/388.7, 530/389.2, 530/389.6

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KWIC	Draw Desc	Image
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☐ 7. Document ID: US 5367057 A

L2: Entry 7 of 10

File: USPT

Nov 22, 1994

US-PAT-NO: 5367057

DOCUMENT-IDENTIFIER: US 5367057 A

TITLE: Tyrosine kinase receptor flk-2 and fragments thereof

DATE-ISSUED: November 22, 1994

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 530/350; 530/403

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KWIC	Draw Desc	Image
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☐ 8. Document ID: US 5283354 A

L2: Entry 8 of 10

File: USPT

Feb 1, 1994

US-PAT-NO: 5283354

DOCUMENT-IDENTIFIER: US 5283354 A

TITLE: Nucleic acids encoding hematopoietic stem cells receptors flk-1

DATE-ISSUED: February 1, 1994

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 536/23.5; 435/69.1, 530/350, 530/403

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KWIC	Draw Desc	Image
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☐ 9. Document ID: US 5270458 A

L2: Entry 9 of 10

File: USPT

Dec 14, 1993

US-PAT-NO: 5270458

DOCUMENT-IDENTIFIER: US 5270458 A

TITLE: Nucleic acids encoding fragments of hematopoietic stem cell receptor flk-2

DATE-ISSUED: December 14, 1993

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 536/23.5; 435/320.1, 435/69.1, 530/350, 530/403

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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KIMC	Draw Desc	Image
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☐ 10. Document ID: US 5185438 A

L2: Entry 10 of 10

File: USPT

Feb 9, 1993

US-PAT-NO: 5185438

DOCUMENT-IDENTIFIER: US 5185438 A

**** See image for Certificate of Correction ****TITLE: Nucleic acids encoding hencatoporetic stem cell receptor flk-2

DATE-ISSUED: February 9, 1993

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
<u>Lemischka; Ihor R.</u>	Princeton	NJ		

US-CL-CURRENT: 536/23.2; 435/320.1, 435/69.1, 530/350, 530/403

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------

KIMC	Draw Desc	Image
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Term	Documents
FLK-2.USPT,PGPB.	70
FLK-2S	0
(1 AND FLK-2).USPT,PGPB.	10
(L1 AND 'FLK-2').USPT,PGPB.	10

Display Format:

-

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identifying ligands which stimulate stem cell hematopoiesis
? s flk(w)2

2948 FLK
8736730 2

S4 279 FLK(W)2

? s s4 and py<1993

Processing

Processing

279 S4
32335638 PY<1993

S5 4 S4 AND PY<1993

? rd s5

...completed examining records

S6 1 RD S5 (unique items)

? t s6/3/all

6/3/1 (Item 1 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All.rts. reserv.

07768231 BIOSIS NO.: 000092071602

A RECEPTOR TYROSINE KINASE SPECIFIC TO HEMATOPOIETIC STEM AND PROGENITOR
CELL-ENRICHED POPULATIONS

AUTHOR: MATTHEWS W; JORDAN C T; WIEGAND G W; PARDOLL D; LEMISCHKA I R

AUTHOR ADDRESS: DEP. MOLECULAR BIOL., PRINCETON UNIV., PRINCETON, N.J.
08540.

JOURNAL: CELL 65 (7). 1991. 1143-1152. 1991

FULL JOURNAL NAME: Cell

CODEN: CELLB

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

?

TEM:OS - DIALOG OneSearch

File 5: Biosis Previews(R) 1969-2003/May W3
(c) 2003 BIOSIS

*File 5: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 73: EMBASE 1974-2003/May W3
(c) 2003 Elsevier Science B.V.

*File 73: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 155: MEDLINE(R) 1966-2003/May W3
(c) format only 2003 The Dialog Corp.

*File 155: Medline has been reloaded and accession numbers have changed. Please see HELP NEWS 155.

File 399: CA SEARCH(R) 1967-2003/UD=13821
(c) 2003 American Chemical Society

*File 399: Use is subject to the terms of your user/customer agreement. Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description

? e au=lemischka ihor ?

Ref	Items	Index-term
E1	40	AU=LEMISCHKA I.R.
E2	9	AU=LEMISCHKA IHOR
E3	0	*AU=LEMISCHKA IHOR ?
E4	36	AU=LEMISCHKA IHOR R
E5	1	AU=LEMISCHKA, I. R.
E6	6	AU=LEMISCHKA, IHOR
E7	25	AU=LEMISCHKA, IHOR R.
E8	1	AU=LEMISH D
E9	10	AU=LEMISH G T
E10	4	AU=LEMISH G.T.
E11	3	AU=LEMISH I
E12	1	AU=LEMISH I.

Enter P or PAGE for more

? s e1-e7

40	AU=LEMISCHKA I.R.
9	AU=LEMISCHKA IHOR
0	AU=LEMISCHKA IHOR ?
36	AU=LEMISCHKA IHOR R
1	AU=LEMISCHKA, I. R.
6	AU=LEMISCHKA, IHOR
25	AU=LEMISCHKA, IHOR R.

S1 117 E1-E7

? s s1 and (flk(W)2)

Processing

117	S1
2948	FLK
8736730	2
279	FLK(W)2

S2 3 S1 AND (FLK(W)2)

? rd s2

...completed examining records

S3 2 RD S2 (unique items)

? t s3/7/all

3/7/1 (Item 1 from file: 73)

DIALOG(R) File 73: EMBASE

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04722255 EMBASE No: 1991215609

A receptor tyrosine kinase specific to hematopoietic stem and progenitor

cell-enriched populations

Matthews W.; Jordan C.T.; Wiegand G.W.; Pardoll D.; Lemischka I.R.
Department of Molecular Biology, Princeton University, Princeton, NJ
08540 United States
Cell (CELL) (United States) 1991, 65/7 (1143-1152)
CODEN: CELLB ISSN: 0092-8674
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

To elucidate the molecular biology of the hematopoietic stem cell, we have begun to isolate genes from murine cell populations enriched in stem cell activity. One such cDNA encodes a novel receptor tyrosine kinase, designated fetal liver kinase-2 or **flk-2**, which is related to the W locus gene product c-kit. Expression analyses suggest an extremely restricted distribution of **flk-2**. It is expressed in populations enriched for stem cells and primitive uncommitted progenitors, and is absent in populations containing more mature cells. Therefore, this receptor may be a key signal transducing component in the totipotent hematopoietic stem cell and its immediate self-renewing progeny.

3/7/2 (Item 1 from file: 399)
DIALOG(R) File 399:CA SEARCH(R)
(c) 2003 American Chemical Society. All rts. reserv.

126289031 CA: 126(22)289031p PATENT
Recombinant production of human gene flk-2 protein kinase extracellular domain and use for identifying ligands which stimulate stem cell hematopoiesis
INVENTOR(AUTHOR): Lemischka, Ihor R.
LOCATION: USA
ASSIGNEE: Princeton University
PATENT: United States ; US 5621090 A DATE: 19970415
APPLICATION: US 906397 (19920626) *US 679666 (19910402) *US 728913 (19910628) *US 793065 (19911115) *US 813593 (19911224)
PAGES: 55 pp. Cont.-in-part of U.S. 5,185,438. CODEN: USXXAM LANGUAGE: English CLASS: 536023500; C07H-021/00A
SECTION:
CA203002 Biochemical Genetics
CA207XXX Enzymes
CA213XXX Mammalian Biochemistry
IDENTIFIERS: gene flk2 protein kinase ligand screening, human gene flk2 protein kinase sequence, cDNA sequence flk2 protein kinase human, hematopoiesis stem cell stimulation flk2 ligand
DESCRIPTORS:
Genes (animal)...
flk-2; recombinant prodn. of human gene flk-2 protein kinase extracellular domain and use for identifying ligands which stimulate stem cell hematopoiesis
cDNA sequences... Hematopoietic stem cell... Ligands... mRNA... Protein sequences...
recombinant prodn. of human gene flk-2 protein kinase extracellular domain and use for identifying ligands which stimulate stem cell hematopoiesis
Hematopoiesis...
stem cell; recombinant prodn. of human gene flk-2 protein kinase extracellular domain and use for identifying ligands which stimulate stem cell hematopoiesis
CAS REGISTRY NUMBERS:
139569-91-8 146215-22-7 162394-09-4 nucleotide sequence; recombinant prodn. of human gene flk-2 protein kinase extracellular domain and use for identifying ligands which stimulate stem cell hematopoiesis
80449-02-1P 139569-26-9 146215-24-9 155077-32-0P recombinant prodn. of human gene flk-2 protein kinase extracellular domain and use for

egin 5,73,155,399
24may03 08:13:40 User208760 Session D2312.2
\$0.00 0.071 DialUnits File410
\$0.00 Estimated cost File410
\$0.01 TELNET
\$0.01 Estimated cost this search
\$0.28 Estimated total session cost 0.149 DialUnits

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removal, customized scheduling. See HELP ALERT.
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*File 155: Medline has been reloaded and accession numbers have
changed. Please see HELP NEWS 155.
File 399:CA SEARCH(R) 1967-2003/UD=13821
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Set	Items	Description
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? s flk(w)2		
	2948	FLK
	8736730	2
S1	279	FLK(W)2
? s flk(w)2(10n)(human)		
Processing		
	2948	FLK
	8736730	2
	19097961	HUMAN
S2	43	FLK(W)2(10N)(HUMAN)
? rd s2		
...completed examining records		
S3	24	RD S2 (unique items)
? t s3/3/all		

3/3/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

13435527 BIOSIS NO.: 200200064348
Nucleic acids encoding soluble **human flk-2** extracellular
domain
AUTHOR: Lemischka I R
AUTHOR ADDRESS: Princeton, N.J.**USA
JOURNAL: Official Gazette of the United States Patent and Trademark Office
Patents 1197 (3):p1935 April 15, 1997
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Citation
LANGUAGE: English

3/3/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

13419152 BIOSIS NO.: 200200047973
Tyrosine kinase receptor **human flk-2**-specific antibodies
AUTHOR: Lemischka I R
AUTHOR ADDRESS: Princeton, N.J.**USA
JOURNAL: Official Gazette of the United States Patent and Trademark Office
Patents 1189 (3):p2100 Aug. 20, 1996
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Citation
LANGUAGE: English

3/3/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

13275375 BIOSIS NO.: 200100482524
Soluble Flk-2 sequence.
AUTHOR: Yang Zhi(a)
AUTHOR ADDRESS: (a)Palo Alto, CA**USA
JOURNAL: Official Gazette of the United States Patent and Trademark Office
Patents 1246 (2):pNo Pagination May 8, 2001
MEDIUM: e-file
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Abstract
LANGUAGE: English

3/3/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

13110077 BIOSIS NO.: 200100317226
Storage of factor VIII (FVIII) in the alpha-granules of human platelets
following retroviral transduction and transplantation of human CD34+
cells into NOD-SCID mice.
AUTHOR: Wilcox David A(a); Rosenberg Jonathan B; Johnson Bryon D(a);
Montgomery Robert R(a)
AUTHOR ADDRESS: (a)Department of Pediatrics, Medical College of Wisconsin,
Milwaukee, WI**USA
JOURNAL: Blood 96 (11 Part 1):p803a November 16, 2000
MEDIUM: print
CONFERENCE/MEETING: 42nd Annual Meeting of the American Society of
Hematology San Francisco, California, USA December 01-05, 2000
SPONSOR: American Society of Hematology
ISSN: 0006-4971
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

3/3/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

12412955 BIOSIS NO.: 200000166457
Identification of CD19-B220+c-Kit+Flt3/Flk-2+ cells as early B lymphoid
precursors before pre-B-I cells in juvenile mouse bone marrow.
AUTHOR: Ogawa Minetaro(a); ten Boekel Edwin; Melchers Fritz
AUTHOR ADDRESS: (a)Department of Molecular Genetics, Graduate School of
Medicine, Kyoto University, Shogoin-Kawaharacho 53, Sakyo-ku, Kyoto,
606-8507**Japan
JOURNAL: International Immunology. 12 (3):p313-324 March, 2000

ISSN: 0953-8178
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

3/3/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

12301577 BIOSIS NO.: 200000059444
Ex vivo generation of CD34+ cells from CD34- hematopoietic cells.
AUTHOR: Nakamura Yoshihiko; Ando Kiyoshi(a); Chargui Jamel; Kawada Hiroshi;
Sato Tadayuki; Tsuji Takashi; Hotta Tomomitsu; Kato Shunichi
AUTHOR ADDRESS: (a)Department of Hematology, Tokai University School of
Medicine, Bohseidai, Isehara, Kanagawa**Japan
JOURNAL: Blood 94 (12):p4053-4059 Dec. 15, 1999
ISSN: 0006-4971
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

3/3/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

12258591 BIOSIS NO.: 200000012093
SZF1: A novel KRAB-zinc finger gene expressed in CD34+ stem/progenitor
cells.
AUTHOR: Liu Cheng; Levenstein Mark; Chen Joseph; Tsifrina Elina; Yonescu
Raluc; Griffin Constance; Civin Curt I; Small Donald(a)
AUTHOR ADDRESS: (a)The Johns Hopkins Oncology Center, 600 North Wolfe
Street, Rm. 3-109, Baltimore, MD, 21287-5001**USA
JOURNAL: Experimental Hematology (Charlottesville) 27 (2):p313-325 Feb.,
1999
ISSN: 0301-472X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

3/3/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

12161736 BIOSIS NO.: 199900456585
Modulation of haematopoietic progenitor development by FLT-3 ligand.
AUTHOR: Banu Naheed; Deng Bijia; Lyman Stewart D; Avraham Hava(a)
AUTHOR ADDRESS: (a)Division of Experimental Medicine, Beth Israel Deaconess
Medical Center, Harvard Institutes of Medicine, 4 Blackfan Circle, 3rd
Floor, Boston, MA, 02115**USA
JOURNAL: Cytokine 11 (9):p679-688 Sept., 1999
ISSN: 1043-4666
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

3/3/9 (Item 9 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

11622695 BIOSIS NO.: 199800404830

Isolation and characterization of a cDNA for human, mouse, and rat
full-length stem cell growth factor, a new member of C-type lectin
superfamily.

AUTHOR: Mio Hiroyuki(a); Kagami Naofumi; Yokokawa Sachiko; Kawai Hironori;
Nakagawa Satoshi; Takeuchi Kyoko; Sekine Susumu; Hiraoka Atsunobu

AUTHOR ADDRESS: (a)Pharm. Res. Inst., Kyowa Hakko Kogyo Co. Ltd., 1188
Shimotogari, Nagaizumi-cho, Sunto-gun, Shizu**Japan

JOURNAL: Biochemical and Biophysical Research Communications 249 (1):p
124-130 Aug. 10, 1998

ISSN: 0006-291X

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

3/3/10 (Item 10 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

10851909 BIOSIS NO.: 199799473054

Expression of multiple forms of fetal liver kinase-2 (flk-2
/flt-3) ligand in cultured human keratinocytes.

AUTHOR: Morita Eishin(a); Tanaka Toshihiko; Shinoda Sumumu; Kameyoshi
Yoshikazu; Yamamoto Shoso; Lee Dong-Geun; Sugiyama Masanori

AUTHOR ADDRESS: (a)Dep. Dermatol., Hiroshima Univ. Sch. Med., Kasumi 1-2-3,
Minami-ku, Hiroshima 734**Japan

JOURNAL: Archives of Dermatological Research 289 (3):p177-179 1997

ISSN: 0340-3696

RECORD TYPE: Citation

LANGUAGE: English

3/3/11 (Item 11 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

10219695 BIOSIS NO.: 199698674613

FLT3/FLK-2 (STK-1) ligand does not stimulate human
megakaryopoiesis in vitro.

AUTHOR: Ratajczak Mariusz Z; Ratajczak Janina; Ford John; Kregnow Robert;
Marlicz Wojtek; Gewirtz Alan M(a)

AUTHOR ADDRESS: (a)513B-Stellar-Chance Lab., Univ. Penna. Sch. Med., 422
Curie Blvd., Philadelphia, PA 19104**USA

JOURNAL: Stem Cells (Dayton) 14 (1):p146-150 1996

ISSN: 1066-5099

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

3/3/12 (Item 12 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

10110680 BIOSIS NO.: 199698565598

Isolation and characterization of a monoclonal antibody binding to the
extracellular domain of the flk-2 tyrosine kinase receptor.

AUTHOR: Rose Caroline; Rockwell Patricia; Yang Jian-Quing; Pytowski
Bronislaw; Goldstein Neil I(a)

AUTHOR ADDRESS: (a)Immunol./Monoclonal Antibodies Dep., ImClone Systems

Inc., 180 Varick St., New York, NY 10014**USA
JOURNAL: Hybridoma 14 (5):p453-459 1995
ISSN: 0272-457X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

3/3/13 (Item 13 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

09713826 BIOSIS NO.: 199598168744
FLK-2/FLT-3 ligand regulates the growth of early myeloid progenitors isolated from human fetal liver.
AUTHOR: Muench Marcus O; Roncarolo Maria Grazia; Menon Satish; Xu Yuming; Kastelein Robert; Zurawski Sandra; Hannum Charles H; Culpepper Janice; Lee Frank; Namikawa Reiko(a)
AUTHOR ADDRESS: (a)DNAX Res. Inst. Mol. Cellular Biol., 901 California Ave., Palo Alto, CA 94304-1104**USA
JOURNAL: Blood 85 (4):p963-972 1995
ISSN: 0006-4971
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

3/3/14 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

09126484 BIOSIS NO.: 199497134854
STK-1, the **human** homology of **Flk-2/Flt-3**, is selectively expressed in CD34+ **human** bone marrow cells and is involved in the proliferation of early progenitor/stem cells.
AUTHOR: Small Donald(a); Levenstein Mark; Kim Eunkyung; Carow Cathy; Amin Shahina; Rockwell Patricia; Witte Larry; Burrow Christopher; Ratajczak Mariusz Z; et al
AUTHOR ADDRESS: (a)Oncol. Cent., Dep. Pediatr., Johns Hopkins Univ. Sch. Med., 600 North Wolfe Street, Baltimore, M**USA
JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 91 (2):p459-463 1994
ISSN: 0027-8424
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

3/3/15 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

09098771 BIOSIS NO.: 199497107141
STK-1, a **human** homolog of **FLK-2/FLT3**, is aberrantly expressed in **human** leukemias and may be involved in the growth and/or differentiation of hematopoietic stem/progenitor cells.
AUTHOR: Small D(a); Levenstein M; Kim E; Carow C E; Amin S; Ratajczak M; Gewirtz A M; Civin C I
AUTHOR ADDRESS: (a)Dep. Oncol., Johns Hopkins Univ. Sch. Lab. Med., Baltimore, MD**USA
JOURNAL: Blood 82 (10 SUPPL. 1):p325A 1993
CONFERENCE/MEETING: Thirty-fifth Annual Meeting of the American Society of Hematology St. Louis, Missouri, USA December 3-7, 1993
ISSN: 0006-4971

RECORD TYPE: Citation

LANGUAGE: English

3/3/16 (Item 1 from file: 73)

DIALOG(R)File 73:EMBASE

(c) 2003 Elsevier Science B.V. All rts. reserv.

10630874 EMBASE No: 2000096239

Identification of CD19sup -B220sup +c-Kitsup +Flt3/Flk-2sup + cells as early B lymphoid precursors before pre-B-I cells in juvenile mouse bone marrow

Ogawa M.; Ten Boekel E.; Melchers F.

M. Ogawa, Department of Molecular Genetics, Graduate School of Medicine, Kyoto University, Shogoin-Kawaharacho 53, Sakyo-ku, Kyoto 606-8507 Japan
International Immunology (INT. IMMUNOL.) (United Kingdom) 2000, 12/3 (313-324)

CODEN: INIME ISSN: 0953-8178

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 58

3/3/17 (Item 2 from file: 73)

DIALOG(R)File 73:EMBASE

(c) 2003 Elsevier Science B.V. All rts. reserv.

10520866 EMBASE No: 1999431983

Ex vivo generation of CD34sup + cells from CD34sup - hematopoietic cells

Nakamura Y.; Ando K.; Chargui J.; Kawada H.; Sato T.; Tsuji T.; Hotta T.; Kato S.

Dr. K. Ando, Department of Hematology, Tokai University School of Medicine, Isehara, Kanagawa 259-1183 Japan

Blood (BLOOD) (United States) 1999, 94/12 (4053-4059)

CODEN: BLOOA ISSN: 0006-4971

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 21

3/3/18 (Item 3 from file: 73)

DIALOG(R)File 73:EMBASE

(c) 2003 Elsevier Science B.V. All rts. reserv.

05636203 EMBASE No: 1994041406

STK-1, the **human** homolog of **Flk-2/Flt-3**, is selectively expressed in CD34sup + **human** bone marrow cells and is involved in the proliferation of early progenitor/stem cells

Small D.; Levenstein M.; Kim E.; Carow C.; Amin S.; Rockwell P.; Witte L.; Burrow C.; Ratajczak M.Z.; Gewirtz A.M.; Civin C.I.

Department of Pediatrics, Oncology Center, Johns Hopkins Univ. Sch. of Medicine, 600 North Wolfe Street, Baltimore, MD 21287 United States

Proceedings of the National Academy of Sciences of the United States of America (PROC. NATL. ACAD. SCI. U. S. A.) (United States) 1994, 91/2 (459-463)

CODEN: PNASA ISSN: 0027-8424

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

3/3/19 (Item 1 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

(c) 2003 American Chemical Society. All rts. reserv.

134085068 CA: 134(7)85068m JOURNAL

Murine stromal cell line HESS-5 maintains reconstituting ability of ex vivo-generated hematopoietic stem cells from human bone marrow and cytokine-mobilized peripheral blood

AUTHOR(S): Shimakura, Yasuhito; Kawada, Hiroshi; Ando, Kiyoshi; Sato, Tadayuki; Nakamura, Yoshihiko; Tsuji, Takashi; Kato, Shunichi; Hotta, Tomomitsu

LOCATION: Department of Internal Medicine, Tokai University School of Medicine, Kanagawa, Japan, 259-1193

JOURNAL: Stem Cells (Miamisburg, Ohio) DATE: 2000 VOLUME: 18 NUMBER: 3

PAGES: 183-189 CODEN: STCEJ ISSN: 1066-5099 LANGUAGE: English

PUBLISHER: AlphaMed Press

3/3/20 (Item 2 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

(c) 2003 American Chemical Society. All rts. reserv.

131196610 CA: 131(15)196610q JOURNAL

Rapid ex vivo expansion of human umbilical cord hematopoietic progenitors using a novel culture system

AUTHOR(S): Kawada, Hiroshi; Ando, Kiyoshi; Tsuji, Takashi; Shimakura, Yasuhito; Nakamura, Yoshihiko; Chargui, Jamel; Hagihara, Masao; Itagaki, Hiroyuki; Shimizu, Takashi; Inokuchi, Sadaki; Kato, Shunichi; Hotta, Tomomitsu

LOCATION: Research Center for Genetic Engineering and Cell Transplantation, JT Inc., Kanagawa, Japan, 259-1193

JOURNAL: Exp. Hematol. (N. Y.) DATE: 1999 VOLUME: 27 NUMBER: 5

PAGES: 904-915 CODEN: EXHMA6 ISSN: 0301-472X

PUBLISHER ITEM IDENTIFIER: 0301-472X(99)00012-0 LANGUAGE: English

PUBLISHER: Elsevier Science Inc.

3/3/21 (Item 3 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

(c) 2003 American Chemical Society. All rts. reserv.

131196608 CA: 131(15)196608v JOURNAL

Ex vivo expansion of human cord blood stem cells and its application to gene therapy

AUTHOR(S): Ando, Kiyoshi; Kawada, Hiroshi; Shimizu, Takashi; Tsuji, Takashi; Nakamura, Yoshihiko; Kimura, Minoru; Miyatake, Hiroko; Shimakura, Yasuhito; Inokuchi, Sadaki; Kato, Shunichi; Hotta, Tomomitsu

LOCATION: Research Center for Genetic Engineering and Cell Transplantation, Department of Internal Medicine, Tokai University School of Medicine, Kanagawa, Japan, 259-1193

JOURNAL: Int. Congr. Ser. DATE: 1999 VOLUME: 1175 NUMBER: Tissue Engineering for Therapeutic Use 3 PAGES: 1-14 CODEN: EXMDA4 ISSN:

0531-5131 LANGUAGE: English PUBLISHER: Elsevier Science B.V.

3/3/22 (Item 4 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

(c) 2003 American Chemical Society. All rts. reserv.

126289031 CA: 126(22)289031p PATENT

Recombinant production of human gene flk-2 protein kinase extracellular domain and use for identifying ligands which stimulate stem cell hematopoiesis

INVENTOR(AUTHOR): Lemischka, Ihor R.

LOCATION: USA

ASSIGNEE: Princeton University

PATENT: United States ; US 5621090 A DATE: 19970415

APPLICATION: US 906397 (19920626) *US 679666 (19910402) *US 728913

(19910628) *US 793065 (19911115) *US 813593 (19911224)
PAGES: 55 pp. Cont.-in-part of U.S. 5,185,438. CODEN: USXXAM LANGUAGE:
English CLASS: 536023500; C07H-021/00A

3/3/23 (Item 5 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2003 American Chemical Society. All rts. reserv.

120290838 CA: 120(23)290838q PATENT
Soluble analogs of the mouse fetal liver kinase FLK-2 hemopoietic factor
INVENTOR(AUTHOR): Yang, Zhi
LOCATION: USA
ASSIGNEE: Systemix, Inc.
PATENT: PCT International ; WO 9401576 A1 DATE: 940120
APPLICATION: WO 93US6404 (930707) *US 912122 (920709)
PAGES: 21 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12P-021/06A;
C12N-015/00B; A61K-037/00B; C07K-013/00B DESIGNATED COUNTRIES: AU; CA; JP;
KR; NO; PL; RU; UA DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FR; GB; GR
; IE; IT; LU; MC; NL; PT; SE

3/3/24 (Item 6 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2003 American Chemical Society. All rts. reserv.

120154711 CA: 120(13)154711r JOURNAL
Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
receptor: a proliferative factor for primitive hematopoietic cells
AUTHOR(S): Lyman, Stewart D.; James, Laura; Vanden Bos, Tim; de Vries,
Peter; Brasel, Ken; Gliniak, Brian; Hollingsworth, L. T.; Picha, Kathleen
S.; McKenna, Hilary J.; et al.
LOCATION: Immunex Res. and Dev. Corp., Seattle, WA, 98101, USA
JOURNAL: Cell (Cambridge, Mass.) DATE: 1993 VOLUME: 75 NUMBER: 6
PAGES: 1157-67 CODEN: CELLB5 ISSN: 0092-8674 LANGUAGE: English
? s flt3
S4 3794 FLT3
? s s4 and py<1993
Processing
Processing
3794 S4
32335638 PY<1993
S5 20 S4 AND PY<1993
? rd s5
...completed examining records
S6 7 RD S5 (unique items)
? t s6/7/all

6/7/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

08751260 BIOSIS NO.: 199395040611
Expression of the FMS/KIT-like gene **FLT3** in human acute leukemias of
the myeloid and lymphoid lineages.
AUTHOR: Birg Françoise(a); Courcoul Marianne; Rosnet Olivier; Bardin
Florence; Pebusque Marie-Joséphé; Marchetto Sylvie; Tabilio Antonio;
Mannoni Patrice; Birnbaum Daniel
AUTHOR ADDRESS: (a)Unite 119 de l'INSERM, 27, Boulevard Lei Roure, 13009
Marseille**France
JOURNAL: Blood 80 (10):p2584-2593 1992
ISSN: 0006-4971
DOCUMENT TYPE: Article
RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: **FLT3**, a receptor belonging to the FMS/KIT family and localized to 13q12, could play a role in the biology of early hematopoietic progenitor cells. Because FMS and KIT are expressed in both normal progenitors and myeloid leukemias, we looked for **FLT3** expression in fresh human leukemic cells using Northern blot analysis. High levels of **FLT3** expression were detected in 92% of the cases of acute myeloid leukemia (AML) tested, ranging from the M1 to the M5 stages of differentiation assessed in the French-American-British classification. Immature (M0) AML cells, biphenotypic leukemias, and AML with megakaryocytic differentiation (M7 subtype) also expressed the **FLT3** transcript. **FLT3** was also expressed at high levels in acute lymphoid leukemias of T and B origins. Finally, it was not expressed in chronic myeloid leukemias in chronic phase, whereas it was expressed in most blast crisis samples. This pattern of expression of **FLT3** contrasts with the expression of FMS and KIT restricted to myeloid leukemias, and suggests that the **FLT3** product could play a role in the expansion of the leukemic blasts of both the myeloid and lymphoid lineages.

6/7/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08227172 BIOSIS NO.: 000094028136
CHROMOSOMAL LOCALIZATION OF FLT4 A NOVEL RECEPTOR-TYPE TYROSINE KINASE GENE
AUTHOR: GALLAND F; KARAMYSHEVA A; MATTEI M-G; ROSNET O; MARCHETTO S;
BIRNBAUM D
AUTHOR ADDRESS: LAB. MOLECULAR ONCOLOGY, U.119 INSERM, 27 BLVD., LEI ROURE,
13009 MARSEILLE, FR.
JOURNAL: GENOMICS 13 (2). 1992. 475-478. 1992
FULL JOURNAL NAME: Genomics
CODEN: GNMCE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A new human gene encoding a putative receptor-type tyrosine kinase (RTK) was isolated by screening a placenta cDNA library with a mouse **Flt3** probe. The deduced amino acid sequence of the intracellular region of the molecule showed that it was strongly related to the FLT1 and KDR/FLK1 gene products and to a lesser degree to members of the class III RTKs: FMS/CSF1R, PDGFRA/B, KIT, and **FLT3**. The gene was named FLT4. Cosmid clones of the mouse **Flt4** gene were isolated. The human gene was localized to bands q34-q35 of chromosome 5, i.e., slightly telomeric to the CSF1R/PDGFRB tandem of genes, and the mouse homolog to chromosome 11, region A5-B1.

6/7/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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08181055 BIOSIS NO.: 000094004828
GENOMIC ORGANIZATION OF THE HUMAN C-KIT GENE EVOLUTION OF THE RECEPTOR
TYROSINE KINASE SUBCLASS III
AUTHOR: ANDRE C; MARTIN E; CORNU F; HU W-X; WANG X-P; GALIBERT F
AUTHOR ADDRESS: LAB. HEMATOLOGIE EXPERIMENTALE, CENTRE HAYEM, HOPITAL
SAINT-LOUIS, 75475 PARIS CEDEX 10, FR.
JOURNAL: ONCOGENE 7 (4). 1992. 685-691. 1992
FULL JOURNAL NAME: Oncogene
CODEN: ONCNE
RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: The c-kit proto-oncogene encodes a transmembrane tyrosine kinase receptor. It belongs to receptor tyrosine kinase subclass III, which also includes the colony-stimulating factor I receptor (c-fms), platelet-derived growth factor receptors A and B (PDGFRA and PDGFRB), as well as FLT1 and FLT3/FLK2. cis-kit and PDGFRA, c-fms and PDGFRB, FLT1 and FLT3/FLK2 are grouped by pair in three clusters in man on chromosome 4 band q11-q13, chromosome 5 band q31-q33 and chromosome 13 band q12 respectively. Here, we report the genomic organization of the human c-kit gene, which is composed of 21 small coding exons, distributed over 80 kb. Comparison of the c-kit and c-fms oncogenes shows that they share identical exon/intron boundaries in their two kinetic domains, as well as a similar exon/intron organization in the extracytoplasmic domain. Comparison with the kinase domains of tyrosine kinase genes not belonging to subclass III suggests that the exon/intron organization of c-kit and c-fms is a characteristic feature of subclass III. The genomic similarities between c-kit and c-fms, in conjunction with the location in pairs on different chromosomes of the subclass III genes, has led us to hypothesize that cis and trans duplications gave rise to this group of genes.

6/7/4 (Item 4 from file: 5)
DIALOG(R) File 5: Biosis Previews(R)
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07886735 BIOSIS NO.: 000092135727
MURINE **FLT3** A GENE ENCODING A NOVEL TYROSINE KINASE RECEPTOR OF THE PDGFR-CSF1R FAMILY
AUTHOR: ROSNET O; MARCHETTO S; DELAPEYRIERE O; BIRNBAUM D
AUTHOR ADDRESS: U.119 INSERM, 27 BLD LEI ROURE, 13009 MARSEILLE, FR.
JOURNAL: ONCOGENE 6 (9). 1991. 1641-1650. 1991
FULL JOURNAL NAME: Oncogene
CODEN: ONCNE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Receptor-type tyrosine kinases presenting an extracellular region with five immunoglobulin-like domains, and strongly related by sequence similarities in the intracellular region, constitute a family of receptors involved in development and function of various cell lineages. We have isolated and characterized the mouse **Flt3** gene, encoding the sixth member of this family. The **Flt3** gene possesses an open reading frame of 3000 nucleotides, and therefore appears to code for a protein of 1000 amino acids. The deduced structure of the **FLT3** protein presents all the characteristics of a receptor-type kinase of this family. The gene is expressed in placenta, in various adult tissues including gonads and brain, and in hematopoietic cells. The **Flt3** transcript is 3.7 kb long, except in the testis, where two shorter post-meiotic transcripts are detected. These results suggest a role for this novel receptor and its yet unidentified ligand in placenta, gonads and hematopoietic and nervous systems.

6/7/5 (Item 5 from file: 5)
DIALOG(R) File 5: Biosis Previews(R)
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04802506 BIOSIS NO.: 000080105634
IDENTIFICATION OF MULTIPLE VARIANTS OF FAST MUSCLE TROPONIN T IN THE CHICKEN USING MONOCLONAL ANTIBODIES
AUTHOR: BIRD I M; DHOOT G K; WILKINSON J M
AUTHOR ADDRESS: DEP. BIOCHEMISTRY, ROAYL COLLEGE SURGEONS OF ENGLAND,

LINCOLN'S INN FIELDS, LONDON, ENGLAND WC2A 3PN.
JOURNAL: EUR J BIOCHEM 150 (3). 1985. 517-526. 1985
FULL JOURNAL NAME: European Journal of Biochemistry
CODEN: EJBCA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Two monoclonal antibodies, T1/7 and T1/61, were prepared which are specific for chicken fast muscle troponin T. Both are of the IgG.gamma.1 subclass. Both antibodies cross-react strongly with human fast and chicken cardiac troponin T, but while T1/7 reacts weakly with rabbit fast troponin T, T1/61 does not. The antibodies can be used for fiber typing of both chicken and human muscle. The antibodies were used to identify fast troponin T on 2-dimensional maps of proteins from a variety of chicken muscles by electrophoretic transfer to nitrocellulose followed by immunoperoxidase staining. Using this technique 5 variant forms of fast troponin T were identified. Two variants, fBT1 and fBT2, are expressed in breast muscle, while the other 3 fLT1, fLT2 and **fLT3** are expressed in leg muscle. Of the leg muscle variants, fLT1 and fLT2 correspond to the 2 forms described previously. The 3rd variant, **fLT3**, has not been described before and is expressed in muscles which have a high content of slow fibers. In addition to these clearly defined variant forms immunostaining reveals multiple minor variants of troponin T present in leg muscle which may reflect complex RNA processing of the troponin T gene transcript.

6/7/6 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE
(c) 2003 Elsevier Science B.V. All rts. reserv.

04577528 EMBASE No: 1991071571
Isolation and chromosomal localization of a novel FMS-like tyrosine kinase gene
Rosnet O.; Mattei M.-G.; Marchetto S.; Birnbaum D.
U.119 INSERM, 27 Bd. Lei Roure, 13009, Marseille France
Genomics (GENOMICS) (United States) 1991, 9/2 (380-385)
CODEN: GNMCE ISSN: 0888-7543
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

We have isolated and sequenced part of a new gene of the tyrosine kinase family. This gene, called **FLT3**, has strong sequence similarities with members of a group of genes encoding growth factor receptors: FMS, KIT, and PDGFR. We have localized the human **FLT3** gene to chromosome 13, band q12, and its mouse homolog to chromosome 5, region G.

6/7/7 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.

07256996 92119639 PMID: 1310071
FLT4, a novel class III receptor tyrosine kinase in chromosome 5q33-qter.
Aprelikova O; Pajusola K; Partanen J; Armstrong E; Alitalo R; Bailey S K; McMahon J; Wasmuth J; Huebner K; Alitalo K
Department of Virology, University of Helsinki, Finland.
Cancer research (UNITED STATES) Feb 1 1992, 52 (3) p746-8,
ISSN 0008-5472 Journal Code: 2984705R
Contract/Grant No.: CA 21124; CA; NCI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The receptors for at least two hematopoietic growth factors, namely the stem cell factor and colony-stimulating factor 1, belong to class III receptor tyrosine kinases. Here we describe cloning of a partial complementary DNA for FLT4, an additional member of this gene family from human leukemia cells. The FLT4 tyrosine kinase domain is 79% homologous with the previously cloned FLT1 (M. Shibuya et al., Oncogene, 5: 519-524, 1990) tyrosine kinase and maps to the chromosomal region 5q33-qter. We have found FLT4 expression in human placenta, lung, heart, and kidney, whereas the pancreas and brain appeared to contain very little if any FLT4 RNA. The results suggest that FLT4 functions in multiple adult tissues.

Record Date Created: 19920225

Record Date Completed: 19920225

? s flk(W)2

2948 FLK

8736730 2

S7 279 FLK(W)2

? s s7 and py<1993

Processing

Processing

279 S7

32335638 PY<1993

S8 4 S7 AND PY<1993

? rd s8

...completed examining records

S9 1 RD S8 (unique items)

? t s9/7/all

9/7/1 (Item 1 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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07768231 BIOSIS NO.: 000092071602

A RECEPTOR TYROSINE KINASE SPECIFIC TO HEMATOPOIETIC STEM AND PROGENITOR CELL-ENRICHED POPULATIONS

AUTHOR: MATTHEWS W; JORDAN C T; WIEGAND G W; PARDOLL D; LEMISCHKA I R

AUTHOR ADDRESS: DEP. MOLECULAR BIOL., PRINCETON UNIV., PRINCETON, N.J.

08540.

JOURNAL: CELL 65 (7). 1991. 1143-1152. 1991

FULL JOURNAL NAME: Cell

CODEN: CELLB

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: To elucidate the molecular biology of the hematopoietic stem cell, we have begun to isolate genes from murine cell populations enriched in stem cell activity. One such cDNA encodes a novel receptor tryosine kinase, designated fetal liver kinase-2 or **flk-2**, which is related to the W locus gene product c-kit. Expression analyses suggest an extremely restricted distribution of **flk-2**. It is expressed in populations enriched for stem cells and primitive uncommitted progenitors, and is absent in populations containing more mature cells. Therefore, this receptor may be a key signal transduction component in the totipotent hematopoietic stem cell and its immediate self-renewing progeny.

? s s7 and review?

279 S7

3363995 REVIEW?

S10 9 S7 AND REVIEW?

? rd s10

...completed examining records

S11 9 RD S10 (unique items)

? t s11/7/all

11/7/1 (Item 1 from file: 5)

DIALOG(R) File 5: Biosis Previews(R)
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10420380 BIOSIS NO.: 199699041525

Expression of FLT3 receptor and response to FLT3 ligand by leukemia cells.

AUTHOR: Drexler H D

AUTHOR ADDRESS: DSMZ-German Collection Microorganisms Cell Cultures, Dep.

Human Animal Cell Cultures, Mascheroder Weg**Germany

JOURNAL: Leukemia (Basingstoke) 10 (4):p588-599 1996

ISSN: 0887-6924

DOCUMENT TYPE: Literature Review

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: The novel hematopoietic growth factor FLT3 ligand (FL) is the cognate ligand for the FLT3 tyrosine kinase receptor (R), also referred to as **FLK-2** and **STK-1**. The FLT3R belongs to a family of receptor tyrosine kinases involved in hematopoiesis that also includes **KIT**, the receptor for **SCF** (stem cell factor), and **FMS**, the receptor for **M-CSF** (macrophage colony-stimulating factor). Restricted FLT3R expression was seen on human and murine hematopoietic progenitor cells. In functional assays recombinant FL stimulated the proliferation and colony formation of human hematopoietic progenitor cells, i.e. CD34+ cord and peripheral blood, bone marrow and fetal liver cells. Synergy was reported for co-stimulation with G-CSF (granulocyte-CSF), GM-CSF (granulocyte-macrophage CSF), M-CSF, interleukin-3 (IL-3), PIXY-321 (an IL-3/GM-CSF fusion protein) and SCF. In the mouse, FL potentially enhanced growth of various types of progenitor/precursor cells in synergy with G-CSF, GM-CSF, M-CSF, IL-3, IL-6, IL-7, IL-11, IL-12 and SCF. The well-documented involvement of this ligand-receptor pair in physiological hematopoiesis brought forth the question whether FLT3R and FL might also have a role in the pathobiology of leukemia. At the mRNA level FLT3R was expressed by most (80-100%) cases of AML (acute myeloid leukemia) throughout the different morphological subtypes (M0-M7), of ALL (acute lymphoblastic leukemia) of the immunological subtypes T-ALL and BCP-ALL (B cell precursor ALL including pre-pre B-ALL, cALL and pre B-ALL), of AMLL (acute mixed-lineage leukemia), and of CML (chronic myeloid leukemia) in lymphoid or mixed blast crisis. Analysis of cell surface expression of FLT3R by flow cytometry confirmed these observations for AML (66% positivity when the data from all studies are combined), BCP-ALL (64%) and CML lymphoid blast crisis (86%), whereas less than 30% of T-ALL were FLT3R+. The myeloid, monocytic and pre B cell type categories also contained the highest proportions of FLT3R+ leukemia cell lines. In contrast to the selective expression of the receptor, FL expression was detected in 90-100% of the various cell types of leukemia cell lines from all hematopoietic cell lineages. The potential of FL to induce proliferation of leukemia cells in vitro was also examined in primary and continuously cultured leukemia cells. The data on FL-stimulated leukemia cell growth underline the extensive heterogeneity of primary AML and ALL samples in terms of cytokine-inducible DNA synthesis that has been seen with other effective cytokines. While the majority of T-ALL (0-33% of the cases responded proliferatively; mean 11%) and BCP-ALL (0-30%; mean 20%) failed to proliferate in the presence of FL despite strong expression of surface FLT3R, FL caused a proliferative response in a significantly higher percentage of AML cases (22-90%; mean 53%). In the panel of leukemia cell lines examined only myeloid and monocytic growth factor-dependent cell lines increased their proliferation upon incubation with FL, whereas all growth factor-independent cell lines were refractory to stimulation. Combinations of FL with G-CSF, GM-CSF, M-CSF, IL-3, PIXY-321 or SCF and FL with IL-3 or IL-7 had synergistic or additive mitogenic effects on primary AML and ALL cells, respectively. The potent stimulation of the myelomonocytic cell lines was further augmented by addition of bFGF (basic fibroblast growth factor), GM-CSF, IL-3 or SCF. The inhibitory effects of TGF-beta-1 (transforming growth factor-beta-1)

on FL-supported proliferation were abrogated by bFGF. Taken together, these results demonstrate the expression of functional FLT3R capable of mediating FL-dependent mitogenic signaling in a subset of AML and ALL cases and further underline the heterogeneity of AML and ALL samples in their proliferative response to cytokines. The data reviewed here provided clear experimental evidence for the involvement of the FL-FLT3R ligand-receptor interaction in normal and possibly also in leukemic hematopoiesis.

11/7/2 (Item 2 from file: 5)
DIALOG(R) File 5: Biosis Previews(R)
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10243948 BIOSIS NO.: 199698698866
Role of protein tyrosine kinase receptors in cancer: Possibilities for therapeutic intervention.
AUTHOR: Rockwell Patricia(a); Goldstein Neil I
AUTHOR ADDRESS: (a) Immunol./Monoclonal Antibodies Dep., Imclone Systems Inc., 180 Varick St., New York, NY 10014**USA
JOURNAL: Molecular and Cellular Differentiation 3 (4):p315-335 1995
ISSN: 1065-3074
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: For many cancers, oncogenic activation by genetic alterations triggers a dysfunctional cell proliferation that may manifest itself as overexpression of growth factors and their cognate receptors on tumor cells. Secreted growth factors that promote cell proliferation are provided either by surrounding tumor-associated stroma (paracrine) or by the tumor cell itself (autocrine). In addition, receptors on quiescent endothelial cells are activated to stimulate new blood vessel formation (tumor angiogenesis). Therapeutic strategies for suppressing cancer growth and metastasis have focused on targeting the critical proteins that contribute to cancer progression. One approach is blocking the activation of receptors overexpressed in growth factor-dependent tumor cells. This review discusses the use of neutralizing monoclonal antibodies (Mab) to target three important protein tyrosine kinase receptors (PTK) that play a role in malignant transformation: the epidermal growth factor receptor (EGFR), fetal liver kinase-1 (flk-1), and fetal liver kinase-2 (flk-2). Experimental evidence is presented showing the use of neutralizing Mabs as efficacious immunotherapeutics in the treatment of solid tumors (EGFR), acute leukemias (flk-2), and in blocking tumor angiogenesis (flk-1). In addition, preclinical results from studies utilizing human carcinoma xenograft models have shown that a therapeutic approach of antireceptor monoclonal antibodies in combination with chemotherapy is synergistic. These data emphasize (1) the importance of targeting receptors that play a crucial role in tumor growth and progression, (2) the tumor vasculature as a major target for inhibiting tumor growth, and (3) the clinical relevance of these receptors for therapeutic intervention.

11/7/3 (Item 1 from file: 73)
DIALOG(R) File 73: EMBASE
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10675228 EMBASE No: 2000159682
Ex vivo expansion of hematopoietic stem cells and their clinical application
Nakahata T.
Dr. T. Nakahata, Department of Pediatrics, Graduate School of Medicine,

Kyoto University, 54 Kawahara-cho, Shogoin, Sakyo-ku, Kyoto 606-8507
Japan
Biotherapy (BIOTHERAPY (JAPAN)) (Japan) 2000, 14/3 (270-275)
CODEN: BITPE ISSN: 0914-2223
DOCUMENT TYPE: Journal; Review
LANGUAGE: JAPANESE SUMMARY LANGUAGE: ENGLISH; JAPANESE
NUMBER OF REFERENCES: 16

We previously reported that most of immature progenitor cells such as CFU-Blast and LTCIC were included in CD34sup + gp130sup + IL-6Rsup - population, suggesting that sIL-6R/IL-6 but not IL-6 may be potent for the ex vivo expansion of immature progenitor cells. We also demonstrated that most immature progenitors in cord blood expressed c-Kit, Flk 2 /Flt 3 and mpl receptors. A significant ex vivo expansion of human hematopoietic stem cells capable of repopulating in NOD/SCID mice using a combination of stem cell factor (SCF), Flk 2/Flt 3 ligand (FL), thrombopoietin (TPO) and a complex of interleukin (IL)-6 and soluble IL-6 receptor (IL-6/sIL-6R). When fresh cord blood CD34sup + cells and their progenies cultured with SCF+FL+TPO+IL-6/sIL-6R for 7 days were transplanted into NOD/SCID mice, successful engraftment were highly observed in the mice who were transplanted with cultured cells, 10 to 12 weeks after the transplantation. The CD45sup + cells in the recipients engrafted with cultured cells consisted of various lineages and a large number of CD34sup + cells, which formed human hematopoietic colonies in in vitro clonal culture. The fold increase in the long-term repopulating hematopoietic stem cells was estimated at 4.0 by a limiting dilution method. The present study may provide a novel culture method for the expansion of human transplantable hematopoietic stem cells aimed for clinical application.

11/7/4 (Item 2 from file: 73)
DIALOG(R)File 73:EMBASE
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07513354 EMBASE No: 1998418902
Recent progress in identifying genes regulating hematopoietic stem cell function and fate
Jordan C.T.; Van Zant G.
C.T. Jordan, Blood Marrow Transplantation Program, Markey Cancer Center, University Kentucky Medical Center, 800 Rose Street, Lexington, KY 40536 United States
AUTHOR EMAIL: cjordan@pop.uky.edu
Current Opinion in Cell Biology (CURR. OPIN. CELL BIOL.) (United Kingdom) 1998, 10/6 (716-720)
CODEN: COCBE ISSN: 0955-0674
DOCUMENT TYPE: Journal; Review
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 46

Significant advances in the use of genetic and molecular biology strategies have recently begun to identify genes that have a major impact on the determination, commitment and developmental potential of hematopoietic stem cells. Using a variety of experimental strategies, genes such as SCL, GATA-2, HoxB4, Flk-2, c-mpl, dlk, and others have been implicated as important regulators of stem cell growth. In addition, genetic mapping has identified several loci that correlate strongly with stem cell numbers and proliferation.

11/7/5 (Item 3 from file: 73)
DIALOG(R)File 73:EMBASE
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07131889 EMBASE No: 1998019867

Regulation of hematopoiesis by microvascular endothelium

Rafii S.; Mohle R.; Shapiro F.; Frey B.M.; Moore M.A.S.

S. Rafii, Division of Hematology-Oncology, Cornell University Medical College, 1300 York Avenue, New York, NY 10021 United States

Leukemia and Lymphoma (LEUK. LYMPHOMA) (United Kingdom) 1997, 27/5-6 (375-386)

CODEN: LELYE ISSN: 1042-8194

DOCUMENT TYPE: Journal; Review

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 86

The bone marrow microenvironment is a complex three dimensional structure where hematopoietic stem cells proliferate, mature, migrate into the sinusoidal space, and enter the circulation in an exquisitely regulated fashion. Stromal cells within the BM microenvironment provide a suitable environment for self-renewal, proliferation and differentiation of hematopoietic stem cells. Within the hematopoietic microenvironment, whether it is embryonic yolk sac, fetal liver, or adult bone marrow, microvascular endothelium not only acts as a gatekeeper controlling the trafficking and homing of hematopoietic progenitors, but also provides cellular contact and secretes cytokines that allows for the preservation of the steady state hematopoiesis. Recently, homogenous monolayers of bone marrow endothelial cells (BMEC) have been isolated and cultivated in tissue culture. Long term coculture studies have shown that BMEC monolayers are unique type of endothelium and can support long-term proliferation of hematopoietic progenitor cells particularly megakaryocytic and myeloid progenitor cells by constitutive elaboration of lineage-specific cytokines such as G-CSF, GM-CSF, M-CSF, Kit-ligand, IL6, **FLK-2** ligand, and leukemia inhibitory factor. Direct cellular contact between hematopoietic progenitor cells and BMEC monolayers through specific adhesion molecules including beta1, beta2 integrins and selectins play a critical role in trafficking and possibly proliferation of hematopoietic stem cells. Dysfunction of microvascular endothelial cells within the hematopoietic microenvironment may result in stem cell disorders and progression to aplastic anemias, and contribute to graft failure during bone marrow transplantation. Further studies on the role of microvascular endothelium in the regulation of hematopoietic stem cell homing and proliferation may enhance our understanding of the pathophysiology of stem cell and leukemic disorders.

11/7/6 (Item 4 from file: 73)

DIALOG(R) File 73:EMBASE

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06382704 EMBASE No: 1996041629

FLT3/**FLK-2** (STK-1) ligand does not stimulate human megakaryopoiesis in vitro

Ratajczak M.Z.; Ratajczak J.; Ford J.; Kregenow R.; Marlicz W.; Gewirtz A.M.

513B-Stellar Chance Laboratories, University of Pennsylvania, School of Medicine, 422 Curie Blvd., Philadelphia, PA 19104 United States

Stem Cells (STEM CELLS) (United States) 1996, 14/1 (146-150)

CODEN: STCEE ISSN: 1066-5099

DOCUMENT TYPE: Journal; Review

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

It has not yet been determined if the FLT3/**FLK-2** or STK-1 Ligand (STK-1 L)FLT3/**FLK-2** or STK-1 receptor (STK-1R) axis has the ability to regulate human megakaryopoiesis in vitro. To address this question, we exposed normal human CD34sup + marrow mononuclear cells to recombinant human STK-11, alone, or in combination with other growth factors. Colony-forming unit- megakaryocytic/thrombocytes (CFU-Meg) and BEU-E-derived colonies were then enumerated, and effects on colony size and

maturation noted. As assessed by these parameters, STK-11, had no demonstrable effect on megakaryocyte colony formation. Similarly, suppressing STK-1R expression with oligodeoxynucleotides also had no influence on CFU-Meg-derived colony formation. To begin to derive a physiologic explanation for these findings, we examined freshly isolated normal human megakaryocytes for the presence of STK-11, and STK-1R mRNA. In contrast to a growing number of growth factors and growth factor receptors which appear to be expressed by megakaryocytes, normal mature human megakaryocytes express neither STK-1R or STK-1L mRNA. Accordingly, our results led us to hypothesize that if STK-1/STK-1L, have any effects on megakaryocyte development in vitro, they are likely subtle and of uncertain physiologic significance.

11/7/7 (Item 1 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

(c) 2003 American Chemical Society. All rts. reserv.

137061596 CA: 137(5)61596t CONFERENCE PROCEEDING
Effects of Flk-2 and Flt-3 ligands on hematopoietic stem cells
AUTHOR(S): Nakahata, Tatsuhiko
LOCATION: School of Medicine, Kyoto University, Japan,
JOURNAL: Zoketsu Saitokain (Zoketsu Saitokain) EDITOR: Motoyoshi, Kazuo
(Ed), DATE: 2001 PAGES: 198-210 CODEN: 69CBMS LANGUAGE: Japanese
PUBLISHER: Medikaru Rebyusha, Tokyo, Japan
SECTION:
CA215000 Immunochemistry
IDENTIFIERS: review Flk2 Flt3 ligand hematopoietic stem cell
DESCRIPTORS:
Hematopoiesis...
Effects of Flk-2 and Flt-3 ligands on hematopoietic stem cells
Hematopoietins...
FLT3 ligand; Effects of Flk-2 and Flt-3 ligands on hematopoietic stem cells
Hematopoietin receptors...
FLT3 receptors; Effects of Flk-2 and Flt-3 ligands on hematopoietic stem cells
Hematopoietic precursor cell...
stem; Effects of Flk-2 and Flt-3 ligands on hematopoietic stem cells

11/7/8 (Item 2 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

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131168819 CA: 131(13)168819w JOURNAL
B cell development in the mouse from early progenitors to mature B cells
AUTHOR(S): Rolink, Antonius G.; ten Boekel, Edwin; Yamagami, Tamotsu;
Ceredig, Rod; Andersson, Jan; Melchers, Fritz
LOCATION: Basel Institute for Immunology, CH-4005, Basel, Switz.
JOURNAL: Immunol. Lett. DATE: 1999 VOLUME: 68 NUMBER: 1 PAGES: 89-93
CODEN: IMLED6 ISSN: 0165-2478 PUBLISHER ITEM IDENTIFIER:
0165-2478(99)00035-8 LANGUAGE: English PUBLISHER: Elsevier Science
Ireland Ltd.
SECTION:
CA215000 Immunochemistry
IDENTIFIERS: review B cell development progenitor gene tyrosine kinase
DESCRIPTORS:
B cell(lymphocyte)... Cell differentiation...
B cell development in the mouse from early progenitors to mature B cells
Hematopoiesis...
B-cell lymphopoiesis; in B cell development in the mouse from early progenitors to mature B cells

Hematopoietic precursor cell...
 B-cell; B cell development in the mouse from early progenitors to
 mature B cells
 Hemopoietins...
 flk-2 ligand; in B cell development in the mouse from early progenitors
 to mature B cells
 Biomarkers(biological responses)... c-Kit(protein)... Gene,animal...
 Immunoglobulins...
 in B cell development in the mouse from early progenitors to mature B
 cells
 Recombination,genetic...
 rearrangement, Ig genes; in B cell development in the mouse from early
 progenitors to mature B cells
 CAS REGISTRY NUMBERS:
 138359-29-2 in B cell development in the mouse from early progenitors to
 mature B cells

11/7/9 (Item 3 from file: 399)
 DIALOG(R)File 399:CA SEARCH(R)
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123252066 CA: 123(19)252066r JOURNAL
 Flt 3/Flk 2 and its ligand
 AUTHOR(S): Komatsu, Norio
 LOCATION: Jichi Med. Coll., Tochigi, Japan, 329-04
 JOURNAL: Igaku no Ayumi DATE: 1995 VOLUME: 174 NUMBER: 2 PAGES: 131-4
 CODEN: IGAYAY ISSN: 0039-2359 LANGUAGE: Japanese
 SECTION:
 CA213000 Mammalian Biochemistry
 CA203XXX Biochemical Genetics
 IDENTIFIERS: review gene FLT3 receptor ligand hematopoiesis
 DESCRIPTORS:
 Hematopoiesis... Molecular cloning... Receptors, gene FLT3...
 FLT3/FLK2 receptor tyrosine kinase and its ligand in hematopoiesis
 ? ds

Set	Items	Description
S1	279	FLK(W)2
S2	43	FLK(W)2(10N)(HUMAN)
S3	24	RD S2 (unique items)
S4	3794	FLT3
S5	20	S4 AND PY<1993
S6	7	RD S5 (unique items)
S7	279	FLK(W)2
S8	4	S7 AND PY<1993
S9	1	RD S8 (unique items)
S10	9	S7 AND REVIEW?
S11	9	RD S10 (unique items)
? s s7 and (human and murine)		
	279	S7
	19097961	HUMAN
	370744	MURINE
S12	37	S7 AND (HUMAN AND MURINE)
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	S13	20 RD S12 (unique items)
? t s13/3/all		

13/3/1 (Item 1 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
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13171516 BIOSIS NO.: 200100378665

Extensive and long-term ex vivo production of dendritic cells from CD34 positive umbilical cord blood or bone marrow cells by novel culture system using mouse stroma.

AUTHOR: Hagihara Masao(a); Li Changwen; Gansuud Balgansuren; Munkhbat Batmunkh; Inoue Hiroyasu; Shimakura Yasuhito; Tsuchiya Takahide; Ueda Yoko; Oki Masayuki; Ando Kiyoshi; Kato Shunichi; Hotta Tomomitsu

AUTHOR ADDRESS: (a)Department of Hematology and Rheumatology, Tokai University School of Medicine, Bohseidai, Isehara, Kanagawa, 259-1193: masaoaha@is.icc.u-tokai.ac.jp**Japan

JOURNAL: Journal of Immunological Methods 253 (1-2):p45-55 1 July, 2001

MEDIUM: print

ISSN: 0022-1759

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

13/3/2 (Item 2 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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13110077 BIOSIS NO.: 200100317226

Storage of factor VIII (FVIII) in the alpha-granules of human platelets following retroviral transduction and transplantation of human CD34+ cells into NOD-SCID mice.

AUTHOR: Wilcox David A(a); Rosenberg Jonathan B; Johnson Bryon D(a); Montgomery Robert R(a)

AUTHOR ADDRESS: (a)Department of Pediatrics, Medical College of Wisconsin, Milwaukee, WI**USA

JOURNAL: Blood 96 (11 Part 1):p803a November 16, 2000

MEDIUM: print

CONFERENCE/MEETING: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000

SPONSOR: American Society of Hematology

ISSN: 0006-4971

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

13/3/3 (Item 3 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All rts. reserv.

12301577 BIOSIS NO.: 200000059444

Ex vivo generation of CD34+ cells from CD34- hematopoietic cells.

AUTHOR: Nakamura Yoshihiko; Ando Kiyoshi(a); Chargui Jamel; Kawada Hiroshi; Sato Tadayuki; Tsuji Takashi; Hotta Tomomitsu; Kato Shunichi

AUTHOR ADDRESS: (a)Department of Hematology, Tokai University School of Medicine, Bohseidai, Isehara, Kanagawa**Japan

JOURNAL: Blood 94 (12):p4053-4059 Dec. 15, 1999

ISSN: 0006-4971

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

13/3/4 (Item 4 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All rts. reserv.

12278689 BIOSIS NO.: 200000032191

Rapid ex vivo expansion of **human** umbilical cord hematopoietic progenitors using a novel culture system.

AUTHOR: Kawada Hiroshi; Ando Kiyoshi; Tsuji Takashi; Shimakura Yasuhito; Nakamura Yoshihiko; Chargui Jamel; Hagihara Masao; Itagaki Hiroyuki; Shimizu Takashi; Inokuchi Sadaki; Kato Shunichi; Hotta Tomomitsu(a)

AUTHOR ADDRESS: (a)Division of Hematology, Department of Internal Medicine, Tokai University School of Medicine, Bohseidai, Isehara, Kanagawa, 259-1193**Japan

JOURNAL: Experimental Hematology (Charlottesville) 27 (5):p904-915 May, 1999

ISSN: 0301-472X

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

13/3/5 (Item 5 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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12161736 BIOSIS NO.: 199900456585

Modulation of haematopoietic progenitor development by FLT-3 ligand.

AUTHOR: Banu Naheed; Deng Bijia; Lyman Stewart D; Avraham Hava(a)

AUTHOR ADDRESS: (a)Division of Experimental Medicine, Beth Israel Deaconess Medical Center, Harvard Institutes of Medicine, 4 Blackfan Circle, 3rd Floor, Boston, MA, 02115**USA

JOURNAL: Cytokine 11 (9):p679-688 Sept., 1999

ISSN: 1043-4666

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

13/3/6 (Item 6 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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11661939 BIOSIS NO.: 199800443670

Leukemic predisposition of mice transplanted with gene-modified hematopoietic precursors expressing flt3 ligand.

AUTHOR: Hawley Teresa S; Fong Andrew Z C; Griesser Henrik; Lyman Stewart D; Hawley Robert G(a)

AUTHOR ADDRESS: (a)Toronto Hospital, CRCS-424, 67 College St., Toronto, Ontario M5G 2M1**Canada

JOURNAL: Blood 92 (6):p2003-2011 Sept. 15, 1998

ISSN: 0006-4971

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

13/3/7 (Item 7 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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11622695 BIOSIS NO.: 199800404830

Isolation and characterization of a cDNA for **human**, mouse, and rat full-length stem cell growth factor, a new member of C-type lectin superfamily.

AUTHOR: Mio Hiroyuki(a); Kagami Naofumi; Yokokawa Sachiko; Kawai Hironori;

Nakagawa Satoshi; Takeuchi Kyoko; Sekine Susumu; Hiraoka Atsunobu
AUTHOR ADDRESS: (a) Pharm. Res. Inst., Kyowa Hakko Kogyo Co. Ltd., 1188
Shimotogari, Nagaizumi-cho, Sunto-gun, Shizu**Japan
JOURNAL: Biochemical and Biophysical Research Communications 249 (1):p
124-130 Aug. 10, 1998
ISSN: 0006-291X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

13/3/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

10420380 BIOSIS NO.: 199699041525
Expression of FLT3 receptor and response to FLT3 ligand by leukemia cells.
AUTHOR: Drexler H D
AUTHOR ADDRESS: DSMZ-German Collection Microorganisms Cell Cultures, Dep.
Human Animal Cell Cultures, Mascheroder Weg**Germany
JOURNAL: Leukemia (Basingstoke) 10 (4):p588-599 1996
ISSN: 0887-6924
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

13/3/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

10110680 BIOSIS NO.: 199698565598
Isolation and characterization of a monoclonal antibody binding to the
extracellular domain of the flk-2 tyrosine kinase receptor.
AUTHOR: Rose Caroline; Rockwell Patricia; Yang Jian-Quing; Pytowski
Bronislaw; Goldstein Neil I(a)
AUTHOR ADDRESS: (a) Immunol./Monoclonal Antibodies Dep., ImClone Systems
Inc., 180 Varick St., New York, NY 10014**USA
JOURNAL: Hybridoma 14 (5):p453-459 1995
ISSN: 0272-457X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

13/3/10 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

09983617 BIOSIS NO.: 199598438535
Rationale for cytokine combinations for ex vivo expansion of hematopoietic
stem cells.
AUTHOR: Ogawa M(a); Johnson Ralph H
AUTHOR ADDRESS: (a) Dep. Veterans Affairs Med. Center, Charleston, SC**USA
JOURNAL: Experimental Hematology (Charlottesville) 23 (8):p839 1995
CONFERENCE/MEETING: 24th Annual Meeting of the International Society for
Experimental Hematology Duesseldorf, Germany August 27-31, 1995
ISSN: 0301-472X
RECORD TYPE: Citation
LANGUAGE: English

13/3/11 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All rts. reserv.

09546029 BIOSIS NO.: 199598000947

Cellular and molecular characterization of the role of the **FLK-2/FLT-3** receptor tyrosine kinase in hematopoietic stem cells.

AUTHOR: Zeigler Francis C; Bennett Brian D; Jordan Craig T; Spencer Susan D
; Baumhueter Susanne; Carroll Kathleen J; Hooley Jeffrey; Bauer Kenneth;
Matthews William(a)

AUTHOR ADDRESS: (a)Genentech, Inc., 460 Point San Bruno Blvd., South San
Francisco, CA 94080**USA

JOURNAL: Blood 84 (8):p2422-2430 1994

ISSN: 0006-4971

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

13/3/12 (Item 12 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All rts. reserv.

09154020 BIOSIS NO.: 199497162390

Molecular cloning of a ligand for the **FLT3/FLK-2** receptor: A
proliferative factor for early hematopoietic cells.

AUTHOR: Beckmann M Patricia; Vanden Bos Tim; James Laura; Brasel Ken; De
Vries Peter; Picha Kathleen S; Farrah Terry; Hollingsworth L T; Gliniak
Brian; et al

AUTHOR ADDRESS: Immunex Res. and Development Corp., Seattle, WA 98101**USA

JOURNAL: Journal of Cellular Biochemistry Supplement 0 (18B):p175 1994

CONFERENCE/MEETING: Keystone Symposium on Stem Cells Taos, New Mexico, USA
January 31-February 7, 1994

ISSN: 0733-1959

RECORD TYPE: Citation

LANGUAGE: English

13/3/13 (Item 13 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All rts. reserv.

09126484 BIOSIS NO.: 199497134854

STK-1, the **human** homology of **Flk-2/Flt-3**, is selectively
expressed in CD34+ **human** bone marrow cells and is involved in the
proliferation of early progenitor/stem cells.

AUTHOR: Small Donald(a); Levenstein Mark; Kim Eunhyung; Carow Cathy; Amin
Shahina; Rockwell Patricia; Witte Larry; Burrow Christopher; Ratajczak
Mariusz Z; et al

AUTHOR ADDRESS: (a)Oncol. Cent., Dep. Pediatr., Johns Hopkins Univ. Sch.
Med., 600 North Wolfe Street, Baltimore, M**USA

JOURNAL: Proceedings of the National Academy of Sciences of the United
States of America 91 (2):p459-463 1994

ISSN: 0027-8424

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

13/3/14 (Item 14 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2003 BIOSIS. All rts. reserv.

09098771 BIOSIS NO.: 199497107141

STK-1, a **human** homolog of **FLK-2/FLT3**, is aberrantly
expressed in **human** leukemias and may be involved in the growth

and/or differentiation of hematopoietic stem/progenitor cells.
AUTHOR: Small D(a); Levenstein M; Kim E; Carow C E; Amin S; Ratajczak M;
Gewirtz A M; Civin C I
AUTHOR ADDRESS: (a)Dep. Oncol., Johns Hopkins Univ. Sch. Lab. Med.,
Baltimore, MD**USA
JOURNAL: Blood 82 (10 SUPPL. 1):p325A 1993
CONFERENCE/MEETING: Thirty-fifth Annual Meeting of the American Society of
Hematology St. Louis, Missouri, USA December 3-7, 1993
ISSN: 0006-4971
RECORD TYPE: Citation
LANGUAGE: English

13/3/15 (Item 15 from file: 5)
DIALOG(R)File 5:BIOSIS Previews(R)
(c) 2003 BIOSIS. All rts. reserv.

09076690 BIOSIS NO.: 199497085060
Molecular cloning of a ligand for the flt3/flk-2 tyrosine
kinase receptor: A proliferative factor for primitive hematopoietic
cells.
AUTHOR: Lyman Stewart D; James Laura; Vanden Bos Tim; De Vries Peter;
Brasel Ken; Gliniak Brian; Hollingsworth L T; Picha Kathleen S; McKenna
Hilary J; et al
AUTHOR ADDRESS: Immunex Res. Dev. Corp., 51 University St., Seattle, WA
98101**USA
JOURNAL: Cell 75 (6):p1157-1167 1993
ISSN: 0092-8674
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

13/3/16 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE
(c) 2003 Elsevier Science B.V. All rts. reserv.

10520866 EMBASE No: 1999431983
Ex vivo generation of CD34sup + cells from CD34sup - hematopoietic cells
Nakamura Y.; Ando K.; Chargui J.; Kawada H.; Sato T.; Tsuji T.; Hotta T.;
Kato S.
Dr. K. Ando, Department of Hematology, Tokai University School of
Medicine, Isehara, Kanagawa 259-1183 Japan
Blood (BLOOD) (United States) 1999, 94/12 (4053-4059)
CODEN: BLOOA ISSN: 0006-4971
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 21

13/3/17 (Item 2 from file: 73)
DIALOG(R)File 73:EMBASE
(c) 2003 Elsevier Science B.V. All rts. reserv.

05751254 EMBASE No: 1994164622
Molecular cloning of a novel receptor tyrosine kinase gene, STK, derived
from enriched hematopoietic stem cells
Iwama A.; Okano K.; Sudo T.; Matsuda Y.; Suda T.
Department of Cell Differentiation, Molecular Embryology/Genetics Inst.,
Kumamoto Univ. School of Medicine, 2-2-1 Honjo, Kumamoto 860 Japan
Blood (BLOOD) (United States) 1994, 83/11 (3160-3169)
CODEN: BLOOA ISSN: 0006-4971
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

13/3/18 (Item 3 from file: 73)
DIALOG(R)File 73:EMBASE
(c) 2003 Elsevier Science B.V. All rts. reserv.

05636203 EMBASE No: 1994041406
STK-1, the **human** homolog of Flk-2/Flt-3, is selectively expressed in CD34sup + **human** bone marrow cells and is involved in the proliferation of early progenitor/stem cells
Small D.; Levenstein M.; Kim E.; Carow C.; Amin S.; Rockwell P.; Witte L.; Burrow C.; Ratajczak M.Z.; Gewirtz A.M.; Civin C.I.
Department of Pediatrics, Oncology Center, Johns Hopkins Univ. Sch. of Medicine, 600 North Wolfe Street, Baltimore, MD 21287 United States
Proceedings of the National Academy of Sciences of the United States of America (PROC. NATL. ACAD. SCI. U. S. A.) (United States) 1994, 91/2 (459-463)
CODEN: PNASA ISSN: 0027-8424
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

13/3/19 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2003 American Chemical Society. All rts. reserv.

134085068 CA: 134(7)85068m JOURNAL
Murine stromal cell line HESS-5 maintains reconstituting ability of ex vivo-generated hematopoietic stem cells from human bone marrow and cytokine-mobilized peripheral blood
AUTHOR(S): Shimakura, Yasuhito; Kawada, Hiroshi; Ando, Kiyoshi; Sato, Tadayuki; Nakamura, Yoshihiko; Tsuji, Takashi; Kato, Shunichi; Hotta, Tomomitsu
LOCATION: Department of Internal Medicine, Tokai University School of Medicine, Kanagawa, Japan, 259-1193
JOURNAL: Stem Cells (Miamisburg, Ohio) DATE: 2000 VOLUME: 18 NUMBER: 3
PAGES: 183-189 CODEN: STCEJ ISSN: 1066-5099 LANGUAGE: English
PUBLISHER: AlphaMed Press

13/3/20 (Item 2 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2003 American Chemical Society. All rts. reserv.

131196608 CA: 131(15)196608v JOURNAL
Ex vivo expansion of human cord blood stem cells and its application to gene therapy
AUTHOR(S): Ando, Kiyoshi; Kawada, Hiroshi; Shimizu, Takashi; Tsuji, Takashi; Nakamura, Yoshihiko; Kimura, Minoru; Miyatake, Hiroko; Shimakura, Yasuhito; Inokuchi, Sadaki; Kato, Shunichi; Hotta, Tomomitsu
LOCATION: Research Center for Genetic Engineering and Cell Transplantation, Department of Internal Medicine, Tokai University School of Medicine, Kanagawa, Japan, 259-1193
JOURNAL: Int. Congr. Ser. DATE: 1999 VOLUME: 1175 NUMBER: Tissue Engineering for Therapeutic Use 3 PAGES: 1-14 CODEN: EXMDA4 ISSN: 0531-5131 LANGUAGE: English PUBLISHER: Elsevier Science B.V.
?

Set	Items	Description
S1	279	FLK(W)2
S2	43	FLK(W)2(10N)(HUMAN)
S3	24	RD S2 (unique items)
S4	3794	FLT3
S5	20	S4 AND PY<1993
S6	7	RD S5 (unique items)
S7	279	FLK(W)2
S8	4	S7 AND PY<1993
S9	1	RD S8 (unique items)
S10	9	S7 AND REVIEW?
S11	9	RD S10 (unique items)
S12	37	S7 AND (HUMAN AND MURINE)
S13	20	RD S12 (unique items)
?		

GenCore version 5.1.4 ps.4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:53:00 ; Search time 34.4826 Seconds
(without alignments)
2765.606 Million cell updates/sec

Title: US-09-919-408-2

Perfect score: 5264

Sequence: 1 MRALAQRSDRLLLVLSV.....RGGLRAQSPQVQVKKHRRS 992

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5264	100.0	992	A39931	protein-tyrosine k
2	5102	96.9	1000	S18827	Flt3 protein - mou
3	4408.5	83.7	993	A36873	protein-tyrosine k
4	1258.5	23.9	980	TVCTMD	macrophage colony-
5	1247	23.7	941	TVMTVD	protein-tyrosine k
6	1232.5	23.4	978	A49814	protein-tyrosine k
7	1223	23.2	975	TVMSKT	protein-tyrosine k
8	1221.5	23.2	972	TVHUMD	macrophage colony-
9	1220	23.2	954	I51703	c-kit-related kina
10	1215	23.1	977	I45877	protein-tyrosine k
11	1210	23.0	978	S16385	macrophage colony-
12	1198.5	22.8	976	TVMSMD	macrophage colony-
13	1196	22.7	976	TVHUKT	protein-tyrosine k
14	1188.5	22.6	975	T30816	macrophage colony-
15	1181	22.4	960	JN0677	protein-tyrosine k
16	1157.5	22.0	1088	1PFRGA	platelet-derived g
17	1152.5	21.9	1089	1PFHUGA	platelet-derived g
18	1132	21.5	1087	I51552	platelet-derived g
19	1123.5	21.3	1089	I53727	platelet-derived g
20	1098	20.9	1098	1FMSRB	platelet-derived g
21	1078	20.5	1106	1PFHUGB	platelet-derived g
22	1060	20.1	1048	T30815	platelet-derived g
23	998.5	19.0	1338	S09982	protein-tyrosine k
24	984.5	18.7	1336	I60598	Fit-1 tyrosine kin
25	983.5	18.7	1333	I78875	receptor tyrosine
26	980	18.6	1379	2JC4954	vascular endotheli
27	970	18.4	1330	2JA9010	embryonic receptor
28	967.5	18.4	790	1FOMVH2	gag-kit polyprotei
29	965	18.3	1348	2S51656	vascular endotheli

RESULT 1

A39931

protein-tyrosine kinase (EC 2.7.1.112) flk-2, hematopoietic - mouse

C;Species: Mus musculus (house mouse)

C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 04-Feb-2000

C;Accession: A39931

R;Matthews, W.; Jordan, C.T.; Wiegand, G.W.; Pardoll, D.; Lemischka, I.R.

Cell 65, 1143-1152, 1991

A;Title: A receptor tyrosine kinase specific to hematopoietic stem and progenitor cel:

A;Reference number: A39931; MUID:91292518; PMID:1648448

A;Accession: A39931

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-992 <MAT>

A;Cross-references: GB:M64689; NID:g193327; PIDN:AAA37634.1; PID:g193328

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein

F;609-953/Domain: protein kinase homology <KIN>

F;617-625/Region: protein kinase ATP-binding motif

Query Match 100.0%; Score 5264; DB 2; Length 992;

Best Local Similarity 100.0%; Pred. No. 4.7e-262;

Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRALAQRSDRLLLVLSVMILETVTNQDLPVVKCVLISHENNGSSACKPSSYRMVRS	60
Db	1	MRALAQRSDRLLLVLSVMILETVTNQDLPVVKCVLISHENNGSSACKPSSYRMVRS	60
Qy	61	PEDLQCTPRROSEGTVEAATVEAESGSITLQVQLATPGDLSCLWVFKHSLGCQPHFD	120
Db	61	PEDLQCTPRROSEGTVEAATVEAESGSITLQVQLATPGDLSCLWVFKHSLGCQPHFD	120
Qy	121	LQNRGIVSMALINVTETQAGEYLLHIQSERANYTLFTVNRDQTLVLRPRYFRQWENQ	180
Db	121	LQNRGIVSMALINVTETQAGEYLLHIQSERANYTLFTVNRDQTLVLRPRYFRQWENQ	180
Qy	181	DALLCISGEVPEPTVEWVLCSSHRESCKEEGPAVVRKEEKLHELPGTDIRCCARNALGR	240
Db	181	DALLCISGEVPEPTVEWVLCSSHRESCKEEGPAVVRKEEKLHELPGTDIRCCARNALGR	240
Qy	241	ECKTLFTIDLNAQPOSTLPQLFKVGEPLWIRCKAIHVNHGFLTWELDKALEEGSYFE	300
Db	241	ECKTLFTIDLNAQPOSTLPQLFKVGEPLWIRCKAIHVNHGFLTWELDKALEEGSYFE	300
Qy	301	MSTYSTNRNTRMIRILLAFVSSVGRNDTGYTSCSSKHPSQSALVTILEKGFINATSSOEY	360
Db	301	MSTYSTNRNTRMIRILLAFVSSVGRNDTGYTSCSSKHPSQSALVTILEKGFINATSSOEY	360
Qy	361	EIDPYEKEFCFVSRRKAYPRIRCTWIFSQSPCEQGLEGDGYSISKFDHKNKPGYIFY	420
Db	361	EIDPYEKEFCFVSRRKAYPRIRCTWIFSQSPCEQGLEGDGYSISKFDHKNKPGYIFY	420

A,Molecule type: mRNA
A;Residues: 1-993 <SMA>
A;Cross-references: GB:U02687
A;Note: in the authors translation, an additional residue Ala is shown after 420-Ala and
C;Genetics:
A;Map position: 13q12
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP; glycoprotein; phosphotransferase; transmembrane protein; tyrosine-speci
F;608-950/Domain: protein kinase homology <KIN>
F;616-624/Region: protein kinase ATP-binding motif

Query Match 83.7%; Score 4408.5; DB 2; Length 993;
Best Local Similarity 84.0%; Pred. No. 2.8e-218;
Matches 836; Conservative 57; Mismatches 89; Indels 13; Gaps 6;

QY	1	MRALAQRSDRLLLVLSVMILETTVNQDLPVKVLI SHENNSSAGKPSRYMVRGS	60
DB	1	MPALA-RDAGTVPLLVVFSAMI FGTITNQLDPVKVLI INKNDSSVGKSSYPWVSES	59
QY	61	PEDLQTPRRQSEGTVEAATVEA VSGSITLQVLATPGDLSCLWVFKHSSLCQCPHFD	120
DB	60	PEDLGALRQSSGTVEA AAVDVASITLQVLVDAPGNISCLWVFKHSSLCQCPHFD	119
QY	121	LQNRGIVSMALLNWTQAGEYLLHQTSE RANTVLTFTVVRDTQLYVLRPPFRKMEQ	180
DB	120	LQNRGVSMVILKMTETQAGEYLLFQSEATNTYLTFTVIRNTLLYTLRPPFRKMEQ	179
QY	181	DALLCTSEGVPETVEVWLVCSSHRESCKEGPAVRKEEVLHELPGTDIRCCARNALGR	240
DB	180	DALVCISEVSEPFIVEVWLVCDSQGESCKEESPAVVKKEEVLHELPGTDIRCCARNELGR	239
QY	241	ECTKLFTIDLNAQPSTLPQLFLKVGEP LIRKAIHVNHGFGLTWELEDKALEEGSYPE	300
DB	240	ECTRLFTIDLNQTPQTTLPQLFLKVGEP LIRKAVHVNHGFGLTWELENKALEEGSYPE	299
QY	301	MSTYSTNRTMIRILLATFVSSVGRNDTGYTTCSSKHPQSALVTILEKGFINATSSOEY	360
DB	300	MSTYSTNRTMIRILFAFVSSVARNDTGYTTCSSKHPQSALVTIVEKGFINATSSSEY	359
QY	361	EIDPYEKFCSVRPKAPYRIRCTWIFSOAGFPBCEORGLDGYSISKFDHKNKPGEIFY	420
DB	360	EIDQYEEFCSVRPKAPQIRCTWTFSRKFPCEQKGLDNGYSISKFCNKHQPGEIFH	419
QY	421	-AENDDAQFTKMTFLNIRKRPQVLNANASQAQSSSDGYPLPSPMTWKKCSDKSPNCTEEI	479
DB	420	AEENDDAQFTKMTFLNIRRPQVLAEASQAQSCFSDGYPL-SWTWKKCSDKSPNCTEEI	478
QY	480	PEGVWKKANRKVPQGWSSSTLNMSSAGKGLLVKCAYNMGTSCETIFLNSPGPPFFI	539
DB	479	TEGVWNEKANRKVPQGWSSSTLNMSEAIKGLVKCAYNMGTSCETIFLNSPGPPFFI	538
QY	540	QDNISFYATTGLCPFTVLVLILCHYKKQFRYESOLOMTQVGLDNEYFYVDPRDYR	599
DB	539	QDNISFYATTGVCULFIVLVLILCHYKKQFRYESOLOQVQVGTSSDNEYFYVDPRYE	598
QY	600	YDLKWEPPRENLEFGKVLGSGAFGRVNNATAYGISKTGVSIQAVNMLKEKADSCKEAL	659
DB	599	YDLKWEPPRENLEFGKVLGSGAFKVNATAYGISKTGVSIQAVNMLKEKADSSEREAL	658
QY	660	MSELKMMTHLGHNDINVLIGACTLSGPVYLIPYCCYGDLLNLYLRKSRKFHRTWTTEIF	719
DB	659	MSELKMMTQLGSHENIVNLLGACTLSGPVYLIPYCCYGDLLNLYLRKSRKFHRTWTTEIF	718
QY	720	KEHNFSSYPFQAHNSNMSPGSRVQLHPDLQDLSGFNGNSIHSEDEIYENQKLEAEE	779
DB	719	KEHNFSPYPTFQSHNPSMSPGSRVQIHPDSQDLSGLHNGNSFHSEDEIYENQKRL--EE	776
QY	780	EEDLNVLITFEDLLCFAYQVAKGMFEFLFKSCVHRDLAARNVLVTHGKVKVICTDFGLARDI	839
DB	777	EEDLNVLITFEDLLCFAYQVAKGMFEFLFKSCVHRDLAARNVLVTHGKVKVICTDFGLARDI	836
QY	840	LSDSSYVVRGNARLPVKWMAPESLFEGITYTIKSDVWSYGILLWEIFSLGVNYPYPGIPVDA	899

A:Accession: I59083
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 874-972 <RE3>
 A:Cross-references: GB:M14193; NID:gl82521; PIDN:AAA35834.1; PID:gl82522
 R:Nienhuis, A.W.; Bunn, H.F.; Turner, P.H.; Gopal, T.V.; Nash, W.G.; O'Brien, S.
 Cell 42, 421-428, 1985
 A:Title: Expression of the human c-fms proto-oncogene in hematopoietic cells and its del
 A:Reference number: I52772; MUID:85282599; PMID:4028159
 A:Accession: I52772
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 244-295 <RE4>
 A:Cross-references: GB:M11067; NID:gl82674; PIDN:AAA35848.1; PID:g442423
 C:Genetics:
 A:Gene: GDB:CSF1R; FMS
 A:Cross-references: GDB:120600; OMIM:164770
 A:Map position: 5q33.2-5q33.3
 A:Introns: 17/1; 103/1; 198/1; 243/1; 297/1; 361/2; 400/1; 440/2; 504/1; 542/3; 585/1; 6
 C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
 C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
 fic protein kinase
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-972/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
 F:24-512/Domain: extracellular #status predicted <EXT>
 F:35-86/Domain: immunoglobulin homology <IMM1>
 F:120-179/Domain: immunoglobulin homology <IMM2>
 F:217-280/Domain: immunoglobulin homology <IMM3>
 F:316-383/Domain: immunoglobulin homology <IMM4>
 F:412-487/Domain: immunoglobulin homology <IMM5>
 F:513-537/Domain: transmembrane #status predicted <TM>
 F:538-972/Domain: intracellular #status predicted <INT>
 F:580-917/Domain: protein kinase homology <KIN>
 F:588-596/Region: protein kinase ATP-binding motif
 F:42-84,127-177,224-278,419-485/Disulfide bonds: #status predicted
 F:47,73,153,240,335,412,428,480/Binding site: carbohydrate (Aasn) (covalent)
 F:616,633,778/Active site: Lys, Glu, Asp #status predicted
 F:783,796/Binding site: magnesium (Aasn, Asp) #status predicted

Query Match 23.2%; Score 1221.5; DB 1; Length 972;
 Best Local Similarity 32.5%; Pred. No. 3.3e-55;
 Matches 330; Conservative 152; Mismatches 331; Indels 201; Gaps 33;

Qy 76 VYEAATVEAESGSITLQVQLATPGDLSCLWFKHSLGCPHFDLQNRGIVSMAIL-- 132
 Db 22 VIEPSVPELVKCAT--VTLRCVNGSVWDGPPS-----PHTLYSDG--SSILSTN 72
 Qy 133 NVETQAGEYLLHIQSERANYTVLFTVNVNRTQLYVLRPY-----FRKMENODALL-C 185
 Db 73 NATFQNTGTVRCYRTEPGDPLGSAAILHYVKDP-----ARPNVLAQEVVWFEDQALLPC 127
 Qy 186 ISGVPEPTVEWVLCSSHRSCKEKGPAVVRKEK-----VLHE---LF 226
 Db 128 L--L--LTDPLV-----EAGVSLVRVRGRPLMRHTNYSFSPWHGFTIHRAFIQ 171
 Qy 227 GTDIRCCARNALRECTKLTIDLNOAPOSTLP-----OLEFLKVGSPLEIRKCAI 276
 Db 172 SDQYQCSALMG-GR---KVMISIRLKVKQVIPGPALTLPALVIRGAAQIVCSAS 227
 Qy 277 HVNHGFLTWELDKALEEGSYFEMSTYSTNRNIRILLAFVSSVGRNDGTGYTCSS-- 334
 Db 228 SVDVNFDFVLOHNNKTL--AIPOSDPHNNRYQ-KVLTNLNDQVDFQHAGNYSVCVASNV 283
 Qy 335 --KHPSOSALVTILEKGFNATNSQE-EYEDIPYEKFCFVRFKAYPRIR-CTWIFSOAS 390
 Db 284 QGKH-STSMFPRVVSAYLNLSSQNLIQEVTVGEGNLKVMVEAYPLQGFNNWTY----- 338
 Qy 391 FPCQGLEGDGYSISKCDHKNKP-----GEYIFVAEN 423
 Db 339 -----LGPSSDHPQEPKLANATTKOTYRHTFTLSLPRLPSEAGRYSEFLARN 385
 Qy 424 DDAQFTKMTLIRKKQV-----LANASASQASCSGDYPLPSWTWKKCKSDKSPNCTEE 478

Db 386 PGWRALTFELTLRYPPPEVSVIWTFFINGSGT-LICAASGYPPQPNVTLQCSGHTDRCDEA 444
 Qy 479 IPEGVWN-----KKANRKVFGQWVSSSTLNMEAGKGLLVKCCAYNSMGTSCTETFLNSPG 534
 Db 445 QVLQVWDPPPEVLVSQEPFHKTVTQSLLTVETLEHNTYECRAHNSVSGSWAFPIPIASG 504
 Qy 535 PFPPIQNIISFYATIGLC--LPIVIVLIVLICHYKQFRIESOLQMIQVTPGLDNEYF 591
 Db 505 ATHPPDEFLFTPVVACMSIMALLLLLLLYLKQPKYQVRWKIIE--SYEGNSYT 562
 Qy 592 YVPRDYEDLKWEPFRENLEFGKVLGSGAFGRVWNAATAYGISKTGVSIQVAVKMLKEKA 651
 Db 563 FIDPTQLPYNEKEWEPFNNLQFGKTLGAGAPGVKVEATAFGLGKEDAVLKVAVKMLKSTA 622
 Qy 652 DSCKEALMSSELKMTMTHLGHHDNIVNLIGACTLGGPVLIFFEYCCYGDLLNLYRSKRKF 711
 Db 623 HADEKEALMSSELKMTMTHLGHHDNIVNLIGACTHGGPVLVITEYCCYGDLLNLYRSKRKF 680
 Qy 712 HRTWTEIFKEHNFSSYPTFOAHNSNMPGSRREVLPDQLDLSGFGNNGSIHSEDE---- 766
 Db 681 -----AMLGP---SLSPQDPEGVDYKNIHLEKYYVRD 712
 Qy 767 -----IEYENQKLAEE--EEDLNVLTFEDLLCFAYOVAKMEFLEFK 808
 Db 713 SGFSSQGVDTYVEMRPVSTSGNDSFSQDLKEDGRPLELRDLHLHFSSQVAGMAFLASK 772
 Qy 809 SCVRDLAARNVLTHGKVKVICDFGLARDILSDSSVYVRGNARLPVKWMAPESEFEGY 868
 Db 773 NCIHRDVAARNVLTHGKVKVICDFGLARDILSDSSVYVRGNARLPVKWMAPESEFEGY 832
 Qy 869 TIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYKLIQSGFKMEQPFYATEGIYFVMQSC 928
 Db 833 TVQSDVMSYGILLWEIFSLGVNYPGIPVDANFYKLIQSGFKMEQPFYATEGIYFVMQSC 892
 Qy 929 WAFDSRKRPFPNLTSLFGLCOLAEEACITSLHLPKQAAPOQRGGLRAQSPQ 982
 Db 893 WALEPHTHRTPTQQICSLF--QEQAQEDRRERDYNLPSS---RSGSGSSSSE 941

RESULT 9

I51703
 c-kit-related kinase 1 (XKRk1) - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
 C:Accession: I51703
 R:Baker, C.V.; Sharpe, C.R.; Torpey, N.P.; Heasman, J.; Wylie, C.C.
 Mech. Dev. 50, 217-228, 1995
 A:Title: A Xenopus c-kit-related receptor tyrosine kinase expressed in migrating stem
 A:Reference number: I51703; MUID:95344996; PMID:7619732
 A:Accession: I51703
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-954 <BAK>
 A:Cross-references: EMBL:248770; NID:g763033; PIDN:CAA88688.1; PID:g763034
 C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolo
 C:Keywords: Atp
 F:575-915/Domain: protein kinase homology <KIN>
 F:583-591/Region: protein kinase ATP-binding motif

Query Match 23.2%; Score 1220; DB 2; Length 954;
 Best Local Similarity 32.0%; Pred. No. 3.9e-55;
 Matches 315; Conservative 160; Mismatches 321; Indels 188; Gaps 35;

Qy 77 YEATVEAESGSITLQVQLATPGDLSL-----LWFKHSLGCPHFDLQNRGIVSMA 130
 Db 15 YTGDAVPKINDGEDRVTVNVGDKVSLCERDAHLVTLAFQSGLMKKPR-DLKSRLP----- 68
 Qy 131 ILNVET-----QAGEYLLHIQSERANYTVLFTVNVNRTQLYVLRPYFRKME 178
 Db 69 -LNNSETDQFVIILKADLRHIGRYICTNWTQENTSV--SLFVKDPAFPFLDIPDIVTE 125
 Qy 179 NQDAL-LCISEGVPEPTVEWVLCSSHRSCKEKGPAVVRKEKVLHLEFGTDIRC----- 232

Db 126 GADTVGMPF---TDPMDIAI-----EK- -DGSPLPE-----NFTFTDIEAGITIK 169
Qy 233 -----CARNALGR-ECTKLTFTIDLNQAPQSTLQPLFL-----KVCEPLWIRC 273
Db 170 TVOLAFDSCVCSGNGSGTGVKSSSTSIHVKVPKK-VPTVPLSKRQLVKTGEPFVTC 228
Qy 274 KATHVNHGFLTW-ELEDKALEGSGFFENSTYTNRTMIRILLAFVSSVGRNDTGYTCS 332
Db 229 AVLDFVSTVKAQWLDVKEGVTQKAFNRSSNVFSYNLTLS-----DGVPSERSFTQ 282
Qy 333 SSKHPSQ---SALVTILEKGFINATSOE-EYEIDPYEKFCFVRKAYPR-IRCTWIFS 387
Db 283 AENAIGQVNAFTFLDIDVGVNLTVLENTTISVAGDNLVLKVDYDAYPHPDGQVMTYF 342
Qy 388 QASFPCEQRLDGYSISKCDHN-----KPGEIFYAENDDAQTKWF 432
Db 343 NETL---LNTSHYVATK---DEGNRYVSELHLIRLKGTEKGVYFTYTNSSDDASVSF 396
Qy 433 TLNIRKKPOVLANASQAS--CSGYPPLPSWTWKCDKSPNCTEEIPEGVNRK--A 488
Db 397 NIOKTRPEILIAERTSEGTQCVATGFPVPAIQWYFCPSGEORCTDYPLSPVNEKFIQ 456
Qy 489 NRKVFQWSSSTLNMSHAGKLLVKCCAYNSMGTS-----CETIFLNSPGP 535
Db 457 ENSSLGRIVVESTIDVNDLKNKGTQCVASNEVESVFSFAIKEKLRTHLTFT----- 511
Qy 536 FPIQNI SFYATIGLCPPIVVLIVLICHYKKQRYESOLOMI-QVTGPLDNEYFYVD 594
Db 512 -PLL---IGFIAAGL---MCIAVAVLMYKYLQKPKYEIQWVVEING---NNVYIID 560
Qy 595 FRDYEDLKEPRENLEFGKVLGSGAFGRVMNATAYGSKTGVSIQVAVKMLKEKADSC 654
Db 561 PTOLPYDNKWEFPRDLRCFKILGAGAFKVVEATAYGLLKEDSRITVAVKMLKPSAHS 620
Qy 655 EKBALMSLQWTHLGHHDNIIVNLLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRT 714
Db 621 EREALMSLVLYLGHHRKNIIVNLLGACTVGGPTLVITEYCCYGDLLNLYRRKRDSP--- 677
Qy 715 WTIFKEHNFSSYPTFOAHNSNMPGSRVQLHPPDLQSLGFGNSIHSEDEIEYENOK- 773
Db 678 -----ICPKFEDNS-----EALYKYL-----LNRDMGCEGMSEYIDMKP 713
Qy 774 -----RLAEEDENLVITFEDLLCFAYQVAKGMEFLEPKSC 810
Db 714 AVSYVVPYTKDKRRSGFGDQSVSIPEDDL-ALDTEDLNFSQVQAGMFLASKNC 772
Qy 811 VHRDLAARNVLVTHGKVKVVICDFGLARDILSDSSYVVRGNARLPVKWMAPESEFEGYTI 870
Db 773 IHRDLAARNILLTHGRITKICDFGLARDIRNDSNVYVKGARLPVKWMAPESEFHCYVTF 832
Qy 871 KSDVWSYGILLWEIFSLGVNPNYPGIPVDANFYKLIQSGFKMEOPFYATEGIYFVMSQWA 930
Db 833 ESDVWSYGILLWEIFSLGSSPYPRIPVDSFKYKIKDGYRMSPECAPLEMYEIMRSCWN 892
Qy 931 FDSKRPSPFNLTSLFCQLAAEAE 954
Db 893 SDPLKRPFTKQIVQMEQQLSDSK 916

RESULT 10
I45877

protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - aurochs
C:Species: Bos primigenius (aurochs)

C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 20-Apr-2000

C:Accession: I45877

R:Kubota, T.; Hikono, H.; Sasaki, E.; Sakurai, M.

Gene 141, 305-306, 1994

A:Title: Sequence of a bovine c-kit proto-oncogene cDNA.

A:Reference number: I45877; MUID:94215924; PMID:7512939

A:Accession: I45877

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-977 <UB>

A:Cross-references: GB:D16680; NID:G516659; PIDN:BAA04084.1; PID:G516660
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolog
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F:329-395/Domain: immunoglobulin homology <IMM>
F:588-932/Domain: protein kinase homology <KIN>

Query Match 23.1%; Score 1215; DB 2; Length 977;

Best Local Similarity 32.8%; Pred. No. 7.2e-55;

Matches 304; Conservative 141; Mismatches 298; Indels 184; Gaps 28;

Qy 134 VTE-----TQAGEYLLHIQSERANYTVLFTVNVRTQ-LYVLRPPYFRMENQDALLCI-- 186

Db 83 ITEKAEATNTGNYTC---TNKGGLSSSIYVVRDPEKFLFLIDLPLYGKEENDTLVRCLPT 139

Qy 187 -----SSGVEP-TVEVILCSSHRESCKEEGPAVVRKEEVHLFGTDIRC-- 232

Db 140 DPEVTNYSLTGCGKPLPKDLTFV-----ADPKAGITIRNVKREYHRL-----CLH 185

Qy 233 CARNALGRE-CTKLTFTIDLNQAPQS-----TLQPLFKVGEPLWIRCKATHVNHGFLT 285

Db 186 CSANQRCKSMLSKKFTLKVPAAIKAVPVSVSKTSYLLREGEEFAVTCCLKDVSSVDSM 245

Qy 286 WELEDKALEGSGYFEMSTYSTNRTMIRILLAFVSSVGRNDTGYTCSKXHPSSQALVTI 345

Db 246 WIKENSQOTKRAQTKKNSHQGDFSYLRQERLTTISSARVNDSGVFMCYANNFTFGSANVTT 305

Qy 346 LE---KGFINA-TSSQEEYEIDPYEKFCFVRKAYPR-IRCTWIFSQASFPCEQRLDG 400

Db 306 LEVVDKGFINIPMMNTTVFVNDGENVDLVVEYEAYPEKPVHROWIYMNRT----- 355

Qy 401 GYSISKPCDCHK-----NKPGEVIFYAENDDAQTKMFTLINIRKK 439

Db 356 --STDKDDDPKSESNENIRYVNEHLHLRLKGTGGYTFHVSNSDVNSSTVFVYVNTK 413

Qy 440 PQVLANASA--SQASCSSDGYPLPSWTWKCDKSPNCTEEI-PEGVNRKCANRKFVQW 496

Db 414 PEILTHDLRVNGLQCVAAAGFPETIDWYFCPGTEQRCVSPVGPVDVQIQNSVSPFCKL 473

Qy 497 VSSSTLNMSSAGKLLVKCCAYNSMGTS-----CETIFLNSCPGPPFI 539

Db 474 VVYSTIDDSFTKNGTVECRAYNDVGKSSASFNPFAKNSKEQIHAHTLFT-----PLL 527

Qy 540 QDNISFYATTGLCLPFIWLVILVILCHYKKQRYESOLOMI-QVTGPLDNEYFYVDFRDY 598

Db 528 ---IGFVIAAGLMCIFVWIL---TYKYLQKPMYEVQWKVVEING---NNYVIDPTQL 577

Qy 599 EYDLKWEFPRENLEFGKVLGSGAFGRVMNATAYGSKTGVSIQVAVKMLKEKADSCKEA 658

Db 578 PYDHKWEFPNRNLSFGKTLGAGAFKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREA 637

Qy 659 LMSLQWTHLGHHDNIIVNLLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTEI 718

Db 638 LMSLQWTHLGHHDNIIVNLLGACTIGGPTLVITEYCCYGDLLNLYRRKRDSP----- 690

Qy 719 FKEHNFSSYPTFOAHNSNMPGSRVQLHPPDLQSLGFGNSIHSEDEI-----EYENQ 772

Db 691 -----ICSKQEDHAEVALYK-----NLLHSSKSSCNDSTNEYMDM 725

Qy 773 K-----RLAEEDENLVITFEDLLCFAYQVAKGMEFLE 806

Db 726 KPGVSVVVPYTKDKRRSARIGSYIERDVTTPAIMEDELALDLELLSFSYQVAKGMFLA 785

Qy 807 FKSCVHRDLAARNVLVTHGKVKVVICDFGLARDILSDSSYVVRGNARLPVKWMAPESEFEG 866

Db 786 SKNCIHRDLAARNILLTHGRITKICDFGLARDIRNDSNVYVKGARLPVKWMAPESEFENC 845

Qy 867 IYTKSDVWSYGILLWEIFSLGVNPNYPGIPVDANFYKLIQSGFKMEOPFYATEGIYFVMO 926

Db 846 VYTFESDVWSYGILLWEIFSLGSSPYPRIPVDSFKYKIKDGYRMSPECAPLEMYEIMRSCWN 905

Qy 927 SCWAFDSRKRPSFPNLTSLFCQLAAEAE 953

Db 906 TCWDADPLKRPFTKQIVQMEQQLSDSK 932

RESULT 11

S16385
 macrophage colony-stimulating factor 1 receptor precursor - rat
 N;Contains: protein-tyrosine kinase (EC 2.7.1.112) CSF-1R
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Jun-2000
 A;Accession: I60321; S16385
 R;Borycki, A.G.; Guillier, M.; Leibovitch, M.P.; Leibovitch, S.A.
 Growth Factors 6, 209-218, 1992
 A;Title: Molecular cloning of CSF-1 receptor from rat myoblasts. Sequence analysis and
 A;Reference number: I60321; MUID:93001225; PMID:1389227
 A;Accession: I60321
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-978 <RES>
 A;Cross-references: EMBL:X61479; NID:957543; PIDN:CAA43706.1; PID:957544
 A;Note: in Genbank entry RRCSE1, release 113.0, the source is designated as Rattus rattu
 A;Note: submitted to the EMBL Data Library, August 1991
 C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
 C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; kinase-rela
 protein; tyrosine-specific protein kinase
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-978/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
 F;20-515/Domain: extracellular #status predicted <EXT>
 F;35-86/Domain: immunoglobulin homology <IMM1>
 F;120-179/Domain: immunoglobulin homology <IMM2>
 F;217-280/Domain: immunoglobulin homology <IMM3>
 F;316-381/Domain: immunoglobulin homology <IMM4>
 F;410-485/Domain: immunoglobulin homology <IMM5>
 F;516-535/Domain: transmembrane #status predicted <TM>
 F;536-978/Domain: intracellular #status predicted <INT>
 F;578-915/Domain: protein kinase homology <KIN>
 F;586-594/Region: protein kinase ATP-binding motif
 F;42-84,127-177,224-278,417-483/Disulfide bonds: #status predicted
 F;45,73,302,335,389,410,449,478,491/Binding site: carbohydrate (Asn) (covalent) #status
 F;614,631,776/Active site: Lys, Glu, Asp #status predicted
 F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 23.0%; Score 1210; DB 2; Length 978;
 Best Local Similarity 33.5%; Pred. No. 1.3e-54;
 Matches 318; Conservative 147; Mismatches 329; Indels 154; Gaps 31;

Qy 78 EAATVEAEGSITLQVATPGLSLVFKHSLGQCFDILQNGIVSMALNVET 137
 Db 36 ETVTLCRVCSGEWD-----GPISYTWLDPSPGS-----TLTRNATFK 77
 Qy 138 QAGEY-LLHQSEBANYTLFTVNVDTQLV-----LRRPFRKMNQDALL-CIS 187
 Db 78 NTGYRTELEDNPAGSTTI-----HLVYKDPASHWNLLAQEVTVVGEAVLPCL- 128
 Qy 188 EGVPEVTEVWVLCSSHRESCKEAPVVRK-----EEKVLHFLFGTDIRCC 233
 Db 129 --ITDPALK-----DSVSLMREGGRQVLRKTVTFPSAWRGIIRKAKVL-----DSNTYVC 177
 Qy 234 ARNALGRECTKL-FTIDLN-----QAQSTL-PQLFLKV-GEPLWIRCKAHVNHGFLTW 286
 Db 178 KTVNNGRESTSTGLWKNVRVHPPEPQIKLEPSKLVRIRGAAQIVCSATVAEYGFNVIL 237
 Qy 287 ELEDKALE--EGSYFENSTYSTNTMTIRILLAFVSSVGRNDTGYTC-SSSKHPSQSALV 343
 Db 238 KRGTQKLEIPLNSDFQNYKKVRAL-----SLNAVDFQAGIYSCVANSVNGVTRATM 291
 Qy 344 T--ILEKGFINATSQE-EYIDPYEKFCFVRKAYPRIR-CTWIFSQAFFPCEQRLG 399
 Db 292 NFQVVEAYLNLTSQSLQVSGVDSLLVTHADAYPSIOHYNWYTLGPPE-DQKLE 350
 Qy 400 -----DGVISIKFDH--KNKPGEYIFYAENDAAQTKMTNLIRKKPOVLANASQ 450
 Db 351 FITORATYRYTFKFLNRVKASEAQYFLMAQKNAGMNNLTFFELTRYPPPEVSVTWMEVN 410
 Qy 451 AS-----CSSDGYPLPSWTWKCKSKSPNCTEIPGVVN-----KKNRKYVGQWVSSSTL 502

Db 411 GSDVLCDSVGPQPSVTWMECRGHTDRCDQAALQVWMDTHPEVLSQKPFDPKVIQSOL 470
 Qy 503 NMSAGKGLLVKCCAYNSMGTSCETIFLNSPPFPFIQDNISFYATIGLC---LPIIVVL 559
 Db 471 PIGTLKHNTYFCKTHNSVGNSSQYFRAVSLGQSLQLPDESLETPVWVACMSVMSLLVLL 530
 Qy 560 IVLICHKVKQFRYESQLQMIQ-VTGPLDNEYFYVDREYDLKWEFPRENLEFGKVLG 618
 Db 531 LLLLYLKVKQKPYQVWRKILIRYEG---NSYTFIDTQLPYNEKWEFPRNNLQFGKTLG 587
 Qy 619 SGAFGRVNATAYGISKTGVSQVAKMLKEKADSCKEALMSELKMMTHLGHHDHNVNL 678
 Db 588 AGAFGVVEATAFGLGEDAVLKVAVKMLKSTAHADKEALMSELKINSHLQGHENIVNL 647
 Qy 679 LGACTLSGPVYLIFEYCYGDLNLYLRKRE-----KFHRTWTEI 718
 Db 648 LGACTHGGFVLIVITEYCYGDLNLYLRKAEAMLGSLSPGQDSGDSYKNIHLEKKYV 707
 Qy 719 FKEHNFSSYPTFOAHSNSSMPGSRVQLHPDQLSGFNGNSIHSEDETEYENQKRLAE 778
 Db 708 RDSGFS-----SQGVDIYVEMRPVSTSSDSFFKQD-----L 740
 Qy 779 BEEDLNVLTFEDLLCFAYQVAKGMEFLBPKSCVHRDLAARNVLVTHGKYVKICDFGLARD 838
 Db 741 DKEPSRPLELDLHFFSQVAGMAFLASKNCIHRDVAARNVLLTSGHVAKIGDFGLARD 800
 Qy 839 ILSDSYVVRGNARLPVKMAPESLFEIGYITKSDVMSYGILLWEIFSLGVNPPGIPVD 898
 Db 801 IMNDSYVVGKARLPVKMAPESILCYVTYQSDVMSYGILLWEIFSLGLNPPGILVN 860
 Qy 899 ANFYKLIOGFKMEOPFYATEGIYFMOSCAFDKSKSPFNLSFL 946
 Db 861 NKFYKLVDKGQMAQPVFAPKNIYSIMOSCMDELEPRTPTFOQICFL 908

RESULT 12

TVMSMD
 macrophage colony-stimulating factor 1 receptor precursor - mouse
 N;Contains: protein-tyrosine kinase (EC 2.7.1.112) csf1r/fms
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2000
 A;Accession: S01880
 R;Rothwell, V.M.; Rohrschneider, L.R.
 Oncogene Res. 1, 311-324, 1987
 A;Title: Murine c-fms cDNA: cloning, sequence analysis and retroviral expression.
 A;Reference number: S01880; MUID:88217329; PMID:2966922
 A;Accession: S01880
 A;Molecule type: mRNA
 A;Residues: 1-976 <ROT>
 A;Cross-references: EMBL:X06368
 C;Genetics:
 A;Gene: fms
 C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolo
 C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming prote
 fic protein kinase
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-976/Product: macrophage colony-stimulating factor 1 receptor #status predicted <EXT
 F;20-515/Domain: extracellular #status predicted <EXT>
 F;35-86/Domain: immunoglobulin homology <IMM1>
 F;120-179/Domain: immunoglobulin homology <IMM2>
 F;217-280/Domain: immunoglobulin homology <IMM3>
 F;316-381/Domain: immunoglobulin homology <IMM4>
 F;410-485/Domain: immunoglobulin homology <IMM5>
 F;516-535/Domain: transmembrane #status predicted <TM>
 F;536-976/Domain: intracellular #status predicted <INT>
 F;578-914/Domain: protein kinase homology <KIN>
 F;586-594/Region: protein kinase ATP-binding motif
 F;42-84,127-177,224-278,417-483/Disulfide bonds: #status predicted
 F;45,73,302,335,389,410,449,478,491/Binding site: carbohydrate (Asn) (covalent) #stat
 F;614,631,776/Active site: Lys, Glu, Asp #status predicted
 F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

Query Match		22.8%	Score 1198.5;	DB 1;	Length 976;
Best Local Similarity		34.1%	Pred. No. 5e-54;		
Matches 317;		Conservative 148;	Mismatches 347;	Indels 117;	Gaps 31;
QY	78	EAATVEAEGSITLQVOLATPGDLSCLWFKHSSLCQPHFDLQNRGIVSMAILNVTET	137		
DB	36	ETVTLRCVSGNSGVEWD-----GPSIPWILDPSEFGS-----TLTTSNATFK	77		
QY	138	QAGEY-LLHTQSERANYTVLFTVNRVDTQLYV-----LRRPYFRKMNQDALL-CIS	187		
DB	78	NTGYRCTELEDPMAGSTTI-----HLVVKDPAHSMWLLAQEVTVVSGQEAVALPCL-	128		
QY	188	EGVPEPTVEWLVCSHSHRESCKEGBPAVVRKEEKVHLHFLGFTDIR-----CCARNA	237		
DB	129	--ITDPALK-----DSVSLMREGGRQVLRKTVFFSPWRGSIIRKAKVLDNSVTVC	181		
QY	238	LGRECTKL-FTIDLN-----QAQSTL-LPQLPKV-GEPLWIRCKAIHNVHNGFGLTWE	290		
DB	182	NGRESTGTGWLKYNRVHPSPPQIKLEPSKLVRIRGEAAQIVCSATNAEVGFNVILKRGD	241		
QY	291	KALE--EGSYFEMSTYSTNRTMIRILLAFVSSVGRNDTGYTTC--SSSKHPSQSALVT--I	345		
DB	242	TKLEIPUNSFQDNYKKVRAL-----SLNAVDFQDAGIYSCVASNDVGRTRATMNFQV	295		
QY	346	LEKGFINATSQE-EYEIDPYEKFCEFSVRKAYPRIR-CTWIFSQASPPCQRGLE----	399		
DB	296	VEAYNLNTSEQLLOEVSVDGSLILTVHADAYPSIGHYNTWYLGPFPE--DORKLEFITQ	354		
QY	400	---DGVSIKFCDH--KNKPGEYIFYAENDDAQFTKMTNIRKKPOVLANASQAS--	452		
DB	355	RAIYRYTFKFLNRVKASEAGQVFLMAQKAGWNNLTFLTLRYPEVSVVTWMPVNGSDV	414		
QY	453	--CSSDGYPLPSTWTKKCDKSPNCTBEIPEGVNN-----KKANRKVQGWVSSSTLNMSE	506		
DB	415	LFCDVSGYQPPSVTWMECRGHTDCDEAQAHLHNDTHPEVLSQKPFDKVIQSLPIGP	474		
QY	507	AGKGLLVKCAVNSMGTSCTEFLNSGPGPFPIQDNISFYATICLG---LPFIVVLIVLI	563		
DB	475	LKENWTFYCKTHNSVGNSSQYFRAVSLGQSKQLPDESFLTTPVVVACMSVMSLVLL	534		
QY	564	CHKYKKQFRYESQLOMTQ-VTGPDLNBYFYVDPRDYEDLKWEPPEPNLEBFGKVLGSGAF	622		
DB	535	LYKYKQPKYQVRWKIIERYEG---NSYTFIDPTQLPYNEKWEPPRNQLQFGKTLGAGAF	591		
QY	623	GRVNNATAYGTSKTVSIOAVKMLKEKADSCKEALMSELKMTWHLGHNDNIYNLLGAC	682		
DB	592	GKVVETAFGLGKEDAVLKAVKMLKSTAHADKEALMSELKIMSHLGHENIYNLLGAC	651		
QY	683	TLSPGVLLIPEYCCYGDLLNLYRSKRKFHRTWTETIFKEHNFSSYPTFOAHNSSSMPGSR	742		
DB	652	THGGPVLVYTEYCCYGDHLNFLRKAEMHGP-----SLSPQDSGDSYKNIH	701		
QY	743	EVQLHPDQLDQSGFNHNSIHSEDEIYENQKRLAEEBEDLN-----VLTFEDLLCFAYQ	797		
DB	702	LEKKYVRD--SGPSSQGVDTYVEMRPVSTSSDSFFKQDLCKEHSRPLELWDLHFFSSQ	759		
QY	798	VAKQWELEPKSCVHRDLAARNVLVTHGVKVKICDFGLARDILSDSSYVYVGNARLPVKW	857		
DB	760	VAQGMATFLASKNCTHRDVAARNVLLTSGHAKIGDFGLARDIMDSNYVWKGNA-LPVKW	818		
QY	858	MAPSLFEGYTIKSDVMSYGILLWEIFSLGVNPPYGPVDPANFYKLIQSOFKMEQPFYA	917		
DB	819	MAPESIIFDCVITVQSDVMSYGILLWEIFSLGLNYPGIVHVNKKFYKLVKQGYQMAQPVFA	878		
QY	918	TEGIYFVWQSCWAFDSRRKPSFPNLTSL	946		
DB	879	PKNIYSIMQSCWDLDETRRPTFQOICFLL	907		
RESULT 13					
TVHUKT					
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - human					
N;Alternate names: mast/stem cell growth factor receptor; tyrosine kinase receptor c-kit					

C;Species: Homo sapiens (man)
C;Date: 31-Mar-1991 #sequence revision 31-Mar-1991 #text change 21-Jul-2000
C;Accession: S01426; PC1015; K41815; B41815; C41815; I37548; I56954; I54336
R;Yarden, Y.; Kuang, W.J.; Yang-Feng, T.; Coussens, L.; Mumentsh, S.; Dull, T.J.; Ch
EMBO J. 6, 3341-3351, 1987
A;Title: Human proto-oncogene c-kit: a new cell surface receptor tyrosine kinase for
A;Reference number: S01426; MUID:88111521; PMID:2448137
A;Accession: S01426
A;Molecule type: mRNA
A;Residues: 1-976 <VAR>
A;Cross-references: GB:X06182; NID:G34084; PIDN:CAA29548.1; PID:G34085
R;Hu, W.X.; Cornu, F.; Andre, C.; Galibert, F.
Chine Biochem. J. 7, 618-629, 1991
A;Title: Nucleotide sequence of two neighbouring fragments of human c-kit proto-oncogene
A;Reference number: PC1015
A;Accession: PC1015
A;Molecule type: DNA
A;Residues: 412-713 <HW>
A;Note: article in Chinese with English abstract
R;Sprintz, R.A.; Giebel, L.B.; Holmes, S.A.
Am. J. Hum. Genet. 50, 261-269, 1992
A;Title: Dominant negative and loss of function mutations of the c-kit (mast/stem cell)
A;Reference number: A41815; MUID:92133600; PMID:1370874
A;Accession: A41815
A;Molecule type: DNA
A;Residues: 579-583 'L', 585-589 <SPR>
A;Cross-references: GB:578939; NID:G244084; PIDN:AA21234.1; PID:G244085
A;Note: sequence extracted from NCBI backbone (NCBIN:78839, NCBI:78842)
A;Note: disease-related mutant from patient with piebaldism
A;Accession: B41815
A;Molecule type: DNA
A;Residues: 637-641 'SPELPW' <SP2>
A;Cross-references: GB:578943; NID:G244086; PIDN:AA21235.1; PID:G244087
A;Note: sequence extracted from NCBI backbone (NCBIN:78843, NCBI:78844)
A;Note: disease-related mutant from patient with piebaldism
A;Accession: C41815
A;Molecule type: DNA
A;Residues: 556-560 'GDKWK' <SP3>
A;Cross-references: GB:578945; NID:G244088; PIDN:AA21236.1; PID:G244089
A;Note: sequence extracted from NCBI backbone (NCBIN:78845, NCBI:78846)
R;Giebel, L.B.; Strunk, K.M.; Holmes, S.A.; Sprintz, R.A.
Oncogene 7, 2207-2217, 1992
A;Title: Organization and nucleotide sequence of the human KIT (mast/stem cell growth
A;Reference number: I37948; MUID:93064697; PMID:1279499
A;Accession: I37948
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-976 <RES>
A;Cross-references: EMBL:X69301; NID:G34089; PIDN:CAA49159.1; PID:G825686
A;Note: an alternative splice form omitting residues 510-513 is described
R;Yamamoto, K.; Tojo, A.; Aoki, N.; Shibuya, M.
Jpn. J. Cancer Res. 84, 1136-1144, 1993
A;Title: Characterization of the promoter region of the human c-kit proto-oncogene.
A;Reference number: I56954; MUID:94103107; PMID:7506248
A;Accession: I56954
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-22 <RE2>
A;Cross-references: GB:S67773; NID:G459358; PIDN:AA29529.1; PID:G459359
R;Sprintz, R.A.; Holmes, S.A.; Berg, S.Z.; Nordlund, J.J.; Fukui, K.
Hum. Mol. Genet. 2, 1499-1500, 1993
A;Title: A recurrent deletion in the KIT (mast/stem cell growth factor receptor) proto
A;Reference number: I54336; MUID:94061059; PMID:7694728
A;Accession: I54336
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 242-250 <RE3>
A;Cross-references: GB:S67686; NID:G460545; PIDN:AA13996.1; PID:G4261696
C;Genetics:
A;Gene: GDB:KIT
A;Cross-references: GDB:I20117; OMIM:164920
A;Map position: 4q12-q12

Db 445 RPTCNGNNTGLPKQNHQAL--TVEOREEYGAVEVESVFTVGLSNHMTVECVAFNLGV 503
Qy 524 SCTIFLNSPGPPFIODNISFYATIGLC--LPIVVLIVLICHYKKQRYESQLOMIQ 581
Db 504 SSDTFTVE-----VSDKLTSTLGAAGVLAIFLLLLVFLLYKQKRFPRFIRWKIIE 556
Qy 582 VTGPLONEYFYVDRDYEDLKWFEPPRENLEFGKVLGSGAGFRVWVNATAYGISK-TGVSI 640
Db 557 ARE--GNNYTFIDPTOLPYNEKEWPPDKLKGVLGAGAGKVVATEAFLGEDKDNTL 614
Qy 641 QVAVKMLKEKADSCKEALMSELKMHGHDNHNVLNLLGACTLSGPGVYLIFEYCCYGD 700
Db 615 RVAVKMLKANASDEREALMSELKILSHLGHQHNVLNLLGACTYGGPVLVITEYCSLGD 674
Qy 701 LNYLRSKREKFEHTWTEIFKEHNFSSYPTQAHSN-----SSMFGSR 742
Db 675 LNFROKAEFTVNLWMI-----PEIMENSNDYKNCQKWIYRSOGISSTSSST 725
Qy 743 EVOLHPPDLQSGFNGNSIHSEDEIEYENOKRLAEBEEDLNVLTFEDLLCFAYQVAKGM 802
Db 726 YLEWRP-----SQOSHIEASGRKSLCEDNGD--WPLDIDDLRFLSLOVAQL 770
Qy 803 EFLEFKSVHRDLAARNVLVTHGKVKIKDPLGLARDILSDSSYVVRGNARLPVKWMAPE 862
Db 771 DFLASRNCIHRDVAARNVLLTKRVAKICDFGLARDIMWDSNYVVKGNARLPVKWMAPE 830
Qy 863 LFGIYTIKSDVMSYGLLWEIFSLGVNYPGIPVDANFYKLIQSGFKMEOPFYATEGIY 922
Db 831 IFPCVTVSDVMSYGLLWEIFSLGSPYPSMAVDSPFYKWKRGYQMSQDPFALPEIY 890
Qy 923 PVMQSWAFDSRKRPSPNLTSFLGCOLA--EAEAEACIRTSIHLPKQAAPOQRGLRAQS 980
Db 891 MIMKMCNMLEPTERTPTFMSISQMINRLLGQDEGEKLIYRNVQ-PEQVAE----GEACDE 945
Qy 981 PQR 983
Db 946 PKR 948

RESULT 15
JN0677
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - chicken
N/Alternate names: tyrosine kinase receptor kit
C/Species: Gallus gallus (chicken)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C/Accession: JN0677
R/Sasaki, E.; Okamura, H.; Chikamune, T.; Kanai, Y.; Watanabe, M.; Naito, M.; Sakurai, M.
Gene 128, 257-261, 1993
A/Title: Cloning and expression of the chicken c-kit proto-oncogene.
A/Reference number: JN0677; PMID:93292995; PMID:7685729
A/Accession: JN0677
A/Molecule type: mRNA
A/Residues: 1-960 <SAS>
A/Cross-references: DDBJ:DJ13225; NID:g303532; PIDN:BAA02506.1; PID:g303533
A/Experimental source: brain
C/Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C/Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
rotein kinase
F/1-24/Domain: signal sequence #status predicted <SIG>
F/25-960/Product: tyrosine kinase receptor #status predicted <MAT>
F/314-380/Domain: immunoglobulin homology <IMM>
F/573-916/Domain: protein kinase homology <KIN>
F/581-589/Region: protein kinase ATP-binding motif
F/76,135,149,269,286,318,338,356,453,469/Binding site: carbohydrate (Asn) (covalent)

Query Match 22.4%; Score 1181; DB 1; Length 960;
Best Local Similarity 31.8%; Pred. No. 3.9e-53;
Matches 310; Conservative 159; Mismatches 356; Indels 150; Gaps 30;
Qy 45 GSSAGKSSVTRMVRGSPEDIQCTPRROSGTVEAATVEAAGSITLQVOLTATPGDLSC 104
Db 24 GSPVHEESSLVNKGELRLKCN-----EEGPTVWNFQNSDPSAKR 65

Qy 105 L-----WPKHSSLCQCPHFDPQNRGIVSMAILNVTQAGEYLLHIQSERANYTVLFTV 159
Db 66 ISNEKEWHTKNATIRDIGRYECKSKG-----SIVN-----SPVV 99
Qy 160 NVRDTQYLVLRPFRKMNODALLCISEGVPBPTEVWVLCSSHRESCKEGPAVVRKEE 219
Db 100 FVKDPNVLFVDSLIYKGEDSDILLVCPITDPD-VLNFTRKCDGKPLPKMTFIPNPK 158
Qy 220 ---KVLHELPGTDIRCCAR-NALGRECTKLTIDLANCAP-OSTLPOL-----FLKVG 266
Db 159 GIITKNQVRSFKYCQCLAKHNGVEKISEHIP---LNVRPVHKALPVITLSKSYELLKEG 215
Qy 267 EPLMIRKCAIHVNHGFGLTWELEDKALEEGSYFEMSTYSTNRTMIRIILAFVSSVGRNDT 326
Db 216 EEPVTCIIITDVS SVKASWISYKSAIVTSKRNLDGYERK----LTNIRSVGVNDS 271
Qy 327 GYVTCSSKHP--SQSALVTI--LEKGFNATSQE-EYEIDPVEKFCFSVRFKAYPRIR 381
Db 272 GEFTC-QAENPFGKTNATVTLKALAGFVRLFATWNTTIDINAGQNGNLTVYEYAPK-- 328
Qy 382 CTWIFSQASPECEORGLDGYISIKFCDHKNK-----PGEYIF 419
Db 329 -----PKEEVVMYMNETLQNSDHYVYKFTVGNNSYTSSELHLRLKGTGGIYTF 378
Qy 420 YAENDDAQFTQFTLNIRKKPOVLNANASQ--ASCSSDGYPLPSWTWKKCDKSPNCTE 477
Db 379 FVNSDDASSVTFNVYKTKDEILTLDMGLDILQCVATGPPATYIYWFPGTEQRCUD 438
Qy 478 E---IPGWNKKANRKY--FGQWSSSTLNMSBAGLLVKCCAYNSMGTSCEITFLNS 532
Db 439 SPTISPMDVKVSYTNSVPSPERILVESTVNAS-MFKSTGTICCEASSNGDK--SSVFFNF 496
Qy 533 PGPPFTQDNISFYA-----TIGLCLPFIWLVILVILCHYKKQRYESQLOMI-QVTG 584
Db 497 A-----IKEQIRTHLTPLLIAFGVAAGLMCIIVMLIVYILQPKYEVQMKVVEING 551
Qy 585 PLDNEYFVDPDRDYEDLKWFEPPRENLEFGKVLGSGAGFRVWVNATAYGISKTVSIOAV 644
Db 552 ---NNYVYIDPTQLPYDHKWEPPRNRLSFGKTLGAGAGKVVATEAYGLFKSDAAMTVAV 608
Qy 645 KMLKEKADSCKEALMSELKMHGHDNHNVLNLLGACTLSGPGVYLIFEYCCYGDLLNLY 704
Db 609 KMLKPSAHLTEREALMSELKVLVSLGHNINIVNLLGACTIGGPTLIVITEYCCYGDLLN 668
Qy 705 RSKREKP-----HRTWTE--IFKEHNFSSYPTQFQ-HSNSNMPGSRREVQLHPDLSGFN 757
Db 669 RKRKDSPTCPKHEBAEAAVYENLLHQAEPTADAVNEMDMKPGVSYAVPPKADKRPVK 728
Qy 758 GNSHSEDEIEYENOKRLAEBEEDLNVLTFEDLLCPAYQVAKGMEPLEFKSCVHRDLAA 817
Db 729 SGS-----YTQDVTLSMLEDELALDVEDLLSFSYQVAKGMSFLASKNCIHRDLAA 780
Qy 818 RNVLVTHGKVKIKDPLGLARDILSDSSYVVRGNARLPVKWMAPELPEGIYTIKSDVMSY 877
Db 781 RNILLTHGRITKICDPLGLARDIRNDSNVVKGNAARLPVKWMAPEISFNCVTVTFESDVMSY 840
Qy 878 GILLWEIFSLGVNYPGIPVDANFYKLIQSGFKMEOPFYATEGIYFVWQSWAFDSRKR 937
Db 841 GILLWEIFSLGSSPYGMPVDNSKFKYKMKIEGYRMFSPSPPEMYDIMKSCWDADPLQRP 900
Qy 938 SFPNLTSLFGCOLAE 952
Db 901 TFKQIVQLIEQQLSD 915

Search completed: May 24, 2003, 17:00:32

Job time : 41.4826 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:38:45 ; Search time 17.9909 Seconds
(without alignments)
2286.959 Million cell updates/sec

Title: US-09-919-408-2

Perfect score: 5264

Sequence: 1 MRALAQSRDRLLLVLSV.....RGLRAQSPQRQVKIHRERS 992

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	5264	100.0	992	1	FLT3_MOUSE
2	4429.5	84.1	993	1	FLT3_HUMAN
3	1258.5	23.9	980	1	KFMS_FELCA
4	1249.5	23.7	978	1	KFMS_FSVMD
5	1223	23.2	975	1	KIT_MOUSE
6	1222.5	23.2	978	1	KIT_CAPHI
7	1221.5	23.2	972	1	KFMS_HUMAN
8	1219	23.2	977	1	KFMS_MOUSE
9	1215	23.1	977	1	KIT_BOVIN
10	1210	23.0	978	1	KFMS_RAT
11	1207	22.9	975	1	KIT_CANFA
12	1196	22.7	976	1	KIT_HUMAN
13	1181	22.4	960	1	KIT_CHICK
14	1178.5	22.4	978	1	KIT_FELCA
15	1157.5	22.0	1088	1	PGDS_RAT
16	1152.5	21.9	1089	1	PGDS_HUMAN
17	1142.5	21.7	1089	1	PGDS_MOUSE
18	1132	21.5	1087	1	PGDS_XENLA
19	1098	20.9	1098	1	PGDR_MOUSE
20	1078	20.5	1106	1	PGDR_HUMAN
21	998.5	19.0	1338	1	PGRI_HUMAN
22	984.5	18.7	1336	1	VGR1_RAT
23	983.5	18.7	1333	1	VGR1_MOUSE
24	967.5	18.4	370	1	KIT_ESVHZ
25	965	18.3	1348	1	VGR2_COTJA
26	961.5	18.3	1356	1	VGR2_MOUSE
27	954.5	18.1	1298	1	VGR3_HUMAN
28	952	18.1	1363	1	VGR3_MOUSE
29	934	17.7	1343	1	VGR2_RAT
30	926.5	17.6	1367	1	VGR2_MOUSE
31	818	15.5	813	1	FGR2_XENLA
32	810.5	15.4	823	1	CEK3_CHICK
33	791	15.0	821	1	FGR2_HUMAN

RESULT 1

ID	FLT3_MOUSE	STANDARD;	PRT;	992 AA.
AC	Q00342;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	FL cytokine receptor precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor flk-2) (Fetal liver kinase 2) (Tyrosine-protein kinase FLT3).			
GN	FLT3 OR FLT-3 OR FLK-2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
EX	MEDLINE=91292518; PubMed=1648448;			
RA	Matthews W., Jordan C.T., Wiegand G.W., Pardoll D., Lemischka I.R.;			
RT	"A receptor tyrosine kinase specific to hematopoietic stem and progenitor cell-enriched populations.";			
RL	Cell 65:1143-1152(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=92019834; PubMed=1656368;			
RT	Rosnet O., Marchetto S., Delapeyriere O., Birnbaum D.;			
RT	"Murine Flt3, a gene encoding a novel tyrosine kinase receptor of the PDGFR/CSFIR family.";			
RL	Oncogene 6:1641-1650(1991).			
RN	[3]			
RP	CHARACTERIZATION.			
RA	MEDLINE=93205405; PubMed=8384358;			
RA	Maroc N., Rottapel R., Rosnet O., Marchetto S., Lavezzi C., Mannoni P., Birnbaum D., Dubreuil P.;			
RT	"Biochemical characterization and analysis of the transforming potential of the FLT3/FLK2 receptor tyrosine kinase.";			
RL	Oncogene 8:909-918(1993).			
CC	-1- FUNCTION: RECEPTOR FOR THE FL CYTOKINE. HAS A TYROSINE-PROTEIN KINASE ACTIVITY.			
CC	-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- TISSUE SPECIFICITY: HEMATOPOIETIC STEM AND PROGENITOR CELL-ENRICHED POPULATIONS. FOUND IN BRAIN, PLACENTA AND TESTIS.			
CC	-1- SIMILARITY: BELONGS TO THE CSF-1/PDGFR RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.			
CC	-1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			

ALIGNMENTS

34	789	15.0	806	1	CEK2_CHICK	P18460 gallus gall
35	780	14.8	821	1	FGR2_MOUSE	P21803 mus musculu
36	766.5	14.6	819	1	FGR1_CHICK	P21804 gallus gall
37	761.5	14.5	654	1	BFR2_HUMAN	Q01742 homo sapien
38	758.5	14.4	812	1	FGR1_XENLA	P22182 xenopus lae
39	754.5	14.3	822	1	FGR1_HUMAN	P11362 homo sapien
40	751.5	14.3	806	1	FGR3_HUMAN	P22607 homo sapien
41	751.5	14.3	822	1	FGR1_MOUSE	P16092 mus musculu
42	748.5	14.2	822	1	FGR1_RAT	Q04589 rattus norv
43	732	13.9	801	1	FGR3_MOUSE	Q61851 mus musculu
44	698	13.3	802	1	FGR4_HUMAN	P22455 homo sapien
45	697	13.2	808	1	FGR4_MOUSE	Q03142 mus musculu

DR EMBL; M64689; AAA37634.1; --
 DR EMBL; X59398; CAA42041.1; --
 DR PIR; A39931; A39931.
 DR HSP; P11362; IFGK.
 DR MGD; MGI:95559; Flt3.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
 DR signal; Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 992 FL_CYTOKINE RECEPTOR.
 FT DOMAIN 28 544 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 545 564 POTENTIAL.
 FT DOMAIN 565 992 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 611 946 PROTEIN KINASE.
 FT NP_BIND 617 625 ATP (BY SIMILARITY).
 FT BINDING 645 645 ATP (BY SIMILARITY).
 FT ACT_SITE 814 814 BY SIMILARITY.
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 474 474 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 503 503 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 542 542 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 150 150 R -> A (IN REF. 2).
 FT CONFLICT 242 242 C -> S (IN REF. 2).
 FT CONFLICT 726 726 S -> F (IN REF. 2).
 FT CONFLICT 957 979 CIRTSLHPKQAAPQORGGRLAQ -> MYQNMGGNVPHEPS
 FT CONFLICT 983 983 IYQNRPLREASSEP (IN REF. 2).
 FT CONFLICT 983 983 R -> A (IN REF. 2).
 FT SEQUENCE 992 AA; 112639 MW; 407A087853372100 CRC64;

Query Match 100.0%; Score 5264; DB 1; Length 992;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALAQRDRRLLLVLSVILETVNQDLPIVKCVLISHENNNGSAGKPSRYMYRGS 60
 DB 1 MRALAQRDRRLLLVLSVILETVNQDLPIVKCVLISHENNNGSAGKPSRYMYRGS 60
 QY 61 PEDLOCTPRQSEGVVYEAATVEAEGSSITLQVLATPGDLSCLWYFKSSLCQPHFD 120
 DB 61 PEDLOCTPRQSEGVVYEAATVEAEGSSITLQVLATPGDLSCLWYFKSSLCQPHFD 120
 QY 121 LQNRGIVSMALNVTTQAGEYLLHIQSERANYTVLTVNVRTQTLVLRPRPKRMENQ 180
 DB 121 LQNRGIVSMALNVTTQAGEYLLHIQSERANYTVLTVNVRTQTLVLRPRPKRMENQ 180
 QY 181 DALLCISEGVPEPTVEVWLCSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
 DB 181 DALLCISEGVPEPTVEVWLCSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
 QY 241 ECTKLTFTIDLNOAPOSTLPQLFKVGEPLIRCKAIHVNHGFGLTWELEKALEEGSYFE 300
 DB 241 ECTKLTFTIDLNOAPOSTLPQLFKVGEPLIRCKAIHVNHGFGLTWELEKALEEGSYFE 300
 QY 301 MSTYGTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSQSALVTILEKGFINATSSQEEY 360

DB 301 MSTYGTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
 QY 361 EIDPYEKPCFSVRPKAYPRIRCTWIFSPQASPCBORGLEDGYSISKFDHKNKPGEIFY 420
 DB 361 EIDPYEKPCFSVRPKAYPRIRCTWIFSPQASPCBORGLEDGYSISKFDHKNKPGEIFY 420
 QY 421 AENDDAOFTKMTFLNIRKKPOVLANASASQASCSGSDGYPPLSWTWKCKSDKSPNCTEIEP 480
 DB 421 AENDDAOFTKMTFLNIRKKPOVLANASASQASCSGSDGYPPLSWTWKCKSDKSPNCTEIEP 480
 QY 481 EGVWNKKANRKFVQWVSSSTLNSEAGKLLVKKCAVNSMGTSCTIFLNSPGPPFFIQ 540
 DB 481 EGVWNKKANRKFVQWVSSSTLNSEAGKLLVKKCAVNSMGTSCTIFLNSPGPPFFIQ 540
 QY 541 DNISFYATIGLCLPFIIVLIVLI CHYKKQPRYSQLOMIQVTPLDNEYFYVDFRDVEY 600
 DB 541 DNISFYATIGLCLPFIIVLIVLI CHYKKQPRYSQLOMIQVTPLDNEYFYVDFRDVEY 600
 QY 601 DLKWEFPRENLEFGKVLGSGAGFVGMNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
 DB 601 DLKWEFPRENLEFGKVLGSGAGFVGMNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
 QY 661 SELKWMTHLGHNDINVLGACTLSGPVLIFFEYCCYGDLLNLYRSREKPHRTWTEIFK 720
 DB 661 SELKWMTHLGHNDINVLGACTLSGPVLIFFEYCCYGDLLNLYRSREKPHRTWTEIFK 720
 QY 721 EHPSSYPTFOAHSNNSMPGSRVOLHPPLDQSLGFGNSIHSEDEIEYENQKRLAESEE 780
 DB 721 EHPSSYPTFOAHSNNSMPGSRVOLHPPLDQSLGFGNSIHSEDEIEYENQKRLAESEE 780
 QY 781 EDNLVLTFFDLCLCPAYQVAKGMEFLPKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
 DB 781 EDNLVLTFFDLCLCPAYQVAKGMEFLPKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
 QY 841 SDSYVVRGNARLPVKWMAPESLPEGIYTIKSDVMSYGILLWEIFSLGVNVPYGPVVDAN 900
 DB 841 SDSYVVRGNARLPVKWMAPESLPEGIYTIKSDVMSYGILLWEIFSLGVNVPYGPVVDAN 900
 QY 901 FYKLIOGFKMEQPFYATGFIYFMQSWAFDSRKPSFNLTSFLGCOLAEAEACIRT 960
 DB 901 FYKLIOGFKMEQPFYATGFIYFMQSWAFDSRKPSFNLTSFLGCOLAEAEACIRT 960
 QY 961 SIHLPKQAAPOORGLRAQSPORQVKIHRERS 992
 DB 961 SIHLPKQAAPOORGLRAQSPORQVKIHRERS 992

RESULT 2
 FLT3_HUMAN
 ID FLT3_HUMAN STANDARD; PRT; 993 AA.
 AC P36888; Q13414;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FL cytokine receptor precursor [EC 2.7.1.112] (Tyrosine-protein kinase
 DE receptor FLT3) (Stem cell tyrosine kinase 1) (STK-1) (CD135 antigen).
 GN FLT3 OR STK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94119906; PubMed=7507245;
 RA Small D., Levenstein M., Kim E., Carow G., Amin S., Rockwell P.,
 RA Witte L., Burrow C., Ratajczak M.Z., Gewirtz A.M., Civin C.I.,
 RT "STK-1, the human homolog of Flk-2/Flt-3, is selectively expressed in
 RT CD34+ human bone marrow cells and is involved in the proliferation of
 RT early progenitor/stem cells.",
 RL Proc. Natl. Acad. Sci. U.S.A. 91:459-463(1994).
 RN [2]
 RP SEQUENCE FROM N.A.


```

Db 838 SDSNYVVRGNARLPVKWAPESLFEIYTTIKSDVMSYGILLWEIFSLGVNPPGIPVDAN 897
Qy 901 FYKLIQSGKQKQEPFYATEGYFWMQSCWAFDRKPSFNLTSFLGCOLAEAEAC--- 957
Db 898 FYKLIQNGFKQKQEPFYATEGYIYIMQSCWAFDRKPSFNLTSFLGCOLAEAEAYQN 957
Qy 958 -----IRTSIHLPKQAAPOQRG-GLRAQSPQRQVK 986
Db 958 VDCRVSECPHYQNRPPFSREMDLGLLSPOAQQVE 991

RESULT 3
KFMS FELCA
ID KFMS FELCA STANDARD; PRT; 980 AA.
AC P13369;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Macrophage colony stimulating factor I receptor precursor (CSF-1-R)
DE (EC 2.7.1.112) (Fms proto-oncogene) (c-fms).
GN CSF1R OR FMS.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=8907753; PubMed=2849512;
RA Woolford J., McAuliffe A., Rohrschneider L.R.;
RT "Activation of the feline c-fms proto-oncogene: multiple alterations
RT are required to generate a fully transformed phenotype.";
RL Cell 55:965-977(1988).
CC -!- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J03149; AAA30811.1; -
CC PIR: A31636; TVCTMD.
CC HSSP: P11362; IFGK.
CC InterPro: IPR007119; Euk_pkinase.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003598; Ig_C2.
CC InterPro: IPR003600; Ig_Like.
CC InterPro: IPR001824; Tyk_kinaseIII.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF00047; Ig; 3.
CC Pfam: PF00069; pkinase; 1.
CC ProDom: PD000001; Euk_pkinase; 2.
CC SMART: SM00410; IG like; 4.
CC SMART: SM00408; ICG2; 1.
CC SMART: SM00219; Tyrc; 1.
CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE: PS00109; PROTEIN KINASE TYR; 1.
CC PROSITE: PS00240; RECEPTOR TYR_KIN_III; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 19 POTENTIAL.

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FT CHAIN 20 980 MACROPHAGE COLONY STIMULATING FACTOR I
FT DOMAIN 20 509 RECEPTOR.
FT TRANSMEM 510 535 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 536 980 POTENTIAL.
FT DOMAIN 24 104 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 107 197 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 204 298 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 299 397 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 398 502 IG-LIKE C2-TYPE DOMAIN 4.
FT DOMAIN 579 908 IG-LIKE C2-TYPE DOMAIN 5.
FT NP_BIND 585 593 PROTEIN KINASE.
FT BINDING 613 613 ATP (BY SIMILARITY).
FT ACT_SITE 776 776 BY SIMILARITY.
FT DISULFID 42 84 POTENTIAL.
FT DISULFID 127 177 POTENTIAL.
FT DISULFID 224 278 POTENTIAL.
FT MOD_RES 807 807 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 45 45 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 94 94 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 275 275 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 410 410 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 490 490 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 980 AA; 108506 MW; 453CF661E97CF6FF CRC64;

Query Match 23.9%; Score 1258.5; DB 1; Length 980;
Best Local Similarity 32.7%; Pred No. 9.8e-77;
Matches 328; Conservative 168; Mismatches 353; Indels 153; Gaps 32;

Qy 75 TVYEATVEVAESGSIITQVLAATPGDLSCV-----W---VFKHSSIGCQPHFDLQNRG 125
Db 13 TAWHAQGVPIQSPGELVVEPGTITLRCVNGSVEMDGPISPHWNLDLDPSPSI----- 68
Qy 126 IVSMALINVTQAGEYLLHI-----QSERANYTVLTVNVRDQLYVL---RRPY----- 173
Db 69 ---LTTNNATFQNTGT---HCTEPNPGQGNATI-----HLVYKDPARPMKVLQAE 114
Qy 174 FRKMENODALL-CISEGVPEPTVEWLVLCSSHRECKEKGPAVVRKEEVLHFLCTDI-- 230
Db 115 VTVLEGQDALPLCL---LTPALB-----AGSVLRVGRVRLVQRTNYSFSGHGTTHK 166
Qy 231 -----RCCARNALGRECTKL-----FTIDLNQAPQSTL-PQLFLKV-GEPLWIRCK 274
Db 167 AKFTENHVYQCSAR-VDGRTVTSNGIWLKVQKDISGPATLTLEPAELVRIQGEAAQIVCS 225
Qy 275 AIHVNHGFGLTWELEDKALEBGSYFEMSTYSTNRTMIRILLAFVSSVGRNDTGYTTCSSS 334
Db 226 ASNIDVNFVSLRHGDTKL---TISQSQDFHDNRYQ-KVLTNLNDHVSFQDAGNYSCTAT 281
Qy 335 K---HPSQSALVTILEKGFNATSSQB-EYEIDPYEFCFSVRFKAYPRIRC-TWI---- 385
Db 282 NAMGNHSASWFRVRESAYLNLTSEQSLQVTVGKEKVDQVQVKEAYPGLSFNWYVLP 341
Qy 386 FSQASFPCEQRLGLEDGYSISKFCDC-----HKNKPGEYIFYAENDDAQFTKMTFLNIRKPK 441
Db 342 FSDYQDKLDFVTIKDTYRTSTLSLPRKSEAGRYSLARNAGGQNALTFELTLRYYPE 401
Qy 442 VLANASASQAS-----CSSDGYPLPSWTWKCKSDKSPNCTEB---IPEGVWNKANKRVFG 494
Db 402 VRVTMTLINGSDTLLCEASGYPQSPVTVVQCRSHTRCDDESAGLVLEDSHSEVLSQVDFH 461
Qy 495 QWVSSSTLNINSEACKGLLVKCCAYNSMGTSCETIFLNSPGFPFIQDNISFYATIGLC--- 552
Db 462 EVIVHSLAIGTLEHNRTYECRAFNFSVNGSSQTFWPISIGAHTQLPDELLETPVLLTQMS 521
Qy 553 -LPFIVVLVILVILCHYKQKQFRYESQLQMIQVTGPLDNEYFYVDPRDYEDYDLKWEPPREN 611

```


CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
CC 3-KINASE (PI3K).
CC CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; D45168; BAA08116.1; -.
CC DR HSSP; P11362; IFGK.
CC DR InterPro; IPR00719; Euk_pkinase.
CC DR InterPro; IPR003086; Ig_MHC.
CC DR InterPro; IPR003598; Ig_C2.
CC DR InterPro; IPR003600; Ig_Like.
CC DR InterPro; IPR001824; RTKinaseIII.
CC DR InterPro; IPR001245; Tyr_pkinase.
CC DR Pfam; PF00047; Ig; 1.
CC DR Pfam; PF00069; pkinase; 1.
CC DR ProDom; PD000001; Euk_pkinase; 2.
CC DR SMART; SM00410; IG_Like; 2.
CC DR SMART; SM00408; IGC2; 1.
CC DR SMART; SM00219; Tyrc; 1.
CC DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
CC DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
CC DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
CC DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
CC KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
CC KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
CC KW Immunoglobulin domain.
CC FT SIGNAL 1 22 POTENTIAL.
CC FT CHAIN 23 978 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
CC FT DOMAIN 23 521 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 522 544 POTENTIAL.
CC FT DOMAIN 545 978 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 590 939 PROTEIN KINASE.
CC FT BIND 596 604 ATP (BY SIMILARITY).
CC FT BINDING 624 624 ATP (BY SIMILARITY).
CC FT ACT_SITE 794 794 BY SIMILARITY.
CC FT MOD_RES 825 825 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
CC FT CARBOHYD 94 94 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 130 130 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 145 145 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 284 284 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 294 294 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 301 301 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 321 321 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 353 353 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 368 368 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 401 401 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 464 464 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 487 487 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT SEQUENCE 978 AA; 109722 MW; CA4D663F98205CA9 CRC64;
CC SQ
CC Query Match 23.2%; Score 1222.5; DB 1; Length 978;
CC Best Local Similarity 34.0%; Pred. No. 2.5e-74;
CC Matches 306; Conservative 145; Mismatches 319; Indels 131; Gaps 26;
CC
CC QY 134 VTE-----TQAGEYLLHLLQSERANVTYVLTNNVRDQ-LYVLRPRYFRKMNQALLCI-- 186
CC Db 83 ITEKAEATNTGNYTC----TNKGGSSSIYVFRDPEKFLIDLPLYGKEENDTLVRCPLT 139
CC QY 187 -----SEGVPPEP-TVEWVLCSSSHRESCKEAGPAVVRKEEVKLHFGTDIRC-- 232

Db 140 DPEVNTSLTGCCEKGLPKDLTFV-----ADPKAGITIRNVKREYHRL-----CLH 185
QY 233 CARNALGRE-CTKLFITDLNAQPOS-----TLQPLFKVGEPLWIRCKALHVNHFGLT 285
Db 186 CSANQKQKSMLSKKFTLKVRAAKAVPVSVSKTSYLLREGEFAVTCLIKDVSSVDSM 245
QY 286 WELEDKALEEGSYEMSTYSTNRTMIRILLAFVSVSGNDGYTCSSSKHPSQSALVTI 345
Db 246 WIKENSQOQRAQTKNSWHQDPSYLRQERLTISSARVNDGVPFCYANNVTFGSANVTIT 305
QY 346 LE---KGFINA-TSSQBEYEIDPYEKFCFSVRFKAYPR-IRCTWIFSOASFPCEORGLD 400
Db 306 LEVVDKGFINIFPMNTTVFVNDGENVDLVVEYAYPKPQHQIYMNRT----- 355
QY 401 GYSISKCDHK-----NKPGEYIFAENDDAQFTOMFTLINIRKK 439
Db 356 --STDKWDDYPKSESNIRYVNEHLHLRLKGTGGTYTFHVSNSDVNSVTFNVTNATK 413
QY 440 POVLANASA--SQASCSSDGYPLPSWTWKCKSDKSPNCTEEI-PEGVWKKANRKFVGOW 496
Db 414 PEILTHDLVNGMLQCVNAGPEPTIDYFCPTGTEQRCVSPVGPVDVQIQNSSVSPFKGL 473
QY 497 VSSSTLNMSEAGKGLLVKCCAYNSMGTSCTEIFLNSPGPPFFPIODN----- 542
Db 474 VVSTIDDDSTFKHNGTVECRAYNDVGKSSASF-----NPAFKGNKKEQIHAHTLFTPL 527
QY 543 ISFYATIGLCPLFIWLVILVILCHYKKQFVYESLOMT-QVTGPDLDNEYFYVDPRDYED 601
Db 528 IGFVIAAGLMCIFVMIL---TYKYLQKPMYEVQWVVVEING---NNYVYIDPTQLPYD 580
QY 602 LKWEFFRENLEFGKVLGSGAPGRVMNATAYGISKTGVSIQVAVKMLKEKADSCKEALMS 661
Db 581 HKWEFFRNRLSFGKTLGAGAFKGVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMS 640
QY 662 ELKMMTHLGHNDINVLGACTLSGPVYLIPEYCCYDGLNLYRSKRKPKHRTWTE---- 717
Db 641 ELKVLSYLGNHNMVNLGACTIGCTPLVITEYCCYDGLNLYRSKRKPKHRTWTE---- 700
QY 718 --TPKENFSFYPFOAHSNMM---PGSREVQLHPDLQSLSGFNGNSIHSEDELEYENQ 772
Db 701 VALYKLLHLSKESNCNSTNEYMDMKFVSYPVPTKAADK-----RRSARIGSYIRDTV 755
QY 773 KRLAEEEEEDLVLTFFEDLLCFAYQVAKMEFLFKSCVHRDLAARNLVTHGKVKVICD 832
Db 756 PAIMEDDELALDL---EDLLSFSYQVAKGMAFLASKNCIHRDLAARNLLTHGRTIKICD 812
QY 833 FGLARDILSDSSYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPPY 892
Db 813 FGLARDIKDSDNYVVGKGNARLPVKWMAPESLFNCVYTFESDVWSYGIFLWELFSLGSSPY 872
QY 893 PGIPVDANFYKLIOSGFMEQPPYATGIIYFVMSCHAFDSKRKPPSPNLTSLFCQCLAE 952
Db 873 PGMPVDSKFYKMIKEGFRMLSPHAPAEAMYDIMKTCWDADPLKPTFKQIQVLIEKQISE 932
QY 953 A 953
Db 933 S 933

RESULT 7
KFMS HUMAN STANDARD; PRT; 972 AA.
AC P07333;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Macrophage colony stimulating factor I receptor precursor (CSF-1-R)
DE (SC 2.7.1.112) (fms proto-oncogene) (c-fms) (CD115 antigen).
GN CSF1R OR FMS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89239490; PubMed=2524025;
 RA Hampe A., Shamoon B.M., Gobet M., Sherr C.J., Galibert F.;
 RT "Nucleotide sequence and structural organization of the human FMS
 RL proto-oncogene.";
 RN Oncogene Res. 4:9-17 (1989).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86175013; PubMed=2421165;
 RA Cousens L., van Beveren C., Smith A., Mitchell R.L.,
 RA Isacke C.M., Verma I.M., Ullrich A.;
 RT "Structural alteration of viral homologue of receptor proto-oncogene
 RL fms at carboxyl terminus.";
 RN Nature 320:277-280 (1986).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89261741; PubMed=2524648;
 RA Visvader J., Verma I.M.;
 RT "Differential transcription of exon 1 of the human c-fms gene in
 RL placental trophoblasts and monocytes.";
 RN Mol. Cell. Biol. 9:1336-1341 (1989).
 [5]
 RP SEQUENCE OF 1-16 FROM N.A.
 RX MEDLINE=86281820; PubMed=3525854;
 RA Wheeler E.F., Roussel M.F., Hampe A., Walker M.H., Fried V.A.,
 RA Look A.T., Rettemier C.W., Sherr C.J.;
 RT "The amino-terminal domain of the v-fms oncogene product includes a
 RL functional signal peptide that directs synthesis of a transforming
 RT glycoprotein in the absence of feline leukemia virus gag sequences.";
 RN J. Virol. 59:224-233 (1986).
 CC -!- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
 CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -!- DATABASE: NAME=PROW; NOTE=PROW 1:13-21 (2000);
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1999017666.g.htm".
 CC -----
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 CC -----
 DR EMBL; M25786; AAAS8421.1; -;
 DR EMBL; U63963; AAB51696.1; -;
 DR EMBL; M14002; AAB35849.1; -;
 DR EMBL; X03663; CAA27300.1; -;
 DR FIR; S08123; TVHUMD.
 DR HSSP; P11362; 1FGK.
 DR Genew; HGNC:2433; CSF1R.
 DR MIM; 164770; -;
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003086; Ig_MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR003600; Ig like.
 DR InterPro; IPR001824; RTKinaseIII.

DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; IG like; 3.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00219; TYRKG; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain; Repeat; Polymorphism.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 972 MACROPHAGE COLONY STIMULATING FACTOR I
 FT RECEPTOR.
 FT DOMAIN 20 512 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 513 537 POTENTIAL.
 FT DOMAIN 538 972 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 24 104 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 107 197 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 204 298 IG-LIKE C2-TYPE DOMAIN 3.
 FT DOMAIN 299 399 IG-LIKE C2-TYPE DOMAIN 4.
 FT DOMAIN 400 505 IG-LIKE C2-TYPE DOMAIN 5.
 FT DOMAIN 582 910 PROTEIN KINASE.
 FT NP_BIND 588 596 ATP (BY SIMILARITY).
 FT BINDING 616 616 ATP (BY SIMILARITY).
 FT ACT_SITE 778 778 BY SIMILARITY.
 FT DISULFID 42 84 POTENTIAL.
 FT DISULFID 127 177 POTENTIAL.
 FT DISULFID 224 278 POTENTIAL.
 FT DISULFID 419 485 POTENTIAL.
 FT MOD_RES 699 699 PHOSPHORYLATION (AUTO-) (IN VITRO) (BY
 FT MOD_RES 708 708 SIMILARITY).
 FT MOD_RES 809 809 PHOSPHORYLATION (AUTO-) (IN VITRO) (BY
 FT MOD_RES 809 809 SIMILARITY).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 240 240 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 275 275 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 412 412 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 428 428 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 480 480 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 969 969 Y -> C (IN DBSNP:1801271).
 FT CONFLICT 54 54 /FTID=VAR_011953
 FT SEQUENCE 972 AA; 107983 MW; A8D99BE237573FE8 CRC64;
 SQ
 Query Match 23.2%; Score 1221.5; DB 1; Length 972;
 Best Local Similarity 32.5%; Pred No. 2.9e-74;
 Matches 330; Conservative 152; Mismatches 331; Indels 201; Gaps 33;
 QY 76 VYEAAATVEAESGSIITQVQLATPGDLSCLWFKHSSLGCOHPFDLQNRGIVSMAL--- 132
 DB 22 VIEPSVPELVVKGAT--VTLRGVNGSGVWDGPPS-----PHTLYSDG--SSSILSTN 72
 QY 133 NVTQTQAGEYLLHIQSERANYTVLTVNVRTQTLVLRPY-----FRKENQDALL-C 185
 DB 73 NATFQNTGTTRCTEPGDFGLGSSAAIHLYKDP-----ARPNVLAQEVVVFEDQDALLFC 127
 QY 186 ISEGVPEPTVEVWLCSHRESCKEEGPAVVRKEK-----VLHE---LF 226
 DB 128 L-----LTDPLV-----EAGVSLVVRGRPLMRHTNYSFSPWHGTHIRAKIQ 171
 QY 227 GTDIRCCARNALGRECTKLTFTIDLNQAPQSTLP-----QLFLKVGRLPWRCKAI 276

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Db 172 SDYQCSALMG-GR---KVMISIRLKVKQVIGPAPPALTLPVPAELVIRGEAAQIVCSAS 227
Qy 277 HVNHGGLTWELEDKALEESYEMSTYTNRTMIRILLAFVSSVGRNDGYTCSS-- 334
Db 228 SVDVNFDFVLOHNNTKL---AIPQSDFNHRVQ-KVLTLLNQDQVDFQHAGNYSVCASNV 283
Qy 335 --KHPQSALVTILEKGFINATSQB-EYEIDPYEKFCSVRFKAYPRIR-CTWIFSQAS 390
Db 284 QGKH-STSMFRVVEAYNLSEQNLIQEVTVGEGNLKVMVEAYPGLOGFNWY---- 338
Qy 391 FPCQRLGDEGYSISKPCDHKNK-----GEYIFVAEN 423
Db 339 -----LGFSDHQPEPKLANATTKOTYRHTFTLSLPRKPSAGRYSLARN 385
Qy 424 DDAQFTMTFLNTRKPOV-----LANASASQASDSDGYPLPSWTWKCKDSKSPNCTEE 478
Db 386 PGWRALTFTLTLYRPEVSVIWFINGSGT-LLCAASGYPPQPNVTWVLCQSGHGTDRDEA 444
Qy 479 IPEGVNVN---KKNRKFQGVWSSSTLNMSSEAGKLLLVKCCAYNSMGTSCTETIFLNSPG 534
Db 445 QVLQVNDPPYEVLSQEPFKVTVQSLTIVTELEHNOTYECRAHNSVSGSWAFIPISAG 504
Qy 535 PFPPIQDNISFYATIGLC---LFPVIVLIVLCHKYKKQFRYSQLOMQIVTGLDNEYF 591
Db 505 AHTHPDDEFLTPVWVACMSIMALLLLLLLLYKQKPKYQVWVKIIE--SYEGNSYT 562
Qy 592 YVDFRYEYDLKWEFFRENLERGKVLGSGAFGRVMNATAGISKTGYISQVAVKMLKEKA 651
Db 563 FIDPTQLPYNERKEFFRNLIQFGKTLGAGAFGKVVEATAFGLGKEDAVLKVAVKMLKSTA 622
Qy 652 DSEKALMSLKMTHLGHNDHNVLLGACTLGGPVLYLFEYCCYGDLLNVLNRSKREKF 711
Db 623 HADEKALMSLKMHLGHEHNVLLGACTHGGPVLYLFEYCCYGDLLNVLNRSKREKF 680
Qy 712 HRTWTEIFKEHNFSSYPTFOAHNSNMPGSRVQLHPPLDQSGFNNGNSIHSDE----- 766
Db 681 -----AMLGP---SLSPQDPEGGVDYKNIHLEKKYVRD 712
Qy 767 -----IEYENQKLAEE---EEDLNVLTFEDLLCFAYOVAKGMFELEFK 808
Db 713 SGFSQGVDTYVEMRPVSTNSDSFSQDLKGDGRPLELRDLHFSQVAQGNFAFLASK 772
Qy 809 SCVHRDLAARNVLVTHGKVKVICDGLARILSDSSVYVRGNARLPVKVWAPESLFFGIY 868
Db 773 NCIRHDAARNVLVTHGVAKIGDGLARIDMDSNVIVKGNARLPVKVWAPESIFDCVY 832
Qy 869 TIKSDVMSYGILLWEIFSLGVPVPIVDANFYKLQSGFKMEQPPYATEGIYFVMSQC 928
Db 833 TVQSDVMSYGILLWEIFSLGVPVPIVDANFYKLQSGFKMEQPPYATEGIYFVMSQC 892
Qy 929 WAFDSKRPSFPNLTSLGQLAEAEACITSHLPKQAPQORGLRAQSPQ 982
Db 893 WALEPHTPTFOQICSLF--QEQAQEDRRERDYNLPSSS---RSGGSGSSSE 941

RESULT 8
KFMS_MOUSE STANDARD; PRT; 977 AA.
AC P0581; Q9DBH9;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Macrophage colony stimulating factor I receptor precursor (CSF-1-R)
DE (EC 2.7.1.12) (fms proto-oncogene) (c-fms).
GN CSF1R OR CSFMR OR FMS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88217329; PubMed=2966922;
RA Rothwell V.M., Rohrschneider L.R.;

```

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RT "Murine c-fms cDNA: cloning, sequence analysis and retroviral
RL expression.";
RN Oncogene Res. 1:311-324 (1987).
RP REVISIONS.
RA Rothwell V.M.;
RL Submitted (SEP-1988) to the EMBL/GenBank/DBJ databases.
RP REVISIONS.
RA MEDLINE=93181280; PubMed=8441691;
RL MEDLINE=93181280; PubMed=8441691;
RP REVISIONS.
RA "Reassessment of the murine c-fms proto-oncogene sequence.";
RL Nucleic Acids Res. 21:750-750 (1993).
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein N.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RP SEQUENCE OF 1-16 FROM N.A.
RX MEDLINE=93268269; PubMed=8497248;
RA Yue X., Favot P., Dunn T.B., Cassidy A.I., Hume D.A.;
RT "Expression of mRNA encoding the macrophage colony-stimulating factor
RT receptor (c-fms) is controlled by a constitutive promoter and tissue-
RL specific transcription elongation.";
RL Mol. Cell. Biol. 13:3191-3201 (1993).
RP AUTOPHOSPHORYLATION SITES.
RX MEDLINE=90258890; PubMed=2160591;
RA van der Geer P., Hunter T.;
RT "Identification of tyrosine 706 in the kinase insert as the major
RT colony-stimulating factor 1 (CSF-1)-stimulated autophosphorylation
RL site in the CSF-1 receptor in a murine macrophage cell line.";
RL Mol. Cell. Biol. 10:2991-3002 (1990).
CC -1- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1. IT IS A PROTEIN
CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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CC -----
CC EMBL; X06368; CAA29666.1; ALT SEQ.
CC EMBL; AK004947; BAB23691.1;
CC EMBL; S62219; -, NOT_ANNOTATED_CDS.
DR
DR
DR

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DR PIR,*S01880; TVMSMD.
 DR HSP; P11362; IFGK.
 DR MGD; MGI:1339758; CsfI.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR001824; RTK_kinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; IG_Like; 3.
 DR SMART; SM00408; IGG2; 1.
 DR SMART; SM00219; TyfK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 19
 FT CHAIN 20 977
 FT DOMAIN 20 511
 FT TRANSMEM 512 536
 FT DOMAIN 537 977
 FT DOMAIN 24 104
 FT DOMAIN 107 197
 FT DOMAIN 204 298
 FT DOMAIN 299 397
 FT DOMAIN 398 503
 FT DOMAIN 580 913
 FT NP_BIND 586 594
 FT BINDING 614 614
 FT ACT_SITE 776 776
 FT DISULFID 42 84
 FT DISULFID 127 177
 FT DISULFID 224 278
 FT DISULFID 417 483
 FT MOD_RES 697 697
 FT MOD_RES 706 706
 FT MOD_RES 807 807
 FT CARBOHYD 45 45
 FT CARBOHYD 73 73
 FT CARBOHYD 302 302
 FT CARBOHYD 335 335
 FT CARBOHYD 389 389
 FT CARBOHYD 410 410
 FT CARBOHYD 449 449
 FT CARBOHYD 478 478
 FT CARBOHYD 491 491
 FT CONFLICT 446 446
 FT CONFLICT 553 553
 FT CONFLICT 616 616
 FT CONFLICT 744 744
 FT CONFLICT 814 814
 SQ SEQUENCE 977 AA; 109178 MW; 7EDP8310CCF98906 CRC64;
 Query Match 23.2%; Score 1219; DB 1; Length 977;
 Best Local Similarity 33.6%; Pred. No. 4.4e-74;
 Matches 319; Conservative 148; Mismatches 327; Indels 154; Gaps 31;
 QY 78 EAATVEAESGSLTQVLATPGDLSCLWFKHSSSLGCPHFQDLQNRGIVSMALNVTET 137
 Db 36 ETVTLRCVNSGSEWD-----GPISPYWTLDPSGSS-----TLTRNATFK 77
 QY 138 QAGEY-LLHQSERANYTVLFTVNRVDTQLYV-----LRRPYFRMENQDALL-CIS 187
 Db 78 NTGYRTCELEDPWAGSTTI-----HLVVKDPAHWNLLAQEVTVWEGEAVLPCL- 128
 QY 188 EGVPEPTVEWLVCSHRESCKEGPAVRK-----EEKVLHFLGTDIRCC 233

Db 129 --ITDPALK-----DSVSLMEGRGQVLKRTVYFSPWRGFIIRKAKVL-----DSNTYVC 177
 QY 234 ARNALGRECTKL-FTIDLN-----QAQSTL-PQLFLKV-GEPLWIRCKAIHVNHGFLTW 286
 Db 178 KTMVNGRESTGTGLWLVKVRVHPPEPPQIKLEPSKLVIRGEAAQIVCSATNAEAVGNVIL 237
 QY 287 ELEDKALE--EGSYFEMSTYSTNRTMIRILLAFVSSVGRNDTGYTC-SSSKHPSQALV 343
 Db 238 KRGDTKLEIPLNSDFQDNYKKVRAL-----SLNAVFDQDAGIYSCVASNDVGRITATM 291
 QY 344 T--ILEKGFINATSSQE--EYIDPYEKFCFSVRKAYPRIR--CTWIFSOASPFCEORGLE 399
 Db 292 NFQVVEGAYLNLTSQSLQEVSGDSLLITVHADAYPSIQHYNNWTYLGPFPE-DQKLE 350
 QY 400 -----DGYISIKPCDH--KNKPGEYIFYAENDDAQFTKMTNLIRKPKQVLANASQ 450
 Db 351 FITORAIYRYTFLKLVNRVKASEAGQYFLMAQNKAQNNLTFELTLRYPPEVSVTMPVN 410
 QY 451 AS-----CSSDGYPLPSTWTKKSDKSPNCTEIPGVVN-----KKANRKFVCGQWSSSTL 502
 Db 411 GSDVLFCDVSGYPOPSVTWMECRGHTDRCDQAQALQVWNDTHPEVLSQKPFQKVIQSQL 470
 QY 503 NMSEAGKGLLVKCCAYNSMGTSCTIFLNSPGPPFFIQDNISFYATIGLC---LPFIIVL 559
 Db 471 PIGTLKNNMTYFCKTHNSVGNSSQYFRAVSLGQSKQLPDESFTFPVVACMSVMSLLVLL 530
 QY 560 IVLICHYKQFRYESQLQMIQ-VTGPLDNEYFYVDREYDYLKWEPPRENLEFGKVLG 618
 Db 531 LLLLLYKQKPKYQVRWKIIEYEG---NSYTFIDPTQLPYNEKWEPPRNLLQFGKTLG 587
 QY 619 SGAGRVNATAYGISKGVSIQAVVMLKEKADSCKEALMSELKMMTHLGHHDNIVNL 678
 Db 588 AGAFKVVTEATAFGLGKEDAVLVKAVKMLKSTAHADKEALMSELKIMSHLGQHENIVNL 647
 QY 679 LGACTLSGPVYLIPCYCYGDLNLYRSKRE-----KPHRTWTEI 718
 Db 648 LGACTHGGPVLVITEYCCYCGDLLNLFRRKAEAMLGPSLSPGQDSEGDSSYKNIHLEKKYV 707
 QY 719 FKEHNFSSYPTFOAHSNMSMFGSREVQLHPPLDQLSGFGNGNSIHSEDEIEYENQKLABE 778
 Db 708 RRDGSGFS-----SQGVDTYVEMRPVSTSSDSFFKQD-----L 740
 QY 779 BEEDNLVLTFFDLICFAYOVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARD 838
 Db 741 DKEASRPLELDLHFFSQVAGMAFLASKNCIHRDVAARNVLLTSGHVAKIGDFGLARD 800
 QY 839 ILSDSSYVVRGNARLPVKWMAPESLFEGITYIKSDVWSYGILLWEIFSGVNPYGPYVD 898
 Db 801 IMNDSNVVVRGNARLPVKWMAPESLFDCVTVVQSDVWSYGILLWEIFSGVNPYGPYVD 860
 QY 899 ANFYKIQSGFMGPFPFYATYEGIFVMSQWAFDSKRKPSFENLTSFL 946
 Db 861 NKFYKLVKDGQMAQPVFAPKNIYSIMQSCWDLPTREPTFOQICFLL 908
 RESULT 9
 KIT_BOVIN
 ID_KIT_BOVIN STANDARD; PRT; 977 AA.
 AC P43481;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mast/stem cell growth factor receptor precursor (BC 2.7.1.112) (SCRP)
 DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
 GN KIT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=94215924; PubMed=7512939;
 RA Kubota T., Hikono H., Sasaki E., Sakurai M.;
 RT "Sequence of a bovine c-kit proto-oncogene cDNA";
 RL Gene 141:305-306(1994).
 CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
 CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC
 CC EMBL; D16680; BAA04084.1; --
 DR HSP; P11362; IFGK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003600; Ig-like.
 DR InterPro; IPR001824; TKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; IG-like; 2.
 DR SMART; SM00408; IGS2; 1.
 DR SMART; SM00219; TyrcK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 977 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
 FT DOMAIN 23 521 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 522 544 POTENTIAL.
 FT DOMAIN 545 977 CYTOPLASMIC (POTENTIAL).
 FT NP BIND 590 938 PROTEIN KINASE.
 FT BINDING 624 624 ATP (BY SIMILARITY).
 FT ACT SITE 793 793 BY SIMILARITY.
 FT MOD_RES 824 824 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 130 130 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 284 284 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 464 464 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 487 487 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 977 AA; 109685 MW; 4B2719050893B7EF CRC64;

Query Match 23.1%; Score 1215; DB 1; Length 977;
 Best Local Similarity 32.8%; Pred. No. 8.1e-74;
 Matches 304; Conservative 141; Mismatches 298; Indels 184; Gaps 28;

Qy 134 VTE-----TQAGEYLLHIQSERANVTVLFTVNRDQ--LYVLRPRYPFKMENQDALLCI-- 186
 Db 83 ITEKAEATNGNYTC---TNKGLSSSIYVVRDPEKFLDLIDLPYKGEENDTLVRCPDLT 139
 Qy 187 -----SEGVPBP-TVVEWVLCSSHRESCKEKGPAVVRKEKVLHFLGTDIRC-- 232
 Db 140 DPEVTNYSLTGCEGKPLPKDLTFV-----ADPKAGITIRNVKREYHRL-----CLH 185
 Qy 233 CARNALGRE-CTKLTFTIDLNOAPOS-----TLQPLFLKVGEPWIRCKALHVNHGFLGT 285
 Db 186 CSANQRGKSMLSKKFTLKVRAAIKAPVSVSKTSYLLREGEFAVTCCLIKDVSSVDMS 245
 Qy 286 WELLEDKALEEGSYEMSTYSTNRTMIRILLAFVSSVGRNDTGYTCSSSKHPSOSALVTI 345
 Db 246 WIKENSQOTKATQTKNSWHQGFSLRQERLITISARVNDSGVFCVYANNTFGSANVTIT 305
 Qy 346 LE---KGFINA-TSSQBEYEIDPYEKFCFSVRKAYPR-IRCTWIFSOASPCFQORGLD 400
 Db 306 LEVVDKGFINIFPMNMTTVFVNDGENVDLVVEYEAYPKPVHROMIYMRT----- 355
 Qy 401 GYSISKFCDDHK-----NKPGEYIFAENDDQAOTKQFTLNIRKK 439
 Db 356 --STDKNDDYPKSENEINIRYVNEHLHLRLKGTGEGTYTFHVSNSDVNSSVTFNYYVNTK 413
 Qy 440 POVLANASA--SQASCSGDGYPLPSWTWKCKSDKSPNCTEIEI-PEGVWKKANRKFVQW 496
 Db 414 PEILTHDLRVNGMLQCVAAAGPEPTIDWYFCGTQRCSVPVGVVDVQIQNSSVSPPFKL 473
 Qy 497 VSSSTLNMSEAGKGLLVKCCAYNSMGTS-----CETIFLNSPGPPFFI 539
 Db 474 VVYSTIDDSFPKHNGTVECRAYNDVGKSSASFPNPAFKNSKEQIHAHTLFT-----PIL 527
 Qy 540 QDNTSFVATIGLCLPFIIVLVILVILCHYKKQFRYESQLQMI-QVTGPDLDNEYFYVDFRDY 598
 Db 528 ---IGFVIAAGLMCIFVMIL---TYLQKPMYEVQVKVVEEING---NNVYIDPTQL 577
 Qy 599 EYDLKWEFPRENLEFGVLGSGAFGRVNMATAYGTSKGTGVIQVAVKMLKEKADSCKEA 658
 Db 578 PYDHKWEFPNRNLSFGKTLGAGAFGVKVEATAYGLIKSDAAMTVAVRMLKPSAHLTEREA 637
 Qy 659 LMSCLKMWHTHLGHHDNI VNLGACCTLSGPVYLIPEYCCYGDLLNLYRSKRKFKHRTWTET 718
 Db 638 LMSCLKVLSYLGNNHNI VNLGACTIGGTLVITEYCCYGDLLNLYRKRKDSF----- 690
 Qy 719 FKEHNFSSYPTFOAHSNMPGSRVQLHPDLQDLSGNGNSIHSEDEI-----EYBNQ 772
 Db 691 -----ICSKQEDHAEVALYK-----NLLHSKSSCNDSTNEYMDM 725
 Qy 773 K-----RLAEEBEEDLN-----VLTFFDLCCFAYQVAKGMEPLE 806
 Db 726 KPGVSYYVPTKADKRRSARISYIERDVTPTAIMEDEDELDLLEDSFSYQAKGMFLA 785
 Qy 807 FKSCVHRDLAARNVLVTHGKVKVVICDFGLARDILSDSSVYVVRGNARLPVKWMAPESLPEG 866
 Db 786 SKNCIHRDLAARNILLTHGRITKICDFGLARDIKNDSSVYVVRGNARLPVKWMAPESSIFNC 845
 Qy 867 IYTIKSDVMSYGILLWEIFSLGVNYPYGPVDPANPYKLIQSGFKMEQPFYATGYFVWQ 926
 Db 846 VYTFESDVMSYGIPLWELFSLGSSPYGPMVDSKPYKMKEGFRMLSPHAPAEYDIMG 905
 Qy 927 SCWAFDSKRPSPFNLTSLFLGCOLAEA 953
 Db 906 TCWDADPLKRPTFKQIVQLIEKQISES 932
 RESULT 10
 KPMS_RAT
 ID KPMS_RAT STANDARD; PRT; 978 AA.
 AC Q00495;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Macrophage colony stimulating factor I receptor precursor (CSF-1-R)

(EC 2.7.1.112) (fms proto-oncogene) (c-fms).

DE CSF1R OR CSFMR OR FMS.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=Wistar; Tissue=Skeletal muscle;
RA MEDLINE=93001225; PubMed=1389227;
RX Borycki A.G.; Gulliver M.; Leibovitch M.P.; Leibovitch S.A.;
RT "Molecular cloning of CSF-1 receptor from rat myoblasts. Sequence
analysis and regulation during myogenesis.";
RL Growth Factors 6:209-218(1992).
CC -!- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC entities requires a license agreement (see <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X61479; CAA43706.1; -
DR PIR: S16385; S16385.
DR HSP; P11362; IFCG.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR001820; R_KinaseIII.
DR InterPro: IPR001824; R_KinaseIII.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00047; Ig; 4.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 2.
DR SMART: SM00410; IG_Like; 3.
DR SMART: SM00408; IG2; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE: PS00240; RECEPTOR TYR KIN III; 1.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 978 MACROPHAGE COLONY STIMULATING FACTOR I
FT RECEPTOR.
FT
FT DOMAIN 20 511 EXTRACELLULAR (POTENTIAL).
FT TRANSMB 512 536 POTENTIAL.
FT DOMAIN 537 978 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 24 104 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 107 197 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 204 298 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 299 397 IG-LIKE C2-TYPE DOMAIN 4.
FT DOMAIN 398 503 IG-LIKE C2-TYPE DOMAIN 5.
FT DOMAIN 580 914 PROTEIN KINASE.
FT NP_BIND 586 594 ATP (BY SIMILARITY).
FT BINDING 614 614 ATP (BY SIMILARITY).
FT ACT_SITE 776 776 BY SIMILARITY.
FT
FT DISULFID 42 84 POTENTIAL.
FT DISULFID 127 177 POTENTIAL.
FT DISULFID 224 278 POTENTIAL.
FT DISULFID 417 483 POTENTIAL.
FT MOD_RES 697 697 PHOSPHORYLATION (AUTO-) (IN VITRO)

FT	MOD_RES	706	706	(BY SIMILARITY). PHOSPHORYLATION (AUTO-) (IN VIVO)
FT	MOD_RES	807	807	(BY SIMILARITY). PHOSPHORYLATION (AUTO-) (IN VITRO)
FT	CARBOHYD	45	45	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	73	73	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	302	302	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	335	335	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	389	389	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	410	410	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	449	449	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	478	478	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	491	491	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	978 AA; 109264 MW; 0A68456EF56BC7E3 CRC64;		

Query Match 23.0%; Score 1210; DB 1; Length 978;
Best Local Similarity 33.5%; Pred. No. 1.8e-73;
Matches 318; Conservative 147; Mismatches 329; Indels 154; Gaps 31;

QY 78 EAATVEVAESGSITLQVOLATPGDLSCLWVFKHSSILGCPHPDLQNRGIVSMALLNVTTET 137
DB 36 ETVTLRCVNSGVEMD-----GPISPYWTLDPSPGS-----TLTRNATFK 77

QY 138 QAGEY-LLHIQGERANYTVLFTVNRDITLYV-----LRRPYPRKMNODALL-CIS 187
DB 78 NTGYRCTELEDPMAGSTI-----HLYVKDPAHSNNLLAQEVTVVEGQEAVALPCL- 128

QY 188 EGVPEFTVEWLVCSSHRESCKEGPAVVRK-----EBKVHLHELFGTDIROC 233
DB 129 --ITDPALK-----DSVSLMREGGRQVLRKTVVFFSAMRGFIIRKAKVL-----DSNTYVC 177

QY 234 ARNALGRECTKL-FTIDLN-----QAQOSTL-PQLFLKV-GEPLWIRCKAIHVNHGGLTW 286
DB 178 KTMVNGRESTGTGILWKNRVHPPEPQIKLEPSKLVIRGEAAQIVCSATNAEVGNVIL 237

QY 287 ELEDKALE--EGSPEMSTYSTNRMTWIRILLAFVSSVGRNDTGYTC-SSSKHPSOSALV 343
DB 238 KRGDTKLEIPINSDFQDNVYKKVRL-----SLNAVDFQDAGIYSCVASNDVGTATM 291

QY 344 T--ILEKGFINATSQE-EYIDPYVEKFCFSVRKAYPRIR-CTWIFSOASPFCEORGLE 399
DB 292 NFQWVESAYLNTLSEQLQEVSVGDSLTLTVHADAPSIQHYNTVYLGPFPE-DQKLE 350

QY 400 -----DGYSISKCDH--KNKPGEYIFYAENDDAQFTMTFLNIRKPKOVLANASQ 450
DB 351 FITORAIYRYTFKLFLNRVKASEAGQYFLMAQNKAGMNNLTPELTLYRPEVSVTMVNVN 410

QY 451 AS---CSSDGYPLPSWTWKCKSDKSPNCTEIPGVWN-----KANRKYFGOWVSSSTL 502
DB 411 GSDVLFCDVSGIPQPSVTWMECRGHTDRCDQAALQVWMDTHEVLSQKPFDFKVIQSOL 470

QY 503 NMSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGPPFPFIQDNISFYATIGLC---LPFIIVL 559
DB 471 PIGTLKHNWYTFCKTHNSVGNSSQYFRAVSLGSKQLPDESFTPVVAVMSVMSLLVLL 530

QY 560 IVLI CHYKKQPRYESQLQMIQ-VTGPLDNEYVDYDRYEDYDLKWEFFPRENLEFGKVLG 618
DB 531 LLLLLLYKKQPKYQVRWKIERYEG---NSYTFIDPTQLPYNEKWEFFPRNNLQFGKTLG 587

QY 619 SGARGRVMNATAGISKTGVSIOAVKMLKEKADSCKEALMSLKMTHLGHHDNIVNL 678
DB 588 AGAFGKVEATAFGLGKEDAVLKVAVMKLTAKHADEKALMSLKMTHLGHHDNIVNL 647

QY 679 LGACTLSGPGVLIIFYCCYGDLLNLYRSKRE-----KEHRTWTEI 718
DB 648 LGACTHGGFVLVITEYCCYGDLLNLYRSKRE-----KEHRTWTEI 707

QY 719 FKEHNPSSYPTFOAHNSMPCGSRVQLHPPLDQLSGFNGNSIHSDEIEYENQKLAEE 778
DB 708 RRDSGFS-----SQGVDTVVMRPSVSTSSSDSPFKQD-----L 740

QY 779 EEDLNVLTFEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARD 838


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Db 741 DKPSRPLELDLHFSQVQAQAFASKNCIHRDVAARNVLLTSGHAKIGFGLARD 800
QY 839 ILSDSSVYVRGNARLPVKWMAPESEFEGIIYTKSDVMSYGILLWEIPSLGNVPYGPVD 898
Db 801 IMDSNTVYVKGARLPVKWMAPESEFEGIIYTKSDVMSYGILLWEIPSLGNVPYGPILVN 860
QY 899 ANFYKLQSGFKMOPPFYATSGIFVWOSCFADSPKSPNLTSLF 946
Db 861 NKFYKVLKGYQMAQPVAPKPNYISIMOSCWDLBETPRTTQQICFL 908

RESULT 11
KIT_CANFA STANDARD; PRT; 975 AA.
AC Q97799;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN KIT.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99142897; PubMed=9989791;
RA Ma Y., Longley B.J., Wang X., Blount J.L., Langley K., Caughey G.H.;
RT "Clustering of activating mutations in c-KIT's juxtamembrane coding
region in canine mast cell neoplasms.";
RL J. invest. Dermatol. 112:165-170(1999).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
CC 3-KINASE (PI3K).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL; AF04249; AAD02327.1; -.
DR HSSP; P11362; IFGK
DR InterPro; IPR00719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00410; IG like; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; RECEPTOR_TYR_KIN_III; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;

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KW Immunoglobulin domain.
PT SIGNAL 1 24
PT CHAIN 25 975
PT DOMAIN 25 519
PT TRANSMEM 520 542
PT DOMAIN 543 975
PT DOMAIN 588 936
PT NP_BIND 594 602
PT BINDING 622 622
PT ACT_SITE 791 791
PT MOD_RES 822 822
PT CARBOHYD 96 96
PT CARBOHYD 132 132
PT CARBOHYD 147 147
PT CARBOHYD 286 286
PT CARBOHYD 296 296
PT CARBOHYD 303 303
PT CARBOHYD 355 355
PT CARBOHYD 370 370
PT CARBOHYD 403 403
PT CARBOHYD 466 466
PT CARBOHYD 489 489
SQ SEQUENCE 975 AA; 109335 MW; 8F570BDB9P05B1CB CRC64;

Query Match 22.9%; Score 1207; DB 1; Length 975;
Best Local Similarity 31.9%; Pred. No. 2.8e-73;
Matches 330; Conservative 165; Mismatches 375; Indels 166; Gaps 34;

QY 31 LPVTKCVLISHENNGSAGKPSVYMRVGRSPEDLOCTPRRQSEGTVEYAATVEVAESGSI 90
Db 11 LCVLLLLLLLVGTGSS--QPS-----VSPCEPLPSIHPAKSELIVSVDG- 54
QY 91 TLQVLATPGDLSCLVKPHSSLGCPHFDLQNRGIVSMALNVTTQAGEYLLHIQSER 150
Db 55 ELRLSCTDGFVK--WTFE--TLG-QLNENTHNEITEKA-----BAGTGNVTCNR 102
QY 151 ANYTVLFTVNRD--TQLVLRPPYPRKMNQDALLCISGVPEPTVWVLCSSHRESCKE 209
Db 103 DGLRSIYVVRDPAKFLVDLPYKRGNDTLVRC-----PLTDPVTVNYSURGC-- 153
QY 210 EGPAVVRKEEVKLHFLGTDIR-----C--CARNALGRE-CTKLTITDLNQAPOS- 256
Db 154 BGKPLKDLTFAVDPKAGITIRNVKREYHRLCHCSADQKGTVLSKFTLVKRAIRAV 213
QY 257 -----TLPQLFLKVEPELWIRCKAIHVNHGFLTWELEDKALEEGSYFEMSTYSNRTM 311
Db 214 PWSVSKTSSLKEGEAPSVCMCFIKDVSSFVDSMMIKENSQQTNQAQTSNSWHHGDNFEE 273
QY 312 RILLAFVSSVGRNDTYTCSSSKHPSQSALVTILE---KGFINA-TSQEEYEIDPYEK 367
Db 274 ROEKLIISSARVNSDGVPMCVANNTFGSANVTTLLEVVDKGFINIFPMSTTIFVNDGQN 333
QY 368 PCFSVRPKAYPR-IRCTWIFSQASF--PCEQRGLDGYISIKFCDH-----KNKPGY 417
Db 334 VDLIVEEAYPKPHEQWIYNNRTFDKWDYPKSDNESIRYVSELHLTRLKGNEGGTY 393
QY 418 IFYAENDDAQFTKMTLNIRKKPQVLANASQA--SCSSDGYPLPSMTWKCKSDKSPNC 475
Db 394 TFOVNSDVNSSVTFNVYVNTKPEILTHESLTNGMLQCVCVAGPEPAVGWYFCPGAEOQC 453
QY 476 TEEI-PEGVWNNKANRKYVQGWVSSSTLNMSEAGLLVKCCAYNSMGTSCTETPLNSPG 534
Db 454 SVPIGPMQVQNSSLSPSGKLWVQSSIDYSAFKNGTVECRAYNNVGRS--SAFNF--- 508
QY 535 PPFIQDNISFYATIGLCPLPIV-----VLIVLICHKKYKQFRYESOLOMI-QVTGPD 587
Db 509 -FAKEQIHPHTLTPPLIGFVIAAGMMCIIVMILTYKYLQKPMYEVQWKVEEING--- 564
QY 588 NEFYVDFRDYEYDLKWEFFPRENLEFGKVLGSGAFGRVNNATAYGISKTGVSIQAVKML 647
Db 565 NNYVYIDTQLPYDHKWEFFPRNRLSFGKTLGAGAGKVVVEATAYGLIKSDAAMTAVAKML 624
QY 648 KEKADSCKEALMSLKQWTHLGHIDNIVNLIGACTLSGPVYLIFFEYCCYDGLLNLRSK 707

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Db 625 KPSAHLTEREALMSELKVLVSYLGNHNVLLGACTVGGPTLVITEYCCYGLNFLRRK 684
 QY 708 REXFHRWTWTFIKREHNFSSYPTQAHNSNMPGSRVQLHPPLDLQSLGFGNCSHSDEI 767
 Db 685 RDSFICKQEQ---DHG-----EVALYK-----NLHSSKSS 712
 QY 768 -----EYENOK-----RLAEEDDLN-----VLTFEDLLCFA 795
 Db 713 CSDSTNEMDMKGVSVVPTKADKRSARIGSYIERDVTPTAIMEDDELALDLBLSFS 772
 QY 796 YQVAKMGFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDILSDSSYYVRGNARLPV 855
 Db 773 YQVAKMGFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDILSDSSYYVRGNARLPV 832
 QY 856 KWPAPESLFGIYTIKSDVMSYGLLWEISLGVNVPYGPVPDANFYKLQSGFKMQPFP 915
 Db 833 KWPAPESIFNCVYTFESDVMYSYGLFELFSLGSSPPYGPMPVDSKFKYKMKEGFRMLSP 892
 QY 916 YATEGIYFVMSQWAFDSRSPFNLSFLGCOLAEAEACIRTSIHLPKQAAPQORGG 975
 Db 893 HAPAEWDIMKTCDWADPLRPFKQVQLIEKQISDSTN-----HIYSNLAN----- 940
 QY 976 LRAQSPQORVQKIHRR 991
 Db 941 -CSPNPERPVVDHVR 955

RESULT 12
 KIT HUMAN
 ID KIT HUMAN STANDARD; PRT; 976 AA.
 AC P10721;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
 DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit) (CD117 antigen).
 GN KIT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Term placenta, and Fetal brain;
 RX MEDLINE=88111521; PubMed=2448137;
 RA Yarden Y., Kuang W.-J., Yang-Feng T., Coussens L., Munemitsu S.,
 RA Dull T.J., Chen E., Schlessinger J., Francke U., Ullrich A.;
 RT "Human proto-oncogene c-kit: a new cell surface receptor tyrosine
 RT kinase for an unidentified ligand.";
 RL EMBO J. 6:3341-3351(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93064697; PubMed=1279499;
 RA Giebel L.B., Strunk K.M., Holmes S.A., Spritz R.A.;
 RT "Organization and nucleotide sequence of the human KIT (mast/stem
 RT cell growth factor receptor) proto-oncogene.";
 RL Oncogene 7:2207-2217(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97179223; PubMed=9027509;
 RA Andre C., Hampe A., Lachaume P., Martin E., Wang X.P., Manus V.,
 RA Hu W.X., Galibert F.;
 RT "Sequence analysis of two genomic regions containing the KIT and the
 RT FMS receptor tyrosine kinase genes.";
 RL Genomics 39:216-226(1997).
 RN [4]
 RP VARIANT LYS-583.
 RX MEDLINE=92291284; PubMed=1376329;
 RA Fleischman R.A.;
 RT "Human piebald trait resulting from a dominant negative mutant allele
 RT of the c-kit membrane receptor gene.";
 RL J. Clin. Invest. 89:1713-1717(1992).

RN [5]
 RP VARIANT LEU-584.
 RX MEDLINE=92133600; PubMed=1370874;
 RA Spritz R.A., Giebel L.B., Holmes S.A.;
 RT "Dominant negative and loss of function mutations of the c-kit
 RT (mast/stem cell growth factor receptor) proto-oncogene in human
 RT piebaldism.";
 RL Am. J. Hum. Genet. 50:261-269(1992).
 RN [6]
 RP VARIANT ARG-664.
 RX MEDLINE=92020918; PubMed=1717985;
 RA Giebel L.B., Spritz R.A.;
 RT "Mutation of the KIT (mast/stem cell growth factor receptor)
 RT protooncogene in human piebaldism.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8696-8699(1991).
 RN [7]
 RP VARIANT VAL-816.
 RX MEDLINE=94013473; PubMed=7691885;
 RA Furutau T., Tsujimura T., Tono T., Ikeda H., Kitayama H.,
 RA Koshimizu U., Sugahara H., Butterfield J.H., Ashman L.K.,
 RA Kanayama Y., Matsuzawa Y., Kitamura Y., Kanakura Y.;
 RT "Identification of mutations in the coding sequence of the proto-
 RT oncogene c-kit in a human mast cell leukemia cell line causing
 RT ligand-independent activation of c-kit product.";
 RL J. Clin. Invest. 92:1736-1744(1993).
 RN [8]
 RP VARIANTS PIEBALDISM GLY-791 AND VAL-812.
 RX MEDLINE=9332624; PubMed=7687267;
 RA Spritz R.A., Holmes S.A., Itin P., Kuester W.;
 RT "Novel mutations of the KIT (mast/stem cell growth factor receptor)
 RT proto-oncogene in human piebaldism.";
 RL J. Invest. Dermatol. 101:22-25(1993).
 RN [9]
 RP VARIANT PIEBALDISM 893-GLU--PRO-896 DEL.
 RX MEDLINE=96287384; PubMed=8680409;
 RA Riva P., Milani N., Gandolfi P., Larizza L.;
 RT "A 12-bp deletion (7818del12) in the c-kit protooncogene in a large
 RT Italian kindred with piebaldism.";
 RL Hum. Mutat. 6:343-345(1995).
 RN [10]
 RP VARIANT GIST VAL-559 DEL.
 RX MEDLINE=98361155; PubMed=9697690;
 RA Nishida T., Hirota S., Taniguchi M., Hashimoto K., Isozaki K.,
 RA Nakamura H., Kanakura Y., Tanaka T., Takabayashi A., Matsuda H.,
 RA Kitamura Y.;
 RT "Familial gastrointestinal stromal tumours with germline mutation of
 RT the KIT gene.";
 RL Nat. Genet. 19:323-324(1998).
 CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
 CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DISEASE: DEFECTS IN KIT ARE THE CAUSE OF A DEVELOPMENTAL
 CC ABNORMALITY KNOWN AS PIEBALDISM. AN AUTOSOMAL DOMINANT GENETIC
 CC DISORDER OF PIGMENTATION CHARACTERIZED BY CONGENITAL PATCHES OF
 CC WHITE SKIN AND HAIR THAT LACK MELANOCYTES.
 CC -1- DISEASE: DEFECTS IN KIT ARE THE CAUSE OF A GASTROINTESTINAL
 CC STROMAL TUMOR (GIST).
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD117 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd117.htm".
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/KITID127.html".
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DR	ENBL; X6182;	CAA29548.1;	-.
DR	ENBL; X69301;	CAA49159.1;	-.
DR	ENBL; X69302;	CAA49159.1;	JOINED.
DR	ENBL; X69303;	CAA49159.1;	JOINED.
DR	ENBL; X69304;	CAA49159.1;	JOINED.
DR	ENBL; X69305;	CAA49159.1;	JOINED.
DR	ENBL; X69306;	CAA49159.1;	JOINED.
DR	ENBL; X69307;	CAA49159.1;	JOINED.
DR	ENBL; X69308;	CAA49159.1;	JOINED.
DR	ENBL; X69309;	CAA49159.1;	JOINED.
DR	ENBL; X69310;	CAA49159.1;	JOINED.
DR	ENBL; X69311;	CAA49159.1;	JOINED.
DR	ENBL; X69312;	CAA49159.1;	JOINED.
DR	ENBL; X69313;	CAA49159.1;	JOINED.
DR	ENBL; X69314;	CAA49159.1;	JOINED.
DR	ENBL; X69315;	CAA49159.1;	JOINED.
DR	ENBL; X69316;	CAA49159.1;	JOINED.
DR	ENBL; U63834;	AAC50968.1;	-.
DR	PIR; S01426;	TVHUKT.	-.
DR	HSSP; P11362;	LFGK.	-.
DR	Genew; HGNC:6342;	KIT.	-.
DR	MIM; 164920;	-.	-.
DR	MIM; 172800;	-.	-.
DR	MIM; 606764;	-.	-.
DR	InterPro; IPR000719;	Euk_pkinase.	-.
DR	InterPro; IPR003006;	Ig_MHC.	-.
DR	InterPro; IPR003598;	Ig_c2.	-.
DR	InterPro; IPR001824;	RtKinaseIII.	-.
DR	InterPro; IPR001245;	Tyr_pkinase.	-.
DR	Pfam; PF00047;	Ig; 1.	-.
DR	Pfam; PF00069;	pkinase; 1.	-.
DR	ProDom; PD000001;	Euk_pkinase; 2:	-.
DR	SMART; SM00408;	IGC2; 1.	-.
DR	SMART; SM00219;	TyrcK; 1.	-.
DR	PROSITE; PS00107;	PROTEIN_KINASE_ATP; 1.	-.
DR	PROSITE; PS00109;	PROTEIN_KINASE_TYR; 1.	-.
DR	PROSITE; PS00240;	RECEPTOR_TYR_KIN_III; 1.	-.
DR	PROSITE; PSS0011;	PROTEIN_KINASE_DOM; 1.	-.
KW	Proto-oncogene; Tyrosine-protein kinase;	Receptor; Transmembrane;	-.
KW	Transferase; Glycoprotein; Phosphorylation;	ATP-binding; Signal;	-.
KW	Immunoglobulin domain; Disease mutation.	-.	-.
FT	SIGNAL	1	22
FT	CHAIN	23	976
FT	DOMAIN	23	520
FT	TRANSMEM	521	543
FT	DOMAIN	544	976
FT	DOMAIN	589	937
FT	NP_BIND	595	603
FT	BINDING	623	623
FT	ACT_SITE	792	792
FT	MOD_RES	823	823
FT	CARBOHYD	130	130
FT	CARBOHYD	145	145
FT	CARBOHYD	283	283
FT	CARBOHYD	293	293
FT	CARBOHYD	300	300
FT	CARBOHYD	320	320
FT	CARBOHYD	352	352
FT	CARBOHYD	367	367
FT	CARBOHYD	463	463
FT	CARBOHYD	486	486
FT	VARIANT	559	559
FT	FTId=VAR_007965.	-	-
FT	VARIANT	583	583
FT	F -> K (IN PIBALDISM).	-	-
FT	FTId=VAR_004104.	-	-
FT	VARIANT	584	584
FT	F -> L (IN PIBALDISM).	-	-
FT	FTId=VAR_004105.	-	-
FT	VARIANT	664	664
FT	G -> R (IN PIBALDISM).	-	-

FT	VARIANT	791	791	/FTID=VAR_004106.
FT				R -> G (IN PIEBALDISM).
FT				/FTID=VAR_004107.
FT	VARIANT	812	812	G -> V (IN PIEBALDISM).
FT				/FTID=VAR_004108.
FT	VARIANT	816	816	D -> V (IN RAST CELL LEUKEMIA, CONSTITUTIVELY ACTIVATED).
FT				/FTID=VAR_004109.
FT	VARIANT	893	896	MISSING (IN SEVERE PIEBALDISM).
FT				/FTID=VAR_004110.
FT				/FTID=VAR_004111.
FT				/FTID=VAR_004112.
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FT				/FTID=VAR

Db 779 GMAFLASNCNCHRLAARNILLTHGRITKICDGLARDIKDSDNSVVKGNARLPVKWMAP 838
 Qy 861 ESLPEGIYTIKSDVWSGILLWEISLGVNPGIPVDANFVKLIQSFKWEQPPYATEG 920
 Db 839 ESIFNCVITFSDVWSYGIFLWELFSLGSSYPGPNVDSPKMIKEGFRMLSPHAPAE 898
 Qy 921 IYFVQSCWAFDSRKRPFPNLTSPLGQLAEB 953
 Db 899 MYDINKTCWDADPLKRPFTFKQIVOLIEKQISES 931

RESULT 13
 KIT_CHICK STANDARD; PRT; 960 AA.
 AC Q08156; 1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mast/stem cell growth factor receptor precursor (BC 2.7.1.112) (SCFR)
 DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
 GN KIT.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=White leghorn; TISSUE=Brain;
 RX MEDLINE=9329295; PubMed=7685729;
 RA Sasaki E., Okamura H., Chikamune T., Kanai Y., Watanabe M.,
 RA Naito M., Sakurai M.;
 RT "Cloning and expression of the chicken c-kit proto-oncogene.";
 RL Gene 128:257-261 (1993).
 CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
 CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: HIGH IN THE BRAIN AND TESTES AND ALSO
 CC PRESENT IN THE BURSA OF FABRICIUS, HEART, KIDNEY, LUNG, SPLEEN
 CC THYMUS AND OVARY.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC use by non-profit institutions as long as its content is in no way
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DR EMBL; D13225; BAA02506.1; -.
 DR PIR; JN0677; JN0677.
 DR HSSP; P11362; 1FGK.
 DR InterPro; IPR00719; Euk_pkinase.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; ig; 3.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00408; IGG2; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain.
 FT SIGNAL 1 24
 FT CHAIN 25 960
 FT DOMAIN 25 505
 FT TRANSMEM 506 530
 FT DOMAIN 531 960
 FT DOMAIN 575 913
 FT NP_BIND 581 589
 FT BINDING 609 609
 FT ACT_SITE 777 777
 FT MOD_RES 808 808
 FT CARBOHYD 76 76
 FT CARBOHYD 135 135
 FT CARBOHYD 149 149
 FT CARBOHYD 269 269
 FT CARBOHYD 286 286
 FT CARBOHYD 306 306
 FT CARBOHYD 318 318
 FT CARBOHYD 338 338
 FT CARBOHYD 343 343
 FT CARBOHYD 356 356
 FT CARBOHYD 453 453
 FT CARBOHYD 469 469
 FT SEQUENCE 960 AA; 107311 MW; 0E93850527AB68F6 CRC64;

Query Match 22.4%; Score 1181; DB 1; Length 960;
 Best Local Similarity 31.8%; Pred. No. 1.5e-71;
 Matches 310; Conservative 159; Mismatches 356; Indels 150; Gaps 30;
 Qy 45 GSSACKPSYMRVGRSPEDLOCTPRQSEGVYEAATVEAEGSITLQVOLATPGDLSC 104
 Db 24 GSPHEESSLVNKGELRLKCN-----EEGPTWTFQNSDPSAKR 65
 Qy 105 L-----WYFKSSLCQPHFOLQNRGIVSMALNVTETQAGEYLLHIQSERANYTVLFTV 159
 Db 66 ISNEKEWTKATRIDIGRECKSG-----SIVN-----SFYV 99
 Qy 160 NVRTQLVLRPRYFRKMENODALLCISEGVEPTVEWVLCSHRESCKEGBAVVRKEE 219
 Db 100 FVKDPNVLFVDSLIYKEDSDILLVCPDTPD-VLNFTLRKCDGKPLPKNTWFIENPQK 158
 Qy 220 ----KVLHELFGTDIRCCAR-NALGRECTKLTIDINQAP-OSTLPOL-----FLKVG 266
 Db 159 GIITKNVQSFKGYCQCLAKNGVEKISEHIF--LNRPVHKALPVIITLSKSYELLKEG 215
 Qy 267 EPLWIRCKAIHVNHGFLTWLEDKALBEGSYFEMSTYSTNRTMIRILLAFVSSVGRNDT 326
 Db 216 EEFVTCIITVDSSVKASWISYKSAIVTSKRNLDGYERK-----LTNRSVGUNDS 271
 Qy 327 GYITCSSKHP--SQSALVTI--LEKGFINTASOE-EYEIDPYEKFCFSVRFPKAYPRIR 381
 Db 272 GEFTC-QAENPFKGTNAVTLLAKAGFVRLPATWNTTIDINAGONGNLTVEAYPK-- 328
 Qy 382 CTWIFSQASFCEORGLDEGYSISKFDHKNK-----PGEYIF 419
 Db 329 -----PKEEVMYMNTELQNSDHYVFKTVGNNSYTSSELHLRLKGTGGGIYTF 378
 Qy 420 YAENDDAQFTKMTLNIRKKPOVLANASAQ--ASCSSDGYPLPSWTWKKCDKSPNCTE 477
 Db 379 FVNSDASSSTFNVVYVKTKPEILTDLMDLGNLDIOCVATGFPATYIYWFPGTEORCLD 438
 Qy 478 E---IPEGVWNNKANRKY--FGQWVSSSTLNMSEAGKGLLVKCCAYNSMGTSCETIFLNS 532
 Db 439 SPTISPMDVKVSYTNSVSPSEFIRILVESTVNAS-NFKSTGTTCCEASSNGDK-SSVFFNF 496
 Qy 533 PGPPFFIQDNISFYA-----TIGLCLEFFIVLVILVILCHKKYKQFRYESQQLMI-QVTG 584
 Db 497 A-----IKEQIRTHLTFTPLLIAGFAAGLMCIIVMLWYIYLQPKYBQVQWKEING 551
 Qy 585 PLDNEYFYVDFRDYEDLKWEPFRENLEFGKVLGSGAFGRVNNATAYGISKTVGSVQIAV 644

Db 552 ---NNYVVIDTQTPYDHKWEFFRNRLSFGKTLGAGAFGKVVETATAGLFKSDAMTVAV 608
Qy 645 KMLKEKADSCKEALMSLKMTHLGHHDNINVLGLACTLSGPPVLLIFCYCCYGDLLNLYL 704
Db 609 KMLKPSAHLTEREALMSLKYLYGNHININVLGLACTIGPTLVITEYCYGDLLNLYL 668
Qy 705 RSKREKP-----HRTWTE--IPKEHNFSSYPTFOA-HNSNMPGSGREVQLAPLQDLSGFN 757
Db 669 RKRKDSFTCPKHEEAAVYENLLHQAEPTADAVNEMDMKPGVSYAVPPKADKGRPVK 728
Qy 758 GNSIHSEDEIEYENOKRLAEEEDLNLVLTEDLLCFAYQVAKMEFLERKSCVHRDLAA 817
Db 729 SGS-----YTDQVTLMEDELALDVEDLLSFSYQVAKGMSFLASKVCHIRDLAA 780
Qy 818 RNLVTHGKVKIKIDFGGLARDILSDSSVVRGNARLPVKWMAPELFEGIYTIKSDVMSY 877
Db 781 RNLITLTHGRITKICDFGLARDIRNDSNVVKGARLPVKWMAPELFEIYTIKSDVMSY 840
Qy 878 GILLWEIPSLGVNYPGIPVDANFYKLIQSGFKMEQPPYATEGIYFVMSQWAFDSRKR 937
Db 841 GILLWEIPSLGVNYPGIPVDANFYKLIQSGFKMEQPPYATEGIYFVMSQWAFDSRKR 900
Qy 938 SFPNLTSLFLGCOLAE 952
Db 901 TFKQIVQIEQOLSD 915

RESULT 14
KIT_FELCA
ID KIT_FELCA STANDARD; PRT; 978 AA.
AC Q28889;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN KIT.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=95140426; PubMed=7530827;
RA Herbst R., Munemitsu S., Ullrich A.;
RT "Oncogenic activation of v-kit involves deletion of a putative
tyrosine-substrate interaction site.";
RL Oncogene 10:369-379(1995).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
CC 3-KINASE (PI3K).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
PROTEIN KINASES
CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC
CC EMBL; S76596; AAB33207.1; -
DR HSPF; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR001824; RtkinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG_2.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00219; TyfK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 978 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
FT DOMAIN 23 521 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 522 544 POTENTIAL.
FT DOMAIN 545 978 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 590 938 PROTEIN KINASE.
FT NP_BIND 596 604 ATP (BY SIMILARITY).
FT BINDING 624 624 ATP (BY SIMILARITY).
FT ACT_SITE 793 793 BY SIMILARITY.
FT MOD_RES 824 824 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 464 464 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 487 487 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 978 AA; 109449 MW; 6D45472E07440B6B CRC64;

Query Match 22.4%; Score 1178.5; DB 1; Length 978;
Best Local Similarity 31.6%; Pred. No. 2.3e-71;
Matches 313; Conservative 162; Mismatches 373; Indels 143; Gaps 30;

Qy 36 CVLISHENNGSSAGKPSYRMVGRSGPEDLQCTPRQSGTGYEATVVAESGSLTQVQ 95
Db 12 CVLLLLRVQTGSSQPSA-----SPGWSLPSIH-PATSELIVSAGDEIRLL 57
Qy 96 LATPGDLSCLVFKHSSLCQPHFDLQNRGIVSMALNVETQAGEYLLHIQSERANYTV 155
Db 58 CTDFGVK--WTFE--TLG-QSSEITHNEWITEKA---EATNTGNYTC---TNGGGLSS 105
Qy 156 LFTVNVRD--TOLYLVRRPYFRKMENODALLCI-----SEGVPPEP----- 193
Db 106 SIYVVRDPAKFLVLDPLYGKEDHDTLVRCPLDPEVTNLSLRGCEGKPLPKDLTFVTD 165
Qy 194 -----TVEWVLCSSHR--ESCKEGPAPVVRKEEVLHFLFGTDIRCCARNALGRECTKLF 246
Db 166 PKAGITIRNVKREYHRLCLHCSAD-----RKGSVLSKKFTLKVRAAIR-----AVP 212
Qy 247 TIDLNAQAPQSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALBEGSFEMSTYST 306
Db 213 VVVSQASH-----LLREGEFFSYMCLIKDVSSSDVMWIKENSPOTNAQPQSNWHOG 266
Qy 307 NRTWIRILLAFVSSVGRNDTGYYTCTSSSKHPSQSALVTILE---KGFINA-TSSQEEYBI 362
Db 267 DFNFRVQRRLTISSARVNDSGVFMCIYANTTTPGSANVTITLEVAVAGFINIFPMNTTIFV 326
Qy 363 DPYKFCFSVREKAYPR-IRCTWIFSQASFPCEQRLEDGYSISKFDHK-----411
Db 327 NDGENVDLIVEAYPKPEHQRWVYM-----NRTLTDKWEDYPKSDNESIRYVSELH 379

QY 412 -----NKPGYIYFAENDDAQFTMTLNIRKPKQVLANAS--ASQASCSSDSDGVPPLPSW 463
 Db LTRLKNGEGGTYTFQVNSDYNSSVTLNVTNTKPEILTHESLVSGILQCLVAGPEPTV 439
 QY 464 TWKCKSDKSPNCTEEI-PEGVWKKANKRVQGVSSSTLWSEAGKLLVKCCAYNSWG 522
 Db DWYFCPGAQRCPVPGDLVQMNSSVSPGKLVQSSIDYSAPFKNGTVECRASNNGV 499
 QY 523 TSCETIFLNSPGPPFFIODN-----ISFYATIGLCPLFTVVLIVLICHKYK 568
 Db 500 KT--SAFFN----FAFGNSKEQMHPHTLFTPLLIGFVIAAGM----MCIIVMILTYKYL 549
 QY 569 KQFYESQLQMI-QVTGPLDNEYFVDFRDYEDYDLKMFEPRENLEPGKVLGSGAPGRVMN 627
 Db 550 QKPMYEQWKVVEING---NNYVYIDPTQLPYDHKMEFPNRLSFGKTLGAGAFGKVE 606
 QY 628 ATAYGISTGVSIQAVKMLKEKADSEKALMSLKMTHLGHNDINVLNLLGACTLSGP 687
 Db 607 ATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSKLVLSYLNHNMNIVNLLGACTVGGP 666
 QY 688 VYLIFECYCCYGLDLNLYLRSKREK-----HRTWTBIFKEHNFSSYPTFOAHNSNMPGSR 743
 Db 667 TLVITEVCCYGLDLNLFNLRKDSFICKQEDHAEVALYKNI-----LQSKSSCNDSTNE 721
 QY 744 -VOLHPPDLQSLGFGNSIHSSEDEIYENQKRLABEEEDLNVLTFEDLLCFAYQVAKGM 802
 Db 722 YMDMKPGSVYVPTKADRRSARIGSYIERDVTPAIMEDELALDLEDLLSFSYQVAKGM 781
 QY 803 EFLFKSVHRDLAARNVLVTHGKVKICDFGLARDILSDSSVYVYVGNARLPVKWMAPE 862
 Db 782 AFLASKNCIHRDLAARNILLPHGRITKICDFGLARDIKNDSNYVYVGNARLPVKWMAPE 841
 QY 863 LFEGYITKSDVWSYGILLWEIFSLGVNYPYGPVANDANFYKLIOSGFKWKEOPFVATEGIY 922
 Db 842 IFNCVYTFESDWSYGYFLWELFSLGSPYFCMPVDKSYFKWIKRGEFRMLSPERHAPAE 901
 QY 923 FVMQSCWAFDSRKRPSFNLFTSLFGCLQALAE 953
 Db 902 DIMKTCWADPLKRPFKQIVOLIEKQISDS 932

RESULT 15
 PGDS_RAT
 ID PGDS_RAT STANDARD; PRT; 1088 AA.
 AC P20786;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112)
 DE (PDGF-R-alpha).
 GN PDGFRA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=90220609; PubMed=2157969;
 RA Lee K.H., Bowen-Pope D.F., Reed R.R.;
 RT "Isolation and characterization of the alpha platelet-derived growth
 factor receptor from rat olfactory epithelium";
 RL Mol. Cell. Biol. 10:2237-2246(1990).
 RN [2]
 RP SEQUENCE OF 33-524 FROM N.A.
 RX MEDLINE=93305723; PubMed=8318539;
 RA Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;
 RT "Conservation in sequence and affinity of human and rodent PDGF
 ligands and receptors";
 RL Biochim. Biophys. Acta 1173:294-302(1993).
 CC -1- FUNCTION: THIS RECEPTOR BINDS PLATELET-DERIVED GROWTH FACTOR AND
 CC HAS A TYROSINE-PROTEIN KINASE ACTIVITY. THIS RECEPTOR CAN BIND
 CC EITHER PDGF-A OR PDGF-B.

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: DIMER OF EITHER ALPHA-ALPHA, BETA-BETA OR ALPHA-BETA
 CC SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; M63837; AAA40743.1; ALT_INIT.
 DR EMBL; Z14118; CAA78488.1; -.
 DR PIR; A34710; PFRTGA.
 DR HSSP; P11362; 1FGK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR Tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein;
 KW Transferase; Phosphorylation; ATP-binding; Immunoglobulin domain;
 KW SIGNAL.
 FT SIGNAL 1 23
 FT CHAIN 24 1088
 FT DOMAIN 24 524
 FT TRANSMEM 525 548
 FT DOMAIN 549 1088
 FT DOMAIN 592 953
 FT NP_BIND 598 606
 FT BINDING 626 626
 FT ACT_SITE 817 817
 FT MOD_RES 848 848
 FT CARBOHYD 41 41
 FT CARBOHYD 75 75
 FT CARBOHYD 102 102
 FT CARBOHYD 178 178
 FT CARBOHYD 352 352
 FT CARBOHYD 358 358
 FT CARBOHYD 457 457
 FT CARBOHYD 467 467
 FT CONFLICT 150 150
 FT CONFLICT 519 519
 SQ SEQUENCE 1088 AA; 122641 MW; 590C8BB0418801E7 CRC64;
 Query Match 22.0%; Score 1157.5; DB 1; Length 1088;
 Best Local Similarity 32.3%; Pred. No. 6.7e-70;
 Matches 300; Conservative 156; Mismatches 317; Indels 155; Gaps 29;
 QY 122 QNRGIVSMALNVTETQAGE-----YLLHIQSERANVTVLTVNVRDPTQLVVLRRP--- 172
 Db 74 ENNSLFTVLEVVNVAHAHTGWTCTYNNHTQTESE-----IEGRHIYIV---PDPD 124
 QY 173 -YFRMENQDALLCISEG-----VP-----EPTVEWVLCSSHR-----ESCKERG 211
 Db 125 MAFVPLGWTDSLIVVEEDSDAIICLLTTPDPTVTLHNHNLVPSYSDSRQGFNGTFSVG 184

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:51:00 ; Search time 70.9642 seconds
(without alignments)
2880.307 Million cell updates/sec

Title: US-09-919-408-2

Perfect score: 5264

Sequence: 1 MRALAKSRRLLLVLSV.....RGLRAQSPQOVKIHRS 992

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	24.1	976	13 Q9W755	Q9W755 brachydanio
2	1234.5	23.5	974	11 Q63702	Q63702 rattus ratt
3	1232.5	23.4	978	11 Q63116	Q63116 rattus norv
4	1220	23.2	954	13 Q91909	Q91909 xenopus lae
5	1215.5	23.1	974	13 Q98SU3	Q98SU3 danio dangi
6	1215.5	23.1	977	13 Q98SU1	Q98SU1 danio nigro
7	1214	23.1	977	13 Q918N6	Q918N6 brachydanio
8	1209.5	23.0	979	6 Q8WN23	Q8WN23 canis fami
9	1208	22.9	964	6 Q97744	Q97744 sus scrofa
10	1207	22.9	964	6 Q9TQ01	Q9TQ01 sus scrofa
11	1207	22.9	964	6 Q9TQ00	Q9TQ00 sus scrofa
12	1205	22.9	978	6 Q9XS93	Q9XS93 canis fami
13	1204.5	22.9	977	13 Q98SU2	Q98SU2 danio kerri
14	1201	22.8	948	6 Q9TDT7	Q9TDT7 trichosurus
15	1198.5	22.8	977	13 Q98SU4	Q98SU4 danio albol
16	1194	22.7	972	4 Q99662	Q99662 homo sapien

17	1188.5	22.6	975	13 P79750	P79750 fugu rubrip
18	1173	22.3	945	6 Q77589	Q77589 equus cabal
19	1170.5	22.2	724	6 Q9MYN0	Q9MYN0 bos taurus
20	1136	21.6	1059	13 Q9DE49	Q9DE49 brachydanio
21	1126.5	21.4	1087	13 Q9PUF6	Q9PUF6 gallus gall
22	1110	21.1	1097	11 Q8R406	Q8R406 rattus norv
23	1073	20.4	1019	13 Q8UVR8	Q8UVR8 fugu rubrip
24	1060	20.1	1048	13 P79749	P79749 fugu rubrip
25	1013.5	19.3	986	13 Q8UVR9	Q8UVR9 fugu rubrip
26	997.5	18.9	923	6 Q97745	Q97745 sus scrofa
27	980	18.6	1379	13 P79701	P79701 coturnix co
28	974	18.5	1327	13 Q8QHL3	Q8QHL3 gallus gall
29	961	18.3	1363	11 Q912T1	Q912T1 rattus norv
30	957	18.2	1301	13 Q8UWU9	Q8UWU9 brachydanio
31	946	18.0	1173	13 Q9PTL0	Q9PTL0 brachydanio
32	939	17.8	563	11 Q925F7	Q925F7 rattus norv
33	937.5	17.8	1345	11 Q8VCD0	Q8VCD0 mus musculu
34	901.5	17.1	323	11 Q9EQ22	Q9EQ22 rattus norv
35	877.5	16.7	323	11 Q9EQ24	Q9EQ24 rattus norv
36	833	15.8	345	13 Q9PVU7	Q9PVU7 lethenteron
37	820.5	15.6	350	13 Q91416	Q91416 xenopus lae
38	798	15.2	796	13 Q91287	Q91287 pleurodeles
39	793	15.1	766	4 Q96KM2	Q96KM2 homo sapien
40	793	15.1	785	4 Q96KM1	Q96KM1 homo sapien
41	793	15.1	819	4 Q96KM0	Q96KM0 homo sapien
42	791	15.0	824	13 Q90749	Q90749 gallus gall
43	790.5	15.0	806	13 Q90200	Q90200 brachydanio
44	790.5	15.0	820	4 Q96KL9	Q96KL9 homo sapien
45	788.5	15.0	922	13 Q90413	Q90413 brachydanio

ALIGNMENTS

RESULT 1

ID	Q9W755	PRELIMINARY;	PRT;	976 AA.
AC	Q9W755;			
DC	01-NOV-1999 (TRENBLrel. 12, Created)			
DT	01-NOV-1999 (TRENBLrel. 12, Last sequence update)			
DE	01-JUN-2002 (TRENBLrel. 21, Last annotation update)			
DB	Kit receptor tyrosine kinase.			
GN	KIT.			
OS	Brachydanio rerio (Zebrafish) (Zebra danio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
[1]				
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=9396707; PubMed=10393121;			
RX	Parichy D.M., Rawls J.F., Pratt S.J., Whitfield T.T., Johnson S.L.;			
RA	"Zebrafish sparse corresponds to an orthologue of c-kit and is			
RT	required for the morphogenesis of a subpopulation of melanocytes, but			
RT	is not essential for hematopoiesis or primordial germ cell			
RT	development".			
RL	Development 126:3425-3436(1999).			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-			
CC	PROTEIN KINASES.			
DR	EMBL; AF153446; AAD41890.1; -			
DR	HSSP; P11362; 1FGK.			
DR	ZFIN; ZDB-GENE-980526-464; kit.			
DR	InterPro; IPR000719; Euk_pkinase.			
DR	InterPro; IPR003598; Ig_C2.			
DR	InterPro; IPR003600; Ig_Like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR001824; RTKinaseII.			
DR	InterPro; IPR001245; Tyr_pkinase.			
DR	Pfam; PF00047; ig; 3.			
DR	Pfam; PF00069; pkinase; 1.			
DR	ProDom; PD000001; Euk_pkinase; 2.			
DR	SMART; SM00408; IGC2; 1.			

DR SMART; SM00410; IG like; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 976 AA; 109278 MW; A80AA01658C1A2DA CRC64;

Query Match 24.1%; Score 1268; DB 13; Length 976;
Best Local Similarity 36.6%; Pred. No. 1.5e-102;
Matches 318; Conservative 136; Mismatches 302; Indels 110; Gaps 29;

Qy 177 MENODALLCISEGVPETVEVWLCSSHRESCKEKGPAV--VRKEEKVLHFGTDIRCCA 234
Db 138 MNKLNQKC--DGQPLN-----SLRYSASLETGVSQVKRFEFGYCVGTLDAATV 189
Qy 235 RNALGRECTKLTLDLNOAPOSTLP-----QLFLKVGPELWIRCKAIHVNHGFLTWE 287
Db 190 KS--GR-----YQTVRLVDPDPPITLGPQORVLLTGEGKLSLSCSTSNVNSDIANKW 242
Qy 288 LE---DKALBEGSYFEMSTYNTMTIRILLAFVSSVGRNDTGYTCCSSKHPQSQA--- 341
Db 243 APNGVNSVHNSHL-----LTEPIHVTALSLSSVTMQDAGNYSCEAINKEGTAKPV 298
Qy 342 LVLTLEKGFNATS--SOEEVEIDYKPCFVRFKAYPRIC--TWIFSOASFPCEQRLG 399
Db 299 WVNIEYKGFNITSVDNSTRVRAGESLSLRVNMVAYPKPHTFWSYS----- 346
Qy 400 DGYISIKFCOH-----KMKPGYIFVAENDDAQFTKMTLIRK 438
Db 347 -GVKLTNTDTHVTSRTHGNSYTBELKVLRLKVSSEGIYTFSCNLNRDATIQTTEVHVIS 405
Qy 439 KPQVLANASA--SOASCSSDGYPLPSWTW-----KKCSKSPNCTEIEPEGVWNKKAN 489
Db 406 KPOIVSYEGPIDGVQVRCVABGYPTPOIKWYCDLPHSRCSNLL-NATOE-BEDVVTVTMT 463
Qy 490 RKVFGQVSSSTLNMSEAGKLLVKCCAYNSMGTSCTEIFLNSPGPPP---FIQDNISFY 546
Db 464 NPPFGKAVESRLNTKNNYATLE--CVASANGEIVTYLFSISENTVPHEFLTPLLIGFV 521
Qy 547 ATIGLCIPFIWLVILVILCHYKQFRIESOLOMIVTQPLONEFYVDYDFRDEYDLKWEF 606
Db 522 AAAYI-----LVLLILVILYKVMQPKYQIQMKVIE--GIHGNVYVYIDPTQLPYDHOEF 575
Qy 607 PRENLEFGKLGSGAFGRVMNATAYGISTGVSIOVAVKMLKEKADSCKEKALMSLKMM 666
Db 576 PRDKLRFGKTLGSGAFGKVVATAYGMSKADTVMTAVKMLKPSAHATEKEALMSLKVL 635
Qy 667 TLGHNDHINVLGACTLGSVPYLIFFCYCCYGDLLNLYLRSKREKPHRTWTEIFKEHNFS 726
Db 636 SYLGNHINVLGACTVGGPTLVITEYCCFGDLLNLFRLRRRVFYFT---TLGEDAYR 692
Qy 727 YPTQAHNSNMPGSRREVQLHPP--LDOLSGFNAGSIHSEDELEYENQKLAEEEDLN 785
Db 693 NVNQSEPNDSRNG--YNTMKPSVLGILSSNRRSLNKGD--SYSDSDAVSEILQEDGLT 748
Qy 786 LTFEDLLCFAQVAKGMFEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDILSDSY 845
Db 749 LQTELLSFSQVAKGMDFLASKNCIHRDLAARNILLTQGRVAKICDFGLARDITDSDNY 808
Qy 846 VVRGNARLPVKWMAPESLFEGITYIKSDVMSYIGILLWEIFSLGNVPYFGIPVDANFYKLI 905
Db 809 VVKGARLPVKWMSPESEIFECVYTESDVSWSYIGILLWEIFSLGSSPYFCMPVDKSFYKMI 868
Qy 906 QSGFMQOPFVATEGIYFWQSCWAFDRKRPSPFNLTSLFCQLAEA--EACITRTSHL 964
Db 865 KEGYRMSEPFSPSEMYDIMHSCNDADVRKPSFSFKIEQKIESQISDSTKTHIYNFNSRL 928
Qy 965 PKQAPQOGRGLRAQSPQORVKIHERS 992

Db 929 P--AAP-----GPRESSSH---VHLNS 947

RESULT 2
Q63702 PRELIMINARY; PRT; 974 AA.
AC Q63702;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE C-kit receptor tyrosine kinase isoform.
OS Rattus rattus [Black rat].
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BN/FMAI;
RA Tsujimura T., Tono T., Yamazaki M., Nomura S., Kitamura Y.;
RT "Two isoforms of rat c-kit receptor tyrosine kinase.";
RL Nucleic Acids Res. 0:0-0(0).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; X62491; CAA44354.1; -;
DR HSSP; P11362; IFGK.
DR InterPro; IPR00719; Euk_pkinase.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG_Like; 3.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 974 AA; 108955 MW; B9BFAD9BA0DA190D CRC64;

Query Match 23.5%; Score 1234.5; DB 11; Length 974;
Best Local Similarity 32.3%; Pred. No. 1.3e-99;
Matches 323; Conservative 176; Mismatches 340; Indels 161; Gaps 37;

Qy 36 CVLISHENNGSAGKPPSSRYMVRGSPEDLOCTPRQSGTVYEATVVAESGSLTQVQ 95
Db 12 CVLLVLLRGQTGSQPSA-----SPGSPSPSIQPAQSELIVEAGD-TIRLT 57
Qy 96 LATPCDLSCLAVFKHSSILGCGPHFLQNGIVSMALNV-TETQAGEYLLHHTQSERANVT 154
Db 58 CTDPAFVK--WTFE-----ILDVRIENKQSEWIR--EKAEATH 92
Qy 155 VLFT-----VNVRD--TQYVLRPPYFRKMNQDALLCISEGVPEPTV--EWVLC 200
Db 93 KGYTCVSGSGLRSSYIVFVRDPAVLFLVGLPLFGKEDNDALVRC---PLTDPQVSNYSLI 149
Qy 201 SSHRESC-----KEEGPAVVRKEEVLHFGTDIRCCARNALGRECTKLTIDLNQ 252
Db 150 ECDGKSLPTDLKFVNPKNAGITIKNVKRAYHRLC---IRCAAOREGKWMRSDFLTKVRA 206
Qy 253 A-----POSTLPQ---FLKVGPELWIRCKAIHVNHGFGITW-----ELEDKALEE 295
Db 207 AIKAIPVVSVPETSHLLKEGDTFTVICTKDVSTSVDSMWIKLNFQPOSKAQVKNRSHQ 266
Qy 296 GSYFEMSTYSTNRTMIRILLAFVSSVGRNDTGYTCCSSKHPQSQALVT---ILEKGFIN 352

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Db 267 GDF-----NYERQETLT-----ISSARVNDSGVFCFYANNTFGSANVTTLTKVKEGFIN 316
QY 353 --ATSSQBEYEIDPYEKEFCFSVRFKAYPR-IRCTWIFSQSPCCQORGLE-----DGYGIS 405
Db 317 IFPVKNTTVFTVDG--ENVDLVVEFEAYPKPEHQWIYNNRT--PTNRGDEYVKSNDQONI 373
QY 406 KFCDH-----KNKPGGEYIFYAENDDAQFTKMTFLNIRKQPVLAA--NASASQASCSDD 456
Db 374 RYVNELRLTRLKGTGGTYTFLVNSDVSAVTFDVTYVNTKPEILTYDRLMNGRLQCVAA 433
QY 457 GYPLPSWTWKCSKDSKPNCTBEIPE-GVWNKANKRVFGQWSSSTLNWSEAGKGLLVKC 515
Db 434 GFPEPTIDWYFCTGAERQCTVPVPVQIQNASVSPFGKLVVQSSIDSVFRHNGTVEC 493
QY 516 CAYNSMGTSCTETFLNSPGPPFF-----IQDN-----ISFYATIGLCLPFIVVLIVLICH 565
Db 494 KASNAVGKS--SAFEN-----FAFKGNSKEIQIOPHTLFTPLLLIGFVVVYTAGL-----MGIIVWVLAY 543
QY 566 KYKQPRYESQLOMI-QVTGPLDNEYFYVDFRDYEYDLKWEFPRENLEBFGKVLGSAFGR 624
Db 544 KYLQKPMYEVQWKVEEING--NNVYVIDPTQLPYDHKWEFPNRNLSFGKTLGAGAFGK 600
QY 625 VNNATAGISGTGVSIOQAVKMLKEKADSCKEALMSLKMTHLGHHDNIIVNLLGACTL 684
Db 601 VWEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELKVLVSLGNHNNIIVNLLGACTV 660
QY 685 SGPVYLIFCYCCYDGLNLYLRSKREKHTWTETFEKHNFSSTYPTFOAHSSMSPGSRV 744
Db 661 GGPTLVITEYCCYDGLNLYLRSKREKHTWTETFEKHNFSSTYPTFOAHSSMSPGSRV 718
QY 745 QLHPPLDQLSGFN-----GNSIHSEDEIEYENQRLAEEDENLVLTFFDLCLFA 795
Db 719 -----MDMKPGVSVVPTKDKRSARIDSYIERDVTAIMEDDELALDL-----EDLLSFS 770
QY 796 YQVAKGMEFLFKSCVHRDLAARNVLTGHKVVKICDFGLARDILSDSYVVRGNARLPV 855
Db 771 YQVAKGMAFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIRNDSYVVRGNARLPV 830
QY 856 KWMAPESIFEGYITKSDVWSYGLLWEIFSGVNPYPGIVDANFYKLIOSGFKWEOFP 915
Db 831 KWMAPESIFNCVYTFESDVWSYGLLWEIFSGVNPYPGIVDANFYKLIOSGFKWEOFP 890
QY 916 YATEGIVFMOSWAFDSRKPSPFNLSFLGCLQALAEAE 955
Db 891 HAPAAVEMVMTCDWDAPLKPRTFKQVQLIEKQISDSK 930

RESULT 3
Q63116 PRELIMINARY; PRT; 978 AA.
AC Q63116;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C-kit receptor tyrosine kinase.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=92003944; PubMed=1912577;
RA Teijimura T., Hirota S., Nomura S., Niwa Y., Yamazaki M., Tono T.,
RA Morii E., Kim H., Kondo K., Nishimura Y., Kitamura Y.;
RT "Characterization of ws mutant allele of rats: A 12-base deletion in
RT tyrosine kinase domain of c-kit gene.";
RL Blood 78:1942-1946(1991).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; D12524; BAA02094.1; -.
DR HSP; P11362; IFGK.

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DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RYKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig_1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD00001; Euk_pkinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG_Like; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 978 AA; 109341 MW; 0958C33F19889051 CRC64;

Query Match 23.4%; Score 1232.5; DB 11; Length 978;
Best Local Similarity 32.2%; Pred. No. 2e-99;
Matches 323; Conservative 176; Mismatches 340; Indels 165; Gaps 37;

QY 36 CVLISHENNGSGAGKPSVVRGSPEDLQCTPRQSEGTVEAATVEVAESGSIQLQV 95
Db 12 CVLLVLLRGQTGTSQPSA-----SPGFSPPSIQPAQSELIVEAGD-TIRLT 57
QY 96 LATPGDLSCLVFKHSHGCGQPHDLQNRGIVSMALNV-TETQAGEYLLHQTSEYANYT 154
Db 58 CTDPAPVK--WTFE-----ILDVRIENKQSEWIR--EKAEATHT 92
QY 155 VLFT-----VNVRD-TQLVVLRRPYPRKMNQDALLCISEGPEPTV-EWVLC 200
Db 93 GKTYCVSGSLRSSYTVFVRDPFAVLFLVGLPLFGKEDNALVRC---PLTDPQVSNYSLI 149
QY 201 SSHRESC-----KEGPAVVRKEEVLHELFGDTRCCARNALGRECTKLTFTDLNQ 252
Db 150 ECDGKSLFTDLKFVNPVKNAGITIKNVKRAYHRLC---IRCAAQREGKWMRSKFTLKVRA 206
QY 253 A-----POSTLPQL--FLKVGEPFLWIRCKAIHVNHGFLTW-----ELEDKALAE 295
Db 207 AIKAIPVSVVPETSHLLKEGDTFTVICTIKOVSTSDSMWIKLNPQPSKAQVKRNSWHQ 266
QY 296 GSYFEMSTYSTNRNIRILLAPVSVSGRNDTGYTTCSSSKHPSQSALVT---ILEKGFIN 352
Db 267 GDF-----NYERQETLT-----ISSARVNDSGVFCFYANNTFGSANVTTLTKVKEGFIN 316
QY 353 --ATSSQBEYEIDPYEKEFCFSVRFKAYPR-IRCTWIFSQSPCCQORGLE-----DGYGIS 405
Db 317 IFPVKNTTVFTVDG--ENVDLVVEFEAYPKPEHQWIYNNRT--PTNRGDEYVKSNDQONI 373
QY 406 KFCDH-----KNKPGGEYIFYAENDDAQFTKMTFLNIRKQPVLAA--NASASQASCSDD 456
Db 374 RYVNELRLTRLKGTGGTYTFLVNSDVSAVTFDVTYVNTKPEILTYDRLMNGRLQCVAA 433
QY 457 GYPLPSWTWKCSKDSKPNCTBEIPE-GVWNKANKRVFGQWSSSTLNWSEAGKGLLVKC 515
Db 434 GFPEPTIDWYFCTGAERQCTVPVPVQIQNASVSPFGKLVVQSSIDSVFRHNGTVEC 493
QY 516 CAYNSMGTSCTETFLNSPGPPFF-----IQDN-----ISFYATIGLCLPFIVVLIVLICH 565
Db 494 KASNAVGKS--SAFEN-----FAFKGNSKEIQIOPHTLFTPLLLIGFVVVYTAGL-----MGIIVWVLAY 543
QY 566 KYKQPRYESQLOMI-QVTGPLDNEYFYVDFRDYEYDLKWEFPRENLEBFGKVLGSG 620
Db 544 VLAYKQPMYEVQWKVEEING--NNVYVIDPTQLPYDHKWEFPNRNLSFGKTLGAG 600
QY 621 AFGRYMNAATGISTGTVSIOQAVKMLKEKADSCKEALMSLKMTHLGHHDNIIVNLLG 680
Db 601 AFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELKVLVSLGNHNNIIVNLLG 660

```


DE Receptor tyrosine kinase Fms.
GN FMS.
OS Danio dangila.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=127599;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21359118; PubMed=11466528;
RA Parichy D.M., Johnson S.L.;
RT "Zebrafish hybrids suggest genetic mechanisms for pigment pattern
diversification in Danio.";
RL Dev. Genes Evol. 211:319-328 (2001).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
PROTEIN KINASES.
DR EMBL; AF324479; AAKL5301.1; -.
DR HSSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig_c2.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTK_inaseIII.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig_3.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transmembrane.
FT VARIANT 720 A -> T.
SQ SEQUENCE 974 AA; 109902 MW; DE7FD64FD0D7B37 CRC64;

Query Match 23.1%; Score 1215.5; DB 13; Length 974;
Best Local Similarity 34.6%; Pred. No. 6.3e-98;
Matches 339; Conservative 147; Mismatches 32; Indels 153; Gaps 37;

Qy 54 YRMVRGSPEDLQCTPR-RQSEGTVEAATVEAEGSITLQVQLATPGDLSCLVFKHSS 112
Db 13 FGQVQGWSE-----PRIRLSSGAL--ADTDVILDSGS---PLQLCEGDGPVTFI----- 57
Qy 113 LGCQPHDLQNRGI-----VSMALLNVVTTQAGEY-LLHIQSERANYTVLFTVN 160
Db 58 ---PRLAKHKRYISKEVGKSRTRFEKATVDFT----GTYKCIYINGNDSNLSSSVHVF 109
Qy 161 VRDTC-LVY-----LRRYFRKMNQDALLCISGEVPTVEWVLCSSHRECKEKGAPV 214
Db 110 VRDGRVLEVPSTSLR--YVRK-EGEDLLPLCLLDPPDAT-DFIFRMDNGSAAPYGMNAT 165
Qy 215 VRKEKVL-----HELFGTDIRCARNALGRECTLTITDLNQAPQSTLPQLFLK----- 264
Db 166 FDPKGVLRNVHPCFNADYICSAIRGAESKIFSIINVQLRFP-PYVILKREYVVK 224
Qy 265 -VGEPLWIRCKAIHNVHGFGLTWELDKALEEGSYFEMSTYSTNRTMIRILLAFVSSVGR 323
Db 225 LVGERLQISCTNNPNFNSVNVVTHSSRLPKAE--ERSTWEGDLAIESILT-IPSVQL 281
Qy 324 NDTGYTCSKSKHPQSQALVT-----ILEKGF-----NATSQEEYEIDPYKFCPSV 372
Db 282 SDTGNIITCGNEAGANSSTTQLLVVDFPYRLSPKLSKLTHRLDSIEVSGDDVDLGV 341
Qy 373 RFKAY-PRIRCTW---IFSQASFPCEQR--GLEDCYSISKCDHKN--KPGEYIIFYAEND 424

Db 342 WIEAYPPLISHKWEPTSHNASLP-ENRFYNHNDRYEALLFLKRLNFEIGQVTLNVKNR 400
Qy 425 DAQFTKMTLNRKKPQVLAN-ASASQASCSGSDGYPPLPSWTWKKCSKSPNCTEE----- 478
Db 401 VKSASITFDIKMYTKPVARVKNWENTTILSCRSYGPAPASILWYQCTGIRTTCPENTTDLQ 460
Qy 479 -----IPEGVNNKKNRKFQGVQWVSSSTLNMSEAGKLLVKCCAYNSMGTSCTEIFLN 531
Db 461 PIQTHGGVPEG-----ESFGSGVSVLTUG-PNRRMTVVCVAFNLVGGSDTFSSMD 511
Qy 532 SPGPPPTQDNISFYATIGLCCLPFTV--VLIVLICHYKKQFRYESQLQMIQVTPGLDNE 599
Db 512 -----VSDQFTSAMCGSTVAMVVLGILLFIYKYKQKPRYERWKIIEATN--GNN 562
Qy 590 FYVDFRDEYDLKWEFPRENLEFGKVLGSGAFGRVMATAYIGISKTGVSIOQAVVMOLKE 649
Db 563 YTFIDPTQLPYNEKWEFPDRDKLGLKGLTGAGAFGKVVEATAYGLGKEDNITRVAVRMLKA 622
Qy 650 KADSCKEALMSLKMTHLGHHDNIVNLLGACTILSGPVYLIFEYCCYGDLLNLYLSKRE 709
Db 623 SAHPDEREALMSLKLHSLGQHKIVNLLGACTHGGPVLVITEYCCCHGDLNLFKSKAE 682
Qy 710 KPHRTWTEI--FKE-----HNFSSYPTTFOAHNSNMPGS-----REVQLHPPLDQLS 754
Db 683 NFLNFMVITPDPEPMTDYKNISTERMP-VRSDSGSSACSDDHYLDMRPVTSRPTLSSS 741
Qy 755 GFNGNSIHSDEIEYENOKRLAEBEEDNLVTFEDLLCFAYQVAKMGFLEFKSCVHRD 814
Db 742 -----ECQEDSWPLDMDLLRFSQVAQGLDFLAAKNCIHRD 778
Qy 815 LAARNVLVTHGKVKVVICDFGLARDILSDSSYVVGNGARLPVKWMAPESLFEGYTIKSDV 874
Db 779 VAARNVLVTHGKVKVVICDFGLARDIMNDSYVVGNGARLPVKWMAPESEIFECYVTVQSDV 838
Qy 875 WSYGILLWEIFSLGVNYPGPVDANFYKLIQSGFKWEQFPFVATEGIYFVMQSCWAFDSR 934
Db 839 WSYGIMLWEIFSLGKSPYNILVDSKFKYKMKCGQMSRPDPAPPPEMYTIMKWCNLDAA 898
Qy 935 KRSPPNLTSFLGCOLAEAE 955
Db 899 ERPTESKISQMIQRLGETPE 919

RESULT 6
Q98SUI ID Q98SUI PRELIMINARY; PRT; 977 AA.
AC Q98SUI;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Receptor tyrosine kinase Fms.
OS Danio nigrofasciatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=144739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21359118; PubMed=11466528;
RA Parichy D.M., Johnson S.L.;
RT "Zebrafish hybrids suggest genetic mechanisms for pigment pattern
diversification in Danio.";
RL Dev. Genes Evol. 211:319-328 (2001).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
PROTEIN KINASES.
DR EMBL; AF324481; AAKL5303.1; -.
DR HSSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig_c2.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.

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DR InterPro; IPR0031006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR002290; Ser_Chtr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00408; Igc2; 1.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferrase; Transmembrane.
FT VARIANT 60 V -> L.
FT VARIANT 103 A -> S.
FT VARIANT 742 P -> S.
FT VARIANT 899 E -> D.
SQ SEQUENCE 977 AA; 109881 MW; CF54E129FAB10E3E CRC64;

Query Match 23.1%; Score 1215.5; DB 13; Length 977;
Best Local Similarity 33.5%; Pred. No. 6.3e-98;
Matches 334; Conservative 160; Mismatches 356; Indels 147; Gaps 35;

QY 54 YRMVGRSPEDIQTPR-RQSEGTVEATVAESGSITLQVLAATPGDLSCLM---VFK 109
Db 13 FGQVQGWSE-----PRRLNSGAL--ACTDVLDGSG---PLQLVCEGDPVTFPRVAK 62

QY 110 HSLGCGPHDQLQNGIVSMALNVTQAGEX-LLHQSERANVTULTFTVNRDQ-LY 167
Db 63 H-----KRYISKEYGKIRSFREKATVDTGTCKVYINGSDNSLASSVHVFRDRLVF 117

QY 168 V-----LRRPVERKMNODALLCISEGPEPTVEWLVCSSHRECKEGPAAVRKEEKVL 222
Db 118 VSPSSLR--YVRK-EGEDLLPCLLTDPDAT-DPTFRMNGSAAPYGNATFPRKGVL 173

QY 223 ----HELFGTDIRCCARNALGRECTKLFTIDLNAQPSLTQLFLK-----VGEPLMI 271
Db 174 IRNVHPGNADYICSAIRGGAEKVKISINVIOIRLPP-PVYVLRKNEYVVKLGERLQI 232

QY 272 RKAHNVHGFGLTWELDKALEGSEYEMSTYSTNRMIILLAFVSSVGRNDTGYTC 331
Db 233 SCTNNPNFYNNVTWTHSSKRLPRPE--EKSTMEGDLAIESILT-ISSVOLSDTGNITC 289

QY 332 SSKKHPQSALVT---ILEKGINAT---SSQEEY-----EIDPYKFCFSVRFKAPRI 380
Db 290 TQNEAGANSSTQLLVVDEPIYRLSPKLSKLTHRGLSIEVSEGEDVDLGLVLEAYPPL 349

QY 381 RC-TW---IFSQASFPFCBOR--GLEDGYISIKFCDHKNI--KPGEYIFYAENDDAQFTQMF 432
Db 350 TSHWETPTSHNASLP-ENRFVNHNDREYALLFLKRLNFEIGQVTLNVKNSKMSASITP 408

QY 433 TLNTRKPKQVLAN-ASASQACSSDGYPLPSWTKWKKCDKSPNCTEEI-----PGVWNKK 487
Db 409 DIKMYTKPVARVKVNWNTLSRCRSGYPAPSLWTQCTGIRTCPTENTDILQPIQTQVTE 468

QY 488 ANRKVFQGVSSSTLNNSSEAGKLLVKCAVNSMGTSCETIFLNSPGFPFIQDNISFYA 547
Db 469 FQKESFGAVGVESVLTVG-PNRRMTVVCVAFNLVCGQSDTFSMD-----VSQDIFTS 520

QY 548 TIGLCLPPIV--VLIVLICHYKKQFYESQLQMTQVTPGLDNEFYVDFRDYEDLAKWE 605
Db 521 MCGSTVAMVVLGLLLIFMYIKYKQKPRYERWKLIEATN--GNVYTFDPTQLPNEKWE 578

QY 606 PPRENLBFKVLGSGAFGRVNNATYISKTGVSITQAVKMLKEKADSCKEALMSELKM 665
Db 579 FPRDKLKLGLGAGAFGVKVEATYGLGKEDNITRVAVKMLKASAHDPREALMSELKI 638

QY 666 MTHL6HHDNINVLIGACTLISGFVYLIFCYCCYGDLLNVLRSKREKF----- 711

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Db 639 LSHLGQHKNIIVNLIGACTHGGPVLVITEYCCCHGDLNLFSLKAEFLNFMVTIPNFPVPV 698
QY 712 -----HRTW-----TEIFKEHNFSSPTTQAHNSNMPGSRVQLHPPLDQLSGF 756
Db 699 TDYKNVSTERMFVRSDSGISSTCSHDVLDMPVTSRPTNSALDPSDDCQ----- 747
QY 757 NGNSIHSEDEIYEYENQKELAEEDLNLVTFEDLLCFAYOVAKGMEFLFKSCVHRDLA 816
Db 748 -----EDSWPLDMDDLLRFSQVQAQGLDFLAAKNCIHRDVA 783
QY 817 ARNVLVTHGKVKIKCDFGLARDIILSDSSVYVVRGNARLPVKWMAPESLPEGIYTIKSDVMS 876
Db 784 ARNVLLTNSRVAKICDFGLARDIMNDSNVYVVGKARLPVKWMAPESEIFECYVTVQSDVMS 843
QY 877 YGILLWEIFSLGVNYPGIPVDANPYKLIQSGFKWMEQFYATEGIYFVWQSCWAFDSRRK 936
Db 844 YGIMLWEIFSLGKSPYPNILVDSKFYKMKCGYQMSRDPDFAPPENYTIMKMCWNLEAAER 903
QY 937 PSFNLTSFLGCOLAE-AEEACIRTSIHLPKQAAPQ 972
Db 904 PTFKISQMIQMLGETSEBQDQTEYKNIPISEAEVEQ 940

RESULT 7
Q918N6 PRELIMINARY; PRT; 977 AA.
AC Q918N6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fms; CSfIR OR Fms.
GN Brachydanio rerio (Zebrafish) (Zebra daniel).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB;
RX MEDLINE=20323166; PubMed=10862741;
RA Parichy D.M., Ransom D.G., Paw B., Zon L.I., Johnson S.L.;
RT "An orthologue of the kit-related gene fms is required for development
RT of neural crest-derived xanthophores and a subpopulation of adult
RT melanocytes in the zebrafish, Danio rerio."
RL Development 127:3031-3044(2000).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AF240639; AAF76872.1; -.
DR HSP; P11362; IFGK.
DR ZFIN; ZDB-GENE-001205-1; csf1r.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00408; Igc2; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;
KW Receptor; Transferrase; Transmembrane; Tyrosine-protein kinase.
FT VARIANT 238 N -> K.
FT VARIANT 615 V -> M.
SQ SEQUENCE 977 AA; 110187 MW; C91A2F339E746A58 CRC64;

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Query Match      23.1%; Score 1214; DB 13; Length 977;
Best Local Similarity 33.4%; Pred. No. 8.6e-98;
Matches 329; Conservative 157; Mismatches 354; Indels 146; Gaps 34;

Qy 68 PR-RQSEGVTEAATVEAAGSGTTLQVLAATPGDLSCLM---VFKHSSLCQCPHFDLQ 123
Db 22 PRIRLSSGAL--AGTDVILESGS---PIQLVCEGDPVTFPLRLAKH-----KRYISKEV 71

Qy 124 RGVISMALNVTETQAGEY--LHIOSEERANYTLFTVNVDRDQ--LYV-----LRPYPK 176
Db 72 GKIRSFVRKVTVDFTGYKCYWNGNDSNLSSVHVHVRDNRVLFVSPSTSLR--YVRK 129

Qy 177 MENQDALL-CISEGVPEPTVEWLVCSSHRESCKEKGPAVVRKEK-----VLHFLFGTDI 230
Db 130 -EGEDLLPLCL--LTDPEADTFTRMDNGSAAVPGMNIITDPRKGLVLRNVHPGFNADY 185

Qy 231 RCCARNALGRECTKLTFTIDLNAQAPSTLPQLFLK-----VGEPLWIRCKAIHVNHGFG 283
Db 186 ICCARIGAEKVKISFISNIIQRLRFP--PYVYLKRNVEVVLVGERLQISCTTNNPNFYIN 244

Qy 284 LTWELEDKALEEGSYFENSTYTNRTMIRILLAFVSSVGRNDTGYTCSSSKHPSQSALV 343
Db 245 VTWTHSRMLPKAE--EKSTMEGRDLAIESILT-IPSVOLSHGTGNITCTGONEAGANST 301

Qy 344 T---ILEKGFNAT---SSQSEY-----EIDPYEKFCFVRKAYPRIRC-----TWIFSQ 388
Db 302 TOLLVVEEPIRLSPKLSKLTIRGLSTIEVSEGDVDLGVLEIAYPLTSHKWEPTSHN 361

Qy 389 ASFPCEQR--GLEDGYSISKFDHKN--KPGEYIFYAENDDAQFTKMTLNRKPKQVLA 444
Db 362 ASLP-ENRFNHNDRYEALLLLKRLNPEEIGQYTLNVKNMSKASITFDIKNYTKPVAR 420

Qy 445 N-ASASQASCSGDGYPSPWTKCSKSPNCTBEI-----PEGWNKANRKYFQWVSS 499
Db 421 KWNVTTLSCRSYGPAPSIILMYOCTGIRTCPCNTTDLQITQTVFQKESFGAAGVE 480

Qy 500 STLAMSAGKGLLVKCCAVNSMTSCETIFLNSPGFPFFIODNISFYATIGLCLPFIV-- 557
Db 481 SVLTVG-PNRMTVVCVAFNLVQGSDFSMF-----VSDQIFTSAMCGSTVAMVILG 532

Qy 558 VLVILCHYKQKQFYESQLOMIQVTPDLNEYFYVDYFRDYEYDLKWEFFPRENLEFGKVL 617
Db 533 LLLIFMIVKYKQKPYRIWKIIEATN--GNNYTFIDPTQLPYNEKWEFFPRDKLGLKTL 590

Qy 618 GSGAFGRVWNTATAGISKTGVSIVAVQVLKEKADSCEKALMSLKMTHLGHHDNIYN 677
Db 591 GAGAFGKVEATAYGLGKEDNITRVAVQVLKASAPDREALMSLKLTLHLGHKNIYN 650

Qy 678 LLGACTLSGPVVLIFEYCYGDLNLNLSKREKF-----HRTW 715
Db 651 LGACTHGGPVVLITVEYCHGDLNLNLSKREKF-----HRTW 715

Qy 716 -----TEIFKEHNFSSYPTFOAHNSSMFSGREVQLHPDLQLDSFGNGSIHSEDEIE 768
Db 711 VRSDSGISSTCSDHYLDMRPVTSRPTNSALDSSSECQ----- 747

Qy 769 YENQKRLAEEDLNLTFTFEDLLCFAYQVAKGMFLFKSCVHRDRLAARNVLVTHGKV 828
Db 748 -----EDSWPLDMDDLLRFSQVAGLDFLAAKNCIHRDVAARNVLLTNSRVA 795

Qy 829 KICDPGLARDILSDSSVYVGNARIPVKWMAPESEFEGYITTKSDVMSVGIILLWEIFSLG 888
Db 796 KICDPGLARDINDSNYVYVGNARIPVKWMAPESEFECYITVQSDVMSVGIILLWEIFSLG 855

Qy 889 VNPYPGIPVDANFYKLIQSGFQKQOFFVATEGIYFVWMSCNAFDSRKRPSFNLTSFLGC 948
Db 856 KSPYNNILVDSKFYKMKCYQMSRPDPAPPMTYIMKMCWNLDAERPTFSKISQMLQR 915

Qy 949 QLAE--ABEACINTSIHLPKQAAPQR 973
Db 916 MLGETSEQDQTEYKNIPTAEAEQQ 941

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RESULT 8
Q8WN23 ID OSWN23 PRELIMINARY; PRT; 979 AA.
AC OSWN23;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C-KIT.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Zemke D., Yuzbasiyan-Gurkan V.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AF481448; AAL40833.1; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR002290; Ser_Chk_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00410; IG_Like; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Ty_Kc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; UNKNOWN_1.
SQ SEQUENCE 979 AA; 109753 MW; 46C30D5DEB8E33D3 CRC64;

Query Match      23.0%; Score 1209.5; DB 6; Length 979;
Best Local Similarity 31.3%; Pred. No. 2.1e-97;
Matches 332; Conservative 165; Mismatches 369; Indels 195; Gaps 35;

Qy 14 LLVLSVMILVTNVDLPVIAKCVLISHENSGSAGKPSFYSYRMVRGSPEDLQCTPRQSE 73
Db 11 LCVLLLLLLGVTGSSQPSV-----SPGEPSL----- 38

Qy 74 GTVTEAATVEAAGSGTTLQVLAATPGDLSCLWPKHSLGCPHFDLQNRGIVSMAILN 133
Db 39 PSIIHPAKSELIVSGD-ELRLSCTDPGFVK--WTFE--TLG-QLNENTHNEWITEKA--- 89

Qy 134 VTETOAGEYLLHIOSEERANYTLFTVNVDRD-TQLVLRARPYERKMNQDALLCISGVPE 192
Db 90 ----EAGTGTNYTCNRDGLRSIYFVRDPAGLFLVDLPYKSGNDTLVRC----- 138

Qy 193 PTVEWLVCSSHRESCKEKGPAVVRKEEKLHFLFTDIR-----C--CARNALGRE 241
Db 139 PLTPEVTNYSIRGC--EGKPLPKDLTFVADPKAGITIRNVKREYHRLCHCSADQKGT 196

Qy 242 -CTKLTIDLNAQPOS-----TLPQLFKVGEPLWIRCKAIHVNHGFLTWELEDKALE 294
Db 197 VLSKFTLVRAAIRAVPWSVSKTSLKKEGAFSCVCFIKDVSFVDSMWIKENSQQT 256

Qy 295 EGSYFEMSTYTNRTMIRILLAFVSSVGRNDTGYTCSSSKHPSQSALVTLIE---KGF 351
Db 257 NAQTQSNWHHGDGFNFQEKLIITSSARVNDSGVFMVCYANNTFGSANVTTLLEVDKGF 316

Qy 352 NA-TSSQSEYEDIDPYEKFCFVRKAYPR-IRCTWIFSOASF--PCEQRGLDEGYSISKF 407
Db 317 NIFPMSTTIFVNDGENVDLIVEYAYPKPEHQQIYVNRRTTDFKWEYPKSDNESNIRY 376

Qy 408 CDH-----KNKPGEYIFYAENDDAQFTKMTLNRKPKQVLANASQA--SCSSDGY 458
Db 377 VSELHLTRLKNGEGTGYTFQVNSNDVNSSVTFNVYVNTKPEILTLESHTNGMLQCVVAGF 436

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QY 459 PLPSWTWKCKSDKSPNCTEEL-PEGVWKKANRKFVGOWVSSSTLNMSEAGKGLLVKCCA 517
Db 437 PEPADVWFCEGAFQRCVPIGPMVQWQSSLSFGKLVQSSIDYSAFKHNGTVEGRA 496
QY 518 YNSMGTSCEITFLNSPGFFPIQN-----ISFYATIGLCLPFIIVLVILI 563
Db 497 YNNVGRS--SAFFN-----FAFKGNSKEQIHPHTLFTPLLIIGFVIAAGM---MCIIVMIL 546
QY 564 CHKYKQFRVYSQLOMI-QVTGPLDNEFFVYDFRDEYDLKWEFPRENLEFGKVLGSGAF 622
Db 547 TYKYLQPMTEYVQWQVEEING---NNVYIDPTQLPYDHKWEFPNRRLSFGKTLGAGAF 603
QY 623 GRVNATAYGISKTVGSTQVAKMLKADSEKALMSKLMTHLGHHDNIIVNLGAC 682
Db 604 GKVEATAYGLIKSDAAMTAVAKMLKPSAHLTERALMSKLVLSYLGNNVNLGAC 663
QY 683 TLSGPFVYLFEYCCYGBLLNLYRSKREKFRHTWTWEIFEKHNFSYPTFOAHNSMPSGR 742
Db 664 TVGGFTLVITEYCCYGBLLNLYRSKREKFRHTWTWEIFEKHNFSYPTFOAHNSMPSGR 701
QY 743 EVQLHPDLQLSGFNGNSIHSEDI-----EYENQK-----RLAEE 779
Db 702 EVALYK-----NLLHSKSCSDSTNEYMDKPGSVVYPTKADKRRSARIGSYI 751
QY 780 BEDLN-----VLTFEDLLCFAYQVAKGMEFLPKSCVHRDLAARNVLVTHGKVVI 830
Db 752 ERDVTPEIMDEDELDLLEDSYQVAKGMAFLASKNCIHRDLAARNVILTHGRITKI 811
QY 831 CDFGLARDILSDSSVYVGNARLPVKWMAPELFEPIYTIKSDVMSYGILLWEIFSLGVN 890
Db 812 CDFGLARDIKNSVYVGNARLPVKWMAPELFCVYTFESDVMSYGIPLWELFSLGSS 871
QY 891 PYGIPVDANFYKLIQSGFKMEQFPYATEGYIFWQSCWAFDSKRPFPNLTSLFGCOL 950
Db 872 PYGMPVDSKFYKIKEGFRMLSEHAPAEYDINKTCWDADPLKRPPTFKQIVOLIEKQI 931
QY 951 AEAEACIRTSIHLPKQAPQOGLRAQSPQROVKIHRER 991
Db 932 SDSTN-----HIYSNLN-----CSPNRPVPVDSVR 959

RESULT 9
O97744
ID O97744 PRELIMINARY; PRT: 964 AA.
AC O97744;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Mast/stem cell growth factor receptor (Fragment).
GN KIT1*0101.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HAMPSHIRE BREED; TISSUE=LEUKOCYTE;
RX MEDLINE=98391767; PubMed=9724328;
RA Marklund S., Kijas J., Rodriguez-Martinez H., Roennstrand L., Funa K.,
RA Moller M., Edfors-Lilja I., Andersson L.;
RT "Molecular evolution of the dominant white phenotype in the domestic
RT pig.";
RL Genome Res. 8:826-833 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HAMPSHIRE BREED; TISSUE=LEUKOCYTE;
RA Marklund S.;
RL Thesis (1997), Department of Animal Breeding and Genetics,
RL Swedish University of Agricultural Sciences, Uppsala, SWEDEN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DB EMBL; AJ242228; CAAL1196.1; -.

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DR HSSP; P11362; lFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003593; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR Glycoprotein; Immunoglobulin domain, Phosphorylation; Receptor;
KW Transmembrane; Tyrosine-protein kinase.
FT NON_TER 964 964
SQ SEQUENCE 964 AA; 108287 MW; 90E72EDFABI35887 CRC64;

Query Match 22.9%; Score 1208; DB 6; Length 964;
Best Local Similarity 32.6%; Pred. No. 2.8e-97;
Matches 319; Conservative 168; Mismatches 362; Indels 130; Gaps 32;

QY 38 LISHENNGSSAGKSSVMVGRSGEDLOCTPRRSEGTVEVAAATVEVAESSITIQVQLA 97
Db 16 LLLRVQTGSS--QPSV-----SPEEL-----SPPSIHPAKSELIVSAGD-EIRLFT 59
QY 98 TPGDLCLWFKHSSSLGCQPHFDLQNRGIVSMALINVTQAGEYLLHIQSERA----- 151
Db 60 DPG--SVKWTPE--TLG-----OLSENTHAEWIV---EKAEAMNTG 93
QY 152 NYTVL-----FTVNVDRDQ-LYVLRPPYFRKMNODAL-----LCISE 188
Db 94 NYTCNEGGLSSIIYVVRDPEKLFVDVPLYGK-EDNDALVRCPLTPEVTNYSLTGE 152
QY 189 GVPEP-TVEWVLCSSHRESCKEKGAVVRKEKVLHLEFGTDIRC--CARNALGRE-CTK 244
Db 153 GKPLPKDLTFV-----ADPKAGITIRNVKREYHRL-----CLHCSANQGGKSVLSK 198
QY 245 LFTIDLNAQPOS-----TLPLQLKVEPLWIRCKATHVNHGFLGTWELEDKALEESY 298
Db 199 KFTLKVRAAIRAVPWAIVSKASYLLREGEFAVMCLIKDVSSSVSDSMW-IRENSOTKAQV 257
QY 299 FEMSTYSTNRMTIRILLAFVSSVGRNDTGYVTCSSSKHPSOSALVTILE---KGFINA-T 354
Db 258 KNSWHQGDNFNLQERLTISSARVNDSGVPMCYANNTFGSANVTTLTLEVDKGFINIFP 317
QY 355 SSQEEYEIDPYEKFCFSVRKAYPR-IRCTWIFSO--ASFPEQGRLEDGYISIKFDHK 411
Db 318 MMNTTVFVNDGEDVDLIVEYEAYPEKPEHRQWLYMNRATATDKWEDYPKSENEISRVSEL 377
QY 412 N-----KPEEYIFYAENDDAQFTYKMTLNRKQPVLAN--ASASQASCSDDGYPLPS 462
Db 378 HLRLKGTGEGTYTFLVSNADVNSSVTVNVYNTKPEILTHDRLMNGLMQCVAAGPEPT 437
QY 463 WTWKCSDKSPNCTEEL-PEGVWKKANRKFVGOWVSSSTLNMSEAGKGLLVKCCAYNSM 521
Db 438 IDWTFPGTEQRCSVPVGVVDVQIQNSVSPFGKLVIIHSSIDYSAFKHNGTVEGRA 497
QY 522 GTSCEITFLNSPGFFPIQNISFYATIGLCLPFTV-----VLIVLICHKYKQFRYES 575
Db 498 GKS--SAFFN-----FAPKEQIHAHTLFTPLLIIGFVIAAGMCIIVMLTYKLPQPMYEV 551
QY 576 QLQMI-QVTGPLDNEFYVDPRDEYDLKWEFPRENLEFGKVLGSGAFGRVNNATAYGIS 634
Db 552 QWKVVEEING---NNVYIDPTQLPYDHKWEFPNRRLSFGKTLGAGAFKVVVEATAYGLI 608
QY 635 KTVGSIQVAVKMLKEKADSEKALMSKLMTHLGHHDNIIVNLGACTLSGPPVLIPEY 694

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609 KSDAAMTVAVKMLKPSAHLTEREALMSKLVSYLGNHNMVNLGLACTIGGPTLVITEY 668
QY 695 CCYGDLLNLYRSKREKPHRTWTETIFKEHNFSSYPTFOAHNSNMPGSRREVOLHPPLDOLS 754
Db 669 CCYGDLLNLYRSKREKPHRTWTETIFKEHNFSSYPTFOAHNSNMPGSRREVOLHPPLDOLS 728
QY 755 GFNGNSIHSEDELEYENOKLAEEDLNVLTFEDLLCFAYQVAKGMEFLFKSCVHRD 814
Db 729 PTKADKRSARIGSYIEROVTPAIMEDELALDLELLSFSYQVAKGMAFLASKNCIHRD 788
QY 815 LAARNVLVTHGKVKVCKDFGLARDILSDSSVYVRGNARLPVKWMAPELSLEGYTIKSDV 874
Db 789 LAARNILLTHGRITKICDFGLARDIKNSDNYVVGKGNARLPVKWMAPELSFNCVYTFESDV 848
QY 875 WSGYILLWEIFSLGVNYPGIPVDANFYKLIOSGKMEQPFYATEGYFYVMOSCAWAFDSR 934
Db 849 WSGYIFLWELFSLGSSPYPGMPVDSKPYKMIKEGFRMLSPHEAPAEWYIMKTCWDADPL 908
QY 935 KRPSFNLTSFLGCQALAE 953
Db 909 KRPTFKQIVOLIEKQISES 927
RESULT 10
Q9TQ01 PRELIMINARY; PRT; 964 AA.
AC Q9TQ01;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Mast/stem cell growth factor receptor (Fragment).
GN KITI-0201.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YORKSHIRE / LANDRACE CROSS; TISSUE=LEUKOCYTE;
RA Marklund S.;
RL Thesis (1997), Department of Animal Breeding and Genetics,
RL Swedish University of Agricultural Sciences, Uppsala, SWEDEN.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=YORKSHIRE / LANDRACE CROSS; TISSUE=LEUKOCYTE;
RX MEDLINE=98391767; PubMed=9724328;
RA Marklund S., Kijas J., Rodriguez-Martinez H., Roennstrand L., Funa K.,
RA Moller M., Edfors-Lilja I., Andersson L.;
RT "Molecular evolution of the dominant white phenotype in the domestic
RT pig.";
RL Genome Res. 8:826-833(1998).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AJ223229; CAAL1197.1; -.
DR HSSP; P11362; 1FGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG like; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
KW Transmembrane; Tyrosine-protein kinase.
FT NON_TER 964 964
SQ SEQUENCE 964 AA; 108315 MW; 996C3C46201358A8 CRC64;
Query Match 22.9%; Score 1207; DB 6; Length 964;
Best Local Similarity 32.6%; Pred. No. 3.5e-97;
Matches 319; Conservative 168; Mismatches 362; Indels 130; Gaps 32;
QY 38 LISHENNAGSAGKPSYRMVGRGSPEDLOCTPRROSECTVVEAATVEVAESGITLQVOLA 97
Db 16 LLURVQTGSS--QPSV-----SPEEL-----SPSIHPAKSELIVSAGD-EIRLPCT 59
QY 98 TPGDLSCLWFKFKSSLCQPHFDLQNRGIVSMALNVNTETQAGEYLLHIQISERA----- 151
Db 60 DFG--SVKTFE--TLG-----QISENTHAEWIV-----EKAEMNTG 93
QY 152 NYTVL-----FTVNVRTQ--LYVLRPYFRKMNODAL-----LCISE 188
Db 94 NYTCTNEGGLSSSIYVVRDPEKLFVDPPLYGK-EDNDALVRCPLDPEVTNYSLTGCE 152
QY 189 GVPEP-TVEWVLCSSHRESCKEKGPAVVRKEKVLHFLGTDIRC--CARNALGEE-CTK 244
Db 153 GKPLPKDLTFV-----ADPKAGITIRNVKREYHRL-----CLHCSANQGKSVLSK 198
QY 245 LFTIDLNOAPOS-----TLPQLFKVGEPLWIRCKAIHVNHGFLTWELDKALEGSY 298
Db 199 KFTLKVRPAARVAVAVASVALLREGEFAVAVCLIKDVSSSVDSWM-IRENSOTKAQV 257
QY 299 FEMSTYSTNRMTIRILLAFVSSVRGNDTGYTSCSSKHPQSQALVTILE---KGFINA-T 354
Db 258 KRNSWHQGDNFRLRQERLTITISSRVNDSGVFMCVANNTFGSANVTTLLEVVDKGFNIFP 317
QY 355 SSOEYEIDPYEKFCSVRPKAYPR-IRCTWIFSQ--ASPPCEORGLDEGYSISKFDCHK 411
Db 318 MNNTTVFVNDGEDVDLIVEYEAYPKPHRQWIMYNRATDKMEDYPKSENSIRYVSEL 377
QY 412 N-----KGEYIFYAENDDAQFTKMTNIRKKPOVLAN--ASASQASCSGDPPLPS 462
Db 378 HLRLKTEGGTYTFLVSNADVNSSVTFNVNTKPEILTHDRLMNGMLQCVAGFPPEPT 437
QY 463 WTWKCKSDKSPNCTEEI--PEGVWNKKANRVFGOWSVSSSTLNMSEAGKGLLVKCCAYNSM 521
Db 438 IDWYFCPGTEORCSVPVGVQIONSVPFGKLVHSSIDYSAFKHNGTVECPAYNDV 497
QY 522 GTCETIFLNSPGPPPIQDNISFYATIGLCPLPIV-----VLIVLICHYKKQFRYES 575
Db 498 GKS--SAFFN---FAPKEQIHAHTLFTPLLIGFVIAAGMMCIIVMILTYKYLQKPMYEV 551
QY 576 QLOMI-QVTGPLDNEYVDPRDYEDLKWEFFRENLEFPGVGLSGARGVNMATAYGIS 634
Db 552 QWKVVEEING---NNYVIIDPTQLPYDHKWEFFPRNRLSPGKTLGAGAFKGVVEATAYGLI 608
QY 635 KTGVSIOVAVKMLKEKADSKCEKALMSKELKMTHLGHHDNIIVNLIGACTLSGPVVLIFEY 694
Db 609 KSDAAMTVAVKMLKPSAHLTEREALMSKLVSYLGNHNMVNLGLACTIGGPTLVITEY 668
QY 695 CCYGDLLNLYRSKREKPHRTWTETIFKEHNFSSYPTFOAHNSNMPGSRREVOLHPPLDOLS 754
Db 669 CCYGDLLNLYRSKREKPHRTWTETIFKEHNFSSYPTFOAHNSNMPGSRREVOLHPPLDOLS 728
QY 755 GFNGNSIHSEDELEYENOKLAEEDLNVLTFEDLLCFAYQVAKGMEFLFKSCVHRD 814
Db 729 PTKADKRSARIGSYIEROVTPAIMEDELALDLELLSFSYQVAKGMAFLASKNCIHRD 788
QY 815 LAARNVLVTHGKVKVCKDFGLARDILSDSSVYVRGNARLPVKWMAPELSLEGYTIKSDV 874
Db 789 LAARNILLTHGRITKICDFGLARDIKNSDNYVVGKGNARLPVKWMAPELSFNCVYTFESDV 848
QY 875 WSGYILLWEIFSLGVNYPGIPVDANFYKLIOSGKMEQPFYATEGYFYVMOSCAWAFDSR 934
Db 849 WSGYIFLWELFSLGSSPYPGMPVDSKPYKMIKEGFRMLSPHEAPAEWYIMKTCWDADPL 908


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QY 935 KRPSFNPNTSLFLGCOLAEA 953
DB 909 KRPTFKQIVOLIEKOISES 927

RESULT 11
Q9TQ00 PRELIMINARY; PRT; 964 AA.
AC Q9TQ00
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Mast/stem cell growth factor receptor (Fragment).
GN KIR1-0202.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YORKSHIRE / LANDRACE CROSS; TISSUE=LEUKOCYTE;
RA Marklund S.;
RL Thesis (1997), Department of Animal Breeding and Genetics,
RL Swedish University of Agricultural Sciences, Uppsala, SWEDEN.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=YORKSHIRE / LANDRACE CROSS; TISSUE=LEUKOCYTE;
RX MEDLINE=98391767; PubMed=9724328;
RA Marklund S., Kijas J., Rodriguez-Martinez H., Roennstrand L., Funa K.,
RA Moller M., Edfors-Lilja I., Andersson L.;
RT "Molecular evolution of the dominant white phenotype in the domestic
RT pig.";
RL Genome Res. 8:826-833(1998).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AJ223230; CAA11198.1; -.
DR HSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG_1.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00113; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
KW Transmembrane; Tyrosine-protein kinase.
FT NON TER 964
SQ SEQUENCE 964 AA; 108287 MW; 1B21292A962E9191 CRC64;

Query Match 22.9%; Score 1207; DB 6; Length 964;
Best Local Similarity 32.6%; Pred. No. 3.5e-97;
Matches 319; Conservative 168; Mismatches 362; Indels 130; Gaps 32;

QY 38 LISHENNGSAGKSYRMVRGSPEDLQCTPRROSEGTVEAATVEAASGITLQVOLA 97
DB 16 LLIRVQTSS--QPSV-----SPEL-----SPSIHPAKSELIVSAGD-EIRLFT 59
KIT.

QY 98 TPGDLSCLVFKHSLGCGQPHFLQNRGIVSMALNVTTQAGYLLHIQISERA----- 151
DB 60 DPG--SVKWTTE--TLG-----QLSENTHAEWIV-----EKAEMMTG 93
KIT.

QY 152 NYTVL-----FTVNRDTQ-LYVLRPPYFRKMNQDAL-----LCISE 189
KIT.

DB 94 NYTCTNEGGLSSSIYVVRDPEKFLVDPPLYCK-EDNDALVRCPLTDPVTNYSLTGE 152
QY 189 GVPEP-TVEWVLCSSHRESCKEGPAVVRKEKVLHFLFTDIRC--CARNALGRE-CTK 244
DB 153 GKPLPKDLTFV-----ADPRAGITIRNVKREYHRL-----CLHCSANOGGKSVLSK 198
QY 245 LFTIDLNAQPOS-----TLPQLFLKVGEPFLWIRKRAIHVNHGFLTWELDKALEGSY 298
DB 199 KFTLKVRRAALRAVPVAVSKASYLLREGGEFAVMCLIKOVSSSVDSNM--IRENSQTAQV 257
QY 299 FEMSTYSTNTRMIRILLIAFVSSVGRNDTGYTTCSSKHPQSQALVTILE---KGFINA-T 354
DB 258 KRNSWHOGDFNRLQEKLTISSRVNDSGVPMCVANNTFGSANVTITLVVDVKGFNIFP 317
QY 355 SSOEYEIDPYEPCFSVRPKAIPR-IRCTWIFSQ--ASFPCEQRGLEDGVSISKFCODHK 411
DB 318 MMNTTTFVNDGEDVDLIVEYEAYPKPEHRQMIYMNRTATDKWEDYPKSENESENIRYVSEL 377
QY 412 N-----KPEYIFYAENDDAQFTKMTLNIRKKPOVLAN--ASASQASCSSGYPLPS 462
DB 378 HLTRLKTEGGTYTFLVSNADVNSSVTFFNVYVNTKPEILTHDRLMNGLMQCVAAGFPDEPT 437
QY 463 WTWKCKSDKSPNCTEEI-PEGVWNKKANRVFGOWSVSSSTLNMSKAGKGLLVKCCAYNSM 521
DB 438 IDWYFCPTQRCSPVPGVDVQIONSSVSFPFGKLVITHSSIDYSAFKHNGTVECRANDV 497
QY 522 GTCETIFLNSPGPFPIQDNI SFYATIGLCPPIV-----VLIVLCHKYKQFYRES 575
DB 498 GKS--SAFFN-----FAFKEQIHATHTFTPLLLIGFVIAAGWMCIIIVMLITYKLOKPMYEV 551
QY 576 OLQMI-QVTGPLDNEYFYVDPROVEYDLKWEFFRENLEFGKVLGSGAGFGRVMNATAYGIS 634
DB 552 QWKVEEING---NNYVYIDPTQLPYDKWEPFRNRLSFGKTLGAGAGFKVVEATAYGLI 608
QY 635 KTVGSIQVAVKMLKEKADSCKEALMSKMTLHGHDMIVNLLGACTLSGPPVLIPEY 694
DB 609 KSDAAMTVAVKMLKPSAHLTEREALMSKLVSLYGNHMIIVNLLGACTIGGPTLVITEY 668
QY 695 CCYGDLNLYLRKREKPHRTWTEIFKEHNFSSYPTFOAHNSNMPGSGREVOLHPDQOLS 754
DB 669 CCYGDLNLLFLRRKDSFICKQEDHAEALYKLLHSSKSSCSDSTNEYMDMKPGVSYYV 728
QY 755 GFNGNSHSDEIEYENQKRLAEEDLNLVLTPEDLICFAYOVAKGMEFLEFKSCVHRD 814
DB 729 PTKADKRARSARIGSYIERDVTPTAIMEDEDLALDLELLSFSYQVAKGNAFKASKNCHRD 788
QY 815 LAARNVLVTHGKVKVVICDFGLARDILSDSSYVVRGNARLPVKWMAPESLFEGYITIKSDV 874
DB 789 LAARNILLTHGRITKICDFGLARDIKDSSYVVRGNARLPVKWMAPESLFNCVYTFESDV 848
QY 875 WSYGILWEITPSLGNVPYGPIDVANDYKLIQSQFKMGPYATGEGYFVNMOSWAFDSR 934
DB 849 WSYGIFLWELPSLGSPPYGPMPVDSKFKYKMLKEGFRMLSPHAPVEMYDIMKTCWDADPL 908
QY 935 KRPSFNPNTSLFLGCOLAEA 953
DB 909 KRPTFKQIVOLIEKOISES 927

RESULT 12
Q9XS93 PRELIMINARY; PRT; 978 AA.
AC Q9XS93
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KIT.
GN C-KIT.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;

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[1]
RN SEQUENCE FROM N.A.
RP TISSUE=CEREELLUM;
RA London C.A., Galli S.J., Yuuki T., Hu Z.-Q., Helfand S.C.,
RA Geisler E.N.;
RT "Spontaneous canine mast cell tumors express tandem duplications in
RT the proto-oncogene c-kit.";
RL Exp. Hematol. 0:0-0(1999).
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AF099030; AAD28369.1; -.
DR HSSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR0003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 2.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00410; IG like; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;
KW Receptor; Transferase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 978 AA; 109651 MW; 5AC31B5AC4E9910F CRC64;

Query Match 22.9%; Score 1205; DB 6; Length 978;
Best Local Similarity 31.5%; Pred. No. 5.4e-97;
Matches 329; Conservative 167; Mismatches 387; Indels 160; Gaps 33;

QY 14 LIAVLVSMILETTNQDLPVVKLVISHENNGSSAGKPSVYRVWVGSPEDLQCTPRQSE 73
DB 11 LCVLLLLLLGVGTGSGQSPS-----SPGPESL----- 38

QY 74 GTVYEATVEVAESGSIITVOLATPGDLSCLWVFHSSLGCPHFDLQNRGIVSMALN 133
DB 39 PSIHAKSELIVSGD-ELSLCTDGFVK-WTFE--TLG-QLNENTHNEWITEKA--- 89

QY 134 VTETQAGEYLLHIOSEKANTVLTNNVRD-TQYVLRYPFRKMNQDALLCISGVPE 192
DB 90 ---EAGHTGNYCTNRDGLSRSIYFVRDPKFLFLVDLPYKGEKNDTLVRC----- 138

QY 193 PTVEWVLCSSHRESCKEAGPAVVRKEKVLHELFGTDIR-----C-CARNALGRE 241
DB 139 PLTDPEVTNYSLRGC--EGKPLKDLTFVADPKAGITIRNVKREYHRLCHLSADQKRT 196

QY 242 -CTKLFTIDLNAPOS-----TLQPLFKVGEPLWIRCKRAIHVNHGFLTWELDKALE 294
DB 197 VLSKKFTLKRAIRAVPVVSVSKTSLLEGEAFSWCFCIKDVSSFVDSMW-----IK 250

QY 295 EGSYFEMSTYST-----NRTMIRILLAFVSSVGRNDTGYTCCSSKHPQSALVTILE-- 347
DB 251 ENSQTNAQTQSNWHHGDFFERQEKLIISARVNDSGVFMVCYANNTFGSANVTITLEV 310

QY 348 -KGFINA-TSSQREYEIDPEKFCFSVRFKAYPR-IRCTWIFSOASF--PCEQRGLDEGY 402
DB 311 DRGFINIFPMSTTIFVNDGENVDLIYVEAYPKPEQOMIYMNRTDKWEDYPKSDNE 370

QY 403 SISKFCDH-----KNKPCGEYFYAENDDAQFTKMTFLAIRKKPOVLANASQA--SC 453
DB 371 SNRIYSELHLTRLKGNEGTYTFQVNSDVNSVTENVYNTKPELITHTESLNGMLQC 430

QY 454 SSDGYPPLPSWTWKCDKSPCTBEI--PEGVWKKANKRVFGQVSSSTLNMSAGKGLL 512
DB 431 VVAGFPPEPAVDWYFPCGAERQCSVPICGMVDVQMGNSSLSPSGLKLVQSSIDYSAFKNGT 490
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QY 513 VKCAVNSMCTSETIFLNSPGPPFIQDN-----ISFYATIGLCPLPIW 558
DB 491 VECRAYNNVGRS--SAFFN---FAFKGNSKEQIHPTLFTPLLIGFVIAAGM---MCI 540

QY 559 LIVLICHYKKQFYESQLQMI-QVTCPLDNEYFYVDFRDEYDLKWEFFRENLEFGKVL 617
DB 541 IVMLITYKYLQKPMYEQVKVBEING---NNVYVIDPTQLPYDHKWEFFPNRLSFGKTL 597

QY 618 GSAFGKRVNATAYGISKTVGSIOVAVKMLKEKADSCKEALMSLKMTHLGHHDNIVN 677
DB 598 GAGAFKGVATAYGLIKSDAAMTAVAKMLKPSAHLTERALMSLKVSLYLNHNMIVN 657

QY 678 LLGACTLSGGEVYLIFFEYCCYGDLLNLSRREKFRHRTWTFEIKHEHNFSSYPTFOAHSS 737
DB 658 LLGACTVGGFTLVITEYCCYGDLLNLSRKRKDSFICKQEDHGEVALYKLLHSSKSSCS 717

QY 738 MPGRREVQLHPPDLQSLGFGNGNSIHSDEIEYENQKRLAEEEDLN-----VLTFF 788
DB 718 DSTNEYMDMKP-----GDSYVVTAKRRSRIGSYIERDVTPTAIMEDDELALDL 768

QY 789 EDLLCFAYOVAKGMEFLFKSCVHRDLAARNVLTHGVKVKICDFGLARDILSDSSVYVR 848
DB 769 EDLLSFSYQVAKGMAFLASKNCHRDLAARNILLTHGRITKICDFGLARDIKNDSNYVVK 828

QY 849 GNARLPVKMAPESLPRGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYKLIQSG 908
DB 829 GNARLPVKMAPESIFNCVYTFESDVMSYGIFLWELSLGSSPYGMPVDSKFKYKMEG 888

QY 909 FKMEQPYATEGIYVWQSAFDSRKRPSFNNLTSLFGCOLAFAEAEACITSIHLPKQA 968
DB 889 FRMLSPHEPAEMVYDINKTCWDADPLKRPSTKQIVQLIEKQISDSTN-----HIYSNL 941

QY 969 APOQRGELRAQSQRQVKIHRER 991
DB 942 AN-----CSPNPERPVVDHSVR 958

RESULT 13
Q98SU2 PRELIMINARY; PRT; 977 AA.
AC Q98SU2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Receptor tyrosine kinase Fms.
OS Danio rerio (Zerr's danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=38750;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21359118; PubMed=11466528;
RA Parichy D.M., Johnson S.L.;
RT "Zebrafish hybrids suggest genetic mechanisms for pigment pattern
RT diversification in Danio.";
RL Dev. Genes Evol. 211:319-328(2001).
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AF324480; AAK15302.1; -.
DR HSSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 4.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00409; IG; 4.
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DR SMART; SM00408; IGC2; 1.
DR SMART; SM00220; S.TK; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN 1.
DR PROSITE; PS00240; RECEPTOR TYR.KIN III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferrase; Transmembrane.
FT VARIANT 31 P -> L.
FT VARIANT 148 L -> F.
FT VARIANT 218 R -> K.
FT VARIANT 263 I -> M.
FT VARIANT 490 R -> K.
FT VARIANT 594 E -> A.
FT VARIANT 614 G -> R.
FT VARIANT 926 N -> T.
FT VARIANT 934 A -> T.
FT VARIANT 938 A -> V.
SQ SEQUENCE 977 AA; AAB2FF2A20D66090 CRC64;
Query Match 22.9%; Score 1204.5; DB 13; Length 977;
Best Local Similarity 32.2%; Pred. No. 5.9e-97;
Matches 334; Conservative 166; Mismatches 363; Indels 173; Gaps 36;
QY 12 LLLVLSVLETVTQDLPVVKVLSHENSSAGKPSYRMVRGSPEDLOCTPRQ 71
DB 5 LLLIGI---LFGQVQSWSEPIRL-----NSGAPAG--TDVLDGSGPLQVLC----- 48
QY 72 SEGVTEAATVEVAESGSIITLQVLAATPGDLSCLVFKHSSSLGQCFHDLQNRGIVSMAI 131
DB 49 -EG-----DGPVIFLPLA-----KH-----KRYISKEVGKIRSFV 79
QY 132 LNVTEQAGEY-LLHIOSEKANYVLTQVNRDQ-LYV---LRPYFRKMNQDALL-C 185
DB 80 EKATVDPTGTGKVCYIINENDSNLSSSVHVFVRDSRVLFVSPSITLRYVRK-EGEDLLLP 138
QY 186 ISEGVPEPTVWVLCSSHRSCKEEG-PAVVRKEEKL---HEFGTDIRCCARNALGR 240
DB 139 L---LTPDQATDLMFRMDNGSAAPYGNATDPDRKGLIRNVHFGFNADYICARIGAE 195
QY 241 ECTKLFTIDLNAQOSTLPQLFLK-----VGEPLMIRKAIHVNHGFGITWELEDKAL 293
DB 196 KVKIFSIINIQLRFP-PYVYLRNEVVKLVGERLQISCTNNPNFYVNVVTHSSRL 254
QY 294 EESYFEMSTYVNRWIRILLAFVSSVGRNDTGYTCSSSKHPSQALVT---ILSKGF 350
DB 255 PKAE--EKSTIEGRLAIESILT-IPVQSDNGNITCTGQNEAGANSSTTQLLVVDEPY 311
QY 351 INAT---SSQEEY-----EIDPYEKFCSVRFKAYPRIC---TWIFSQASPECEOR-- 396
DB 312 IRLSPKLSLTHRGLSIEVSEGDVDLGLVIEAYPLTSHKWTPTSHNASLP-ENRFY 370
QY 397 GLEDGYSISKFOHKN--KGEYIFYAENDDAQFTKFTLNIRKKPQVLAN-ASASQASC 453
DB 371 NHNDRYEALLFLKELNFEIIGYTLNVKNSMKSASITFDIKWTKPVARKVWENVTLSC 430
QY 454 SSDGYPLPSTWTKCSKSNCTEEL---PEGVWNKANKRVFGQVSSSTLNMSAGK 509
DB 431 RSYGYPAISILWYQCTGIRITCPTENTDLPQIQQTVEFKESFGAVGVESVLTVG-PNR 489
QY 510 GLLVKKCAVNSMGTSCSTIFLNSGPPFPFDNISFVATIGLCIFPIV-VLIVLICHKY 567
DB 490 RMTVVCVAFNLVGGSDTFSMD-----VSDQIFTSAMCGSTVAMVVLGILLFIYIKY 542
QY 568 KQPRYESQLQMIQVTPGLONEYFYVDFRDYEDLKWKEFFRENLEFGKVLGSGAGFGRVMN 627
DB 543 KQPRYIRKWIIEATN--GNVYTFIDPTQLPYNEKEFEPRDKLKLKTLGAGEFGKVE 600
QY 628 ATAYIGISKTGYSIQVAVKMLKEKADSCKEALMSLKMTHLGHHDNI VNLGACTLSGP 687
DB 601 ATAYGLCKEDNITGAVAKMLKASAHDPDEREALMSLKLHLGQHKNI VNLGACTHGGP 660

QY 688 VYLIFEYCCYGDLLNLYRSKKEF-----HRTW-----TEI 718
DB 561 VLVITEYCCGDLNLFIRSKAENFLNFWMTIPNPEPMDTKYNVSTERMFVSDSGISST 720
QY 719 FXEHNFSSPTFOAHNSNMPGSRVQLHPLDQLSGFNGSIHSEDEIYENOKRLAE 778
DB 721 CSHYLDMPRPVTSRPTNSTLDSSECC----- 747
QY 779 EEDNLVLTEDLLCFAYQVAKGMFLFKSCVHRDLAARNVLVTHGKVKVXICDPLGARD 838
DB 748 --EDSWPLDMDDLLRFSQVQAQGLDLAAKNCHRDMAARNVLLTNSRVAKICDFGLARD 805
QY 839 ILSDSSVYVRGNARLPVKWMAPESLFEGIYTIKSDVMNSYGILLWEIFSLGVNYPGIPVD 898
DB 806 IMDSNVYVKGARLPVKWMAPESEIFECVTVQSDVMSYGIMLWEIFSLGSPFNILVD 865
QY 899 ANFYKLISQSGFKMEQPPYATEGIYVQMSQWAFDRKRPSPNLTSLFGCOLAE-AEBAC 957
DB 866 SKFYKMIKCGYQMSRDPFAPPMTYIMKMCWNLDAERPTFSKISQMIQRLGETSEQD 925
QY 958 IRTSIHLPKQAAPQOR 973
DB 926 NQEKYKNIPEAAEAQQ 941
RESULT 14
QYTD7
ID QYTD7 PRELIMINARY; PRT; 948 AA.
AC QYTD7;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Stem cell factor receptor (Fragment).
GN C-KIT.
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP SEQUENCE FROM N.A.
RA Lawrence S.B., Greenwood P., Tisdall D.J., McNatty K.P., Fidler A.E.;
RT "Partial cDNA sequence of the c-kit homologue of brushtail possum
RT (Trichosurus vulpecula).";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131209; AAF22141.1;
DR HSSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003598; Ig C2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
KW Immunoglobulin domain; Receptor; Tyrosine-protein kinase.
FT NON_TER 948 948
SQ SEQUENCE 948 AA; 106323 MW; 708E0258FFC4D07D CRC64;
Query Match 22.8%; Score 1201; DB 6; Length 948;
Best Local Similarity 33.0%; Pred. No. 1.2e-96;
Matches 314; Conservative 148; Mismatches 356; Indels 134; Gaps 29;
QY 77 YEATVEVAESGSIITLQVLAATPGDLSCL-----WFKHSSSLGQCFHDLQNRGIVSMA 130
DB 33 YSPSITPARS---QLTVNFGSEIKLSCDLHFVNWTFFENAAAL----HLE-SSRTTETWL 84
QY 131 ILNVTEQAGEYLLHIOSEKANYVLTQVNRDQVLYVLRPRFKMNQDAL----- 183

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Db 85' TTNAQAQDTGRYCT---TNKMGSLSSIIYVFKDPKILFLDLLRYLGNESDALVNCVPVT 141
QY -----LCISGVPEP-----TVEWLCSHRESCKEEGPAVVRKEBKVLH 223
Db 142 PEVNTFTLRUCGKPLPKDLTLIPDIQGIITIKNVK-RSHNKIC-----184
QY 224 ELFGTDIRCCARNALGRECTKLTLDLNOAPOSTLPOL-----FLKVGEBLWIRCKAI 276
Db 195 -----FQCSAQDQGLKSLDRMTLKVRAPOS-VPEVSLLOTQNYLLRGETFQATCMIK 237
QY 277 HYNHGFGLTWELEDKALEBGSFENSTYSTNTMIRILLAFVSSVGRNDTGYTTCSSK- 335
Db 238 DVASSVWSNMWIKDNNRI---STHTOSRHSQDGYAYERODILITISPRVNDVSGVFTCFANNT 294
QY 336 --HPSQSALVTILEKGFINA-TSSOEYEIDPYEKFCFVRKAYPR-IRCTWIFSQASF 391
Db 295 FGPANVTATLKVEKGFINFIPQMTTIFINDGENIDLVEAEAPKPEHLQWIMYNGTV 354
QY 392 PCEQRGLDGYS-----ISKFCOHKNK-----PGEYIFYAENDDAQFTKMTFLNI 436
Db 355 TDKW---DDYTKPGSESTIRYISEL--HLNRLKGTGGGYTFVSNSDVSTSVTFKVIV 408
QY 437 RKPQVILANASQA--SCSSGYPLPSWTWKCKSDKSPNC-TEEIPEGVWKKANRKYV 493
Db 409 KTKPEILTSDRLMGILLQCAAGFPEPTIDWYFCGTEQRCSTSLVPMVDVKTNSMMLPPF 468
QY 494 GOWSSSTLNWSEAGKLLVKCANMCTSCETIFLNSPGPPFFIOTDNI SFATIGLCL 553
Db 469 GKIVVESTIDSAFRNGTVCKASNDVGS--SAFN-----PAIKBQITSHTLFTPLLI 522
QY 554 PFIV-----VLIVLICHYKQFYESLOMI-QVTGLDNEIFYVDFRDYEYDLKWEF 606
Db 523 GFVVAAGLMCVIIITYKYFKPMYEVQWKVEELNG---NNYVYIDTQPLDYHKWEEF 579
QY 607 PRENLEFGKVLGSGAFGRVMNATAYGISTGVSIOVAVKMLKEKADSCKEALMSLKM 666
Db 590 PRNRLSFGKTLGAGAFGKVEATEAGLPSKSDAAMTVAVKMLKPSAHLTREALMSLKV 639
QY 667 THLGHHDINVLIGACTLSGPVYLIFCYCYGDLNLRSEKREKHTWTEIFKEH----722
Db 640 SYLGNHMIANLLGACTIGGPTLVITEYCCYCGDLNLFRLRRKDDSF-----ICSKHEDHA 693
QY 723 NFSSYPTFOAHNSNMPGSR--VOLHPPDLQSLGFGNGNSIHSEDETEYENOKRLAEEBE 781
Db 694 EAALYNLLOSKESSCDGANEMDMKPGVYVVPYKAEKRSARVGSYIERDVTTAIMED 753
QY 782 DLNVLTFEDLLCFAYQVAKMEFLBPKSCVHRDLAARNVLVTHGKVYKICDFGLARDILS 841
Db 754 DELALDIEDLLSFSYQVAKGMSFLASKNCIHRDLAARNILLTHGRITKICDFGLARHIKN 813
QY 842 DSSYVVRGNARLPVKWMADESLEFGIYTTKSDVWSYGILLWIFSLGVNPNYPGIPVDANP 901
Db 814 DSNYVVGNGARLPVKWMADESIFNCVYTPESDVWSYGIFLWELFSLGSSPYFGMPVDSPK 873
QY 902 YKLIOSGFKWEPFYATEGIIYFMOSCAFPDSRSPFNLTSLFGCOLAEA 953
Db 874 YKMIKEGFRMLSPECAPPENYEMKSCWNEDFLORFTFKLIVOLIEBQQLDLS 925

RESULT 15
Q98SU4
ID Q98SU4 PRELIMINARY; PRT; 977 AA.
AC Q98SU4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Receptor tyrosine kinase Fms.
OS Danio albolineatus (pearl danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=27699;
RN [1]
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RP SEQUENCE FROM N.A.
RA MEDLINE=21359118; PubMed=11466528;
RX Parichy D.M., Johnson S.L.;
RT "Zebrafish hybrids suggest genetic mechanisms for pigment pattern
RT diversification in danio.";
RL Dev. Genes Evol. 211:319-328 (2001).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AF324478; AAK15300.1; -.
DR HSSP; P11362; IFCK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig_4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG like; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane.
FT VARIANT 57 57 L -> V.
FT VARIANT 164 164 A -> V.
FT VARIANT 325 325 R -> P.
FT VARIANT 326 326 G -> C.
FT VARIANT 327 327 L -> P.
FT VARIANT 328 328 S -> A.
FT VARIANT 328 328 S -> F.
FT VARIANT 366 366 E -> D.
FT VARIANT 398 398 Q -> K.
FT VARIANT 419 419 K -> R.
FT VARIANT 431 431 P -> R.
FT VARIANT 439 439 T -> S.
FT VARIANT 611 611 N -> I.
FT VARIANT 706 706 I -> T.
FT VARIANT 926 926 S -> T.
FT VARIANT 952 952 E -> D.
SQ SEQUENCE 977 AA; 109802 MW; 109802 MW; PFFAAAE73BDF463B CRC64;

Query Match 22.8%; Score 1198.5; DB 13; Length 977;
Best Local Similarity 33.3%; Pred. No. 2e-96;
Matches 325; Conservative 162; Mismatches 365; Indels 123; Gaps 33;

QY 84 VAESGSITLQVOLATPGDLSCLVWPKHSLGCPHFDLQNRGIV-----SNAILNVT 136
Db 37 IYDGS-----PLQLVCEGDAPVTFL-----PRLAKHKRYISKEVGRSPHVEKATV 84

QY 137 TQAGEY-LLHIQSERANYTVLFTVNVDTQ-LVV-----LRRPYFRKMENODALLCISEG 189
Db 85 DFTGYKYCVINENSDNMSVHVFDVRSRVLFVSPSTSLR--YVRK-EGEDLLPCLLT 141

QY 190 VPEPTVEWYLCSSHRESCKEEGPAVVRKEBKVL-----HELFGTDIRCCARNALGRECTKL 245
Db 142 DEDAT-DFTFRMDNGSAAPYGMNATPDRKGLVLRNVHPGFNADYICSAIGGAEKVSKT 200

QY 246 FTIDLNOAPOSTLPQLFLK-----VGBPLWIRCKAIHNVHGFGLTWELEDKALEBGSY 298
Db 201 FSINITIQRLEFP-PYVYLKRNVEYKLVGKGLQISCTTNNPNFNSYNTVTHSSRMLPKAE- 258

QY 299 FEWSYSTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSQSALVT---ILEKGFINAT- 354
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Db 259 -EKSTMEGRDRAIESILT-IPSVQSDTGNITCTQNEAGANSSTQLLVVDEPYIRLSP 316
Qy 355 --SSOEY-----EIDPYEKCFSPKAYPRIRC-----TWIFSOASFPCEQR--GLEDG 401
Db 317 KLSKLTTHRGSLIEVSEGGDVLGLIAYPPLTSHKWETPTSHNASLP-ENRFYNHNR 375
Qy 402 YSISKFCDHKN--KPGYIFVAENDDAQFTKMTLINIRKKQVLAN-ASASOASCSSDGY 458
Db 376 YEALLFLKRLNFEELGQYTLNVQNSMKASITFDIKMTYKPVAKYKWNVTTLSCPSYGY 435
Qy 459 PLPSWTWKCKSDKSPNCTEEI-----PEGWNKKANRKFQGWVSSSTLNMSEAGGLLVK 514
Db 436 PAPTILWYQCTGIRTCPTENTDLQPIQTQTVFQKESFGAVGESVLTVG-PNRRMTWV 494
Qy 515 CCAYNSMTSCETIFLNSPGPPPTQDNISFYATIGLCLPFIV--VLIVLICHYKQKQFR 572
Db 495 CVAFNLVQGSDDTFSMD-----VSDQIFTSAMCGSTVAMVVLGLLLIFMIYKYKQKPR 547
Qy 573 YESOLQMIQVGTPLDNEYFYVDFRDYEDLKWEPFRENLEFGKVLGSGAFGRVMNATAYG 632
Db 548 YEIRWKIIEATN--GNNTYFDPTQLPYNERWEFFPRDKLGLKTLGACAFKGVVEATAYG 605
Qy 633 ISKTGVSIOQAVKMLKEKADCEKALMSELKMMTHLGHNDNIVNLGACTLSGPPVYLIF 692
Db 606 LGKEDNITRVAVKMLKASAHDPDEREALMSELKILSHLQHKNIIVNLGACTHGGPVLVIT 665
Qy 693 BYCCYGDLLNLYRSKREKPHR-----TWEIFKEHNFSSYPTFOAHNSNMPGS----- 741
Db 666 BYCCHGDLNLFIRSKAENFLNFVMTIPNPFPEMTDYKNVSIERMFVRSDSGISSTCSDHY 725
Qy 742 ---REVQLHPPLDQLSGFNGNSIHSEDEIEYENOKRLAEEBEDLNVLTFEDLLCFAYQV 798
Db 726 LDMRPVTSRPTNSTLDS-----SSCOEDSWPLDMDLLRFSQV 765
Qy 799 AKGMEFLBFCVHRDLAARNVLVTHGKVVKICDFGLARDILSDSSYVVRGNARLPVKWM 858
Db 766 AQGLDFLAAKNCIHRDVAARNVLLTNSRVAKICDFGLAPDIMNDSNYYVVKGNARLPVKWM 825
Qy 859 APESLFEGIYTIKSDVWSYGILLWEIFSLGVNPPYGPIDANFYKLIQSGFKMEOPFYAT 918
Db 826 APESIFEVCYTVQSDVWSYGIMLWEIFSLGKSPYFNILVDSKFYKMKYQMSRDPFAP 885
Qy 919 EGIYFVMSQWAFDSKRKPSPPNLTSLGCOLAE-AEEACIRTSIHLPKOAAPOQGGILR 977
Db 886 PEMYIMKMCWNLDAERPTFSKISQMIQRMIGTSEQODSOEYKNI PAEAEQO--LE 943
Qy 978 AQSPORQVKIHRERS 992
Db 944 SCDPAK---HEEES 954

Search completed: May 24, 2003, 16:59:18
Job time : 78.9642 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:38:17 ; Search time 55.9718 Seconds
(without alignments)
2361.629 Million cell updates/sec

Title: us-09-919-408-2

Perfect score: 5264

Sequence: 1 MRALAQRSDRLLLVLSV.....RGGLRAQSPQVQKIHRRS 992

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5264	100.0	992	14 AAR37502	Murine flk-2. Mus
2	5264	100.0	992	16 AAR67815	Flk2 receptor prot
3	5264	100.0	992	16 AAR67535	Mouse flk-2. Mus
4	5264	100.0	992	17 AAR97418	Human foetal liver
5	5264	100.0	992	18 AAW19874	Murine flk-2 recep
6	5264	100.0	992	20 AAY08616	Murine flk-2 prote
7	5256	99.8	992	14 AAR44994	Murine flk-2 recep
8	5256	99.8	992	14 AAR31375	Murine flk-2. Mus
9	5239	99.5	992	13 AAR28038	Murine flk-2. Mus
10	5102	96.9	1000	16 AAR81868	Flk2/flt3 tyrosine

11	4436.5	84.3	993	16 AAR75961	Human STK-1. Homo
12	4429.5	84.1	993	16 AAR67816	Flk2 receptor prot
13	4429.5	84.1	993	16 AAR67536	Human flk-2. Homo
14	4429.5	84.1	993	17 AAR97419	Murine foetal live
15	4429.5	84.1	993	18 AAW19873	Human flk-2 recep
16	4429.5	84.1	993	20 AAY08617	Human flk-2 protei
17	4426.5	84.0	993	14 AAR37503	Human flk-2. Homo
18	4426.5	84.0	993	14 AAR44995	Human flk-2 recep
19	4420.5	84.0	993	16 AAR81869	Human flk2/flt3 ty
20	4417.5	83.9	1167	14 AAR31376	Human flk-2. Homo
21	4409.5	83.8	983	19 AAR63588	Human receptor typ
22	4408	83.7	986	19 AAR63587	Human receptor typ
23	4404	83.7	986	19 AAR63589	Human receptor typ
24	4404	83.7	994	19 AAR63586	Human receptor typ
25	2806.5	53.3	665	19 AAR63585	Human receptor typ
26	2373.5	45.1	749	19 AAR78002	Protein pMON32390.
27	2226.5	42.3	481	15 AAR47579	Soluble Flk-2. Mu
28	1223.5	23.2	972	23 AAU11935	Colony stimulating
29	1223	23.2	975	22 AAE07144	Murine Kit/stem ce
30	1223	23.2	975	22 AAE07148	Mutant murine Kit/
31	1221.5	23.2	972	23 AAU79039	Human macrophage c
32	1221.5	23.2	972	23 AAU11936	Colony stimulating
33	1221.5	23.2	972	23 AAU11941	Colony stimulating
34	1221.5	23.2	972	23 AAU73585	Colony stimulating
35	1221.5	23.2	1055	22 ABG15479	Novel human diagno
36	1220.5	23.2	972	23 AAU11934	Colony stimulating
37	1220.5	23.2	972	23 AAU11937	Colony stimulating
38	1219.5	23.2	972	23 AAU11940	Colony stimulating
39	1216.5	23.1	972	23 AAU11938	Colony stimulating
40	1215	23.1	977	21 AAY51322	Bovine c-kit bK-1
41	1212.5	23.0	972	23 AAU11939	Colony stimulating
42	1197.5	22.7	2129	22 ABG15478	Novel human diagno
43	1197.5	22.7	2129	22 ABG20749	Novel human diagno
44	1196	22.7	976	22 AAE07145	Human Kit/stem cel
45	1196	22.7	976	22 AAU00375	Human stem cell gr

ALIGNMENTS

RESULT 1

AAAR37502

ID AAR37502 standard; Protein; 992 AA.

XX AAR37502;

AC AAR37502;

DT 19-OCT-1993 (first entry)

XX Murine flk-2.

XX Murine, receptor; protein; tyrosine kinase; pTK; flk-2; primitive;

XX hematopoietic cell; mature; family; conserved; region;

XX catalytic domain; c-kit; fetal liver kinase; flk; fetal; spleen;

XX thymus; adult; brain; bone marrow; multipotential; CFU-Blast colony;

XX hierarchy; transduction; T-lymphoid; lineage.

XX Mus musculus.

XX Key Location/Qualifiers

XX Peptide 1..27

XX Protein /note= "Hydrophobic leader sequence"

XX Domain /note= "Mature murine flk-2"

XX Region /note= "Extracellular receptor domain"

XX Domain /note= "Transmembrane region"

XX Domain /note= "Intracellular catalytic domain"

XX Domain /note= "Catalytic sub-domain"

XX Domain /note= "Catalytic sub-domain"

FT Domain 832..834
 FT /note= "Catalytic sub-domain"
 FT Domain 857..862
 FT /note= "Catalytic sub-domain"
 FT Domain 872..878
 FT /note= "Catalytic sub-domain"
 FT Region 736..812
 FT /note= "flk-2 signature sequence"
 XX W09310136-A.
 XX 27-MAY-1993.
 XX 16-NOV-1992; 92WO-US09893.
 XX 15-NOV-1991; 91US-0793065.
 XX (UYPR-) UNIV PRINCETON.
 XX Lemischka IR;
 XX WPI; 1993-182479/22.
 DR N-PSDB; AAQ40914.
 XX Totipotent haematopoietic stem cell receptors, their ligands and
 PT DNA sequences - for treating anaemia(s) and bone marrow damage
 PT due to e.g. cancer chemotherapy or radiotherapy
 XX Claim 37; Fig 1a; 127pp; English.
 XX This sequence represents the murine receptor protein tyrosine kinase
 CC (ptk), flk-2. The nucleic acid encoding this receptor is expressed
 CC in primitive hematopoietic cells and not in mature hematopoietic
 CC cells. Members of this family of ptk's can be recognised by the
 CC conserved amino acid regions in the catalytic domain. This family
 CC of ptk's also contains c-kit. These new receptors are termed fetal
 CC liver kinases (flk's) after the tissue in which they were discovered.
 CC flk-2 is also expressed in fetal spleen, fetal thymus, adult brain
 CC and adult bone marrow. flk-2 is expressed in individual multipotential
 CC CFU-Blast colonies capable of generating numerous multilineage colonies
 CC upon replating. It is likely therefore, that flk-2 is expressed in
 CC the entire primitive portion of the hematopoietic hierarchy. This is
 CC consistent with flk-2 being important in transducing putative self-
 CC renewal signals from the environment. flk-2 is the first receptor
 CC ptk known to be expressed in the T-lymphoid lineage.
 XX SQ Sequence 992 AA;

Query Match 100.0%; Score 5264; DB 14; Length 992;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALQSRDRLLLVLSVMILETVTTNQLPVIKCVLISHENNGSSAGKPSYRMVRGS 60
 Db 1 MRALQSRDRLLLVLSVMILETVTTNQLPVIKCVLISHENNGSSAGKPSYRMVRGS 60
 Qy 61 PEDLOCTPRQSEGVYEAATVEAESGITLOVQLATPGDLSCLVWPKHSLGQCPHFD 120
 Db 61 PEDLOCTPRQSEGVYEAATVEAESGITLOVQLATPGDLSCLVWPKHSLGQCPHFD 120
 Qy 121 LQNRGIVSMALINVTETQAGEVLLHIQSERANYTVLFTVNVDRDTOLYVLRPYPFRKMNQ 180
 Db 121 LQNRGIVSMALINVTETQAGEVLLHIQSERANYTVLFTVNVDRDTOLYVLRPYPFRKMNQ 180
 Qy 181 DALLCISGEVPEPTVEVWLCSSHRESCKEEGPAVVRKEKVLHFGTDIRCCARNALGR 240
 Db 181 DALLCISGEVPEPTVEVWLCSSHRESCKEEGPAVVRKEKVLHFGTDIRCCARNALGR 240
 Qy 241 ECTKLFITDLNOAPOSTLPQLFKVGEPLWIRCKAIHNVHGFGLTWELEDKALEBSGYFE 300
 Db 241 ECTKLFITDLNOAPOSTLPQLFKVGEPLWIRCKAIHNVHGFGLTWELEDKALEBSGYFE 300
 Qy 301 MSTYTNTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPQSALVTILEKGFNATSSQBEY 360

Db 301 MSTYTNTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPQSALVTILEKGFNATSSQBEY 360
 Qy 361 EIDPYEKFCFSVRFKAYPRIRCTWIFSQASFPCEORGLEDDGYISKFCDHKNKGEYIFY 420
 Db 361 EIDPYEKFCFSVRFKAYPRIRCTWIFSQASFPCEORGLEDDGYISKFCDHKNKGEYIFY 420
 Qy 421 AENDDAOFTKMTNIRKPOVLANASQASCSDDGVPLPSMTWTKKCSDKSPNCTEIP 480
 Db 421 AENDDAOFTKMTNIRKPOVLANASQASCSDDGVPLPSMTWTKKCSDKSPNCTEIP 480
 Qy 481 EGVWKKANRKFVQWVSSSTLNMSKGLLVKCCAYNSMGTSCTETIFLNSPGFPFPIQ 540
 Db 481 EGVWKKANRKFVQWVSSSTLNMSKGLLVKCCAYNSMGTSCTETIFLNSPGFPFPIQ 540
 Qy 541 DNISFYATIGLCLPFIIVLIVLICHKYKKQPRYESQLOMIQVTPGLDNEYFYVDFRDY 600
 Db 541 DNISFYATIGLCLPFIIVLIVLICHKYKKQPRYESQLOMIQVTPGLDNEYFYVDFRDY 600
 Qy 601 DLKWEFFPRENLEFGKVLGSGAGFGRVMNATAYIGISKTGVSIQVAVKMLKEKADSCKEALM 660
 Db 601 DLKWEFFPRENLEFGKVLGSGAGFGRVMNATAYIGISKTGVSIQVAVKMLKEKADSCKEALM 660
 Qy 661 SELKMTHLGHHDNIIVNLLGACTLSGPVYLIFCYCYGDLNLYRSKREKPHRTWTEIFK 720
 Db 661 SELKMTHLGHHDNIIVNLLGACTLSGPVYLIFCYCYGDLNLYRSKREKPHRTWTEIFK 720
 Qy 721 EHNFSSTPTFOAHNSNMPGSRREVQLHPDLQSLGFGNGSIHSEDEIYEYENQKRLAESEE 780
 Db 721 EHNFSSTPTFOAHNSNMPGSRREVQLHPDLQSLGFGNGSIHSEDEIYEYENQKRLAESEE 780
 Qy 781 EDLNVLPEDILLCFAYQVAKGMEFLKSCVHRDLAARNVLVTHGVKVKICDFGLARDIL 840
 Db 781 EDLNVLPEDILLCFAYQVAKGMEFLKSCVHRDLAARNVLVTHGVKVKICDFGLARDIL 840
 Qy 841 SDSSVYVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIFSLGVNPPYGPVPDAN 900
 Db 841 SDSSVYVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIFSLGVNPPYGPVPDAN 900
 Qy 901 FYKLIQSGFKMEQPFYATEGYIFVWQSCWAFDSKRKPSFPNLTSLFGQLAEABACIRT 960
 Db 901 FYKLIQSGFKMEQPFYATEGYIFVWQSCWAFDSKRKPSFPNLTSLFGQLAEABACIRT 960
 Qy 961 SIHLPKQAAPQORGLRAQSPQOVKIHRS 992
 Db 961 SIHLPKQAAPQORGLRAQSPQOVKIHRS 992

RESULT 2
 AAR67815
 ID AAR67815 standard; Protein; 992 AA.
 XX AAR67815;
 AC AC
 XX XX
 DT 16-AUG-1995 (first entry)
 XX XX
 DE Flk2 receptor protein-tyrosine-kinase.
 XX XX
 KW Mouse Flk2; receptor protein-tyrosine-kinase; primitive
 KW hematopoietic cell; fetal liver kinase; diagnostic ligand
 KW isolation; bone marrow disease therapy.
 XX XX
 OS Mus musculus.
 XX XX
 Key Location/Qualifiers
 FH Peptide 1..27
 FT /note= "signal peptide"
 FT Protein 28..992
 FT /note= "mature protein"
 FT Domain 28..544
 FT /note= "extracellular receptor domain"
 FT Domain 545..564
 FT /note= "transmembrane region"

FT Domain 565..992
 FT /note= "intracellular catalytic domain"
 FT Domain 618..623
 FT /note= "catalytic sub-domain"
 FT Domain 811..819
 FT /note= "catalytic sub-domain"
 FT Domain 832..834
 FT /note= "catalytic sub-domain"
 FT Domain 857..862
 FT /note= "catalytic sub-domain"
 FT Domain 872..878
 FT /note= "catalytic sub-domain"
 FT Region 709..785
 FT /note= "signature sequence typical of Flk2"
 XX
 PN WO9500554-A.
 XX
 XX 05-JAN-1995.
 XX
 XX 17-JUN-1994; 94WO-US06944.
 XX
 XX 18-JUN-1993; 93US-0080244.
 PR 21-JUN-1993; 93US-0081508.
 PR 23-NOV-1993; 93US-0157490.
 XX
 XX (UYPR-) UNIV PRINCETON.
 XX
 XX Lemischka IR;
 XX
 XX WPI; 1995-052014/07.
 DR N-PSDB; AAQ81012.
 XX
 XX Ligand for receptor protein tyrosine kinase - useful for the
 PT stimulation of primitive haematopoietic stem cells causing
 PT proliferation and/or differentiation
 XX
 PS Disclosure; Fig 1a; 131pp; English.
 XX
 CC The sequence corresponds to a mouse Flk2 (fetal liver kinase)
 CC receptor protein-tyrosine-kinase, which is expressed in primitive
 CC hematopoietic cells but not in mature hematopoietic cells. The
 CC protein is useful in isolation of receptor ligands, which have
 CC applications in diagnosis of bone marrow disorders and in
 CC stimulating proliferation and/or differentiation of primitive
 CC hematopoietic stem cells.
 XX
 SQ Sequence 992 AA;

Query Match 100.0%; Score 5264; DB 16; Length 992;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALAQRSDRLLLVLSVMILETVNQDLPVTKVLI SHENNGSSAGKPSYRMVRGS 60
 DB 1 MRALAQRSDRLLLVLSVMILETVNQDLPVTKVLI SHENNGSSAGKPSYRMVRGS 60
 QY 61 PEDLOCTPRROSEGVVEAATVEAEGSITLQVLAATPGDLSCLWVFKHSLGCOHPFD 120
 DB 61 PEDLOCTPRROSEGVVEAATVEAEGSITLQVLAATPGDLSCLWVFKHSLGCOHPFD 120
 QY 121 LQNRGIVSMALNVTQAGELVLIHISERANYTVLFTVNVVRDQLVYLRFPYFRKMEQ 180
 DB 121 LQNRGIVSMALNVTQAGELVLIHISERANYTVLFTVNVVRDQLVYLRFPYFRKMEQ 180
 QY 181 DALLCISEGVPEPTVWVLCSSHRESCKEKPAPVVRKEEVLHFLGTDIRCCARNALGR 240
 DB 181 DALLCISEGVPEPTVWVLCSSHRESCKEKPAPVVRKEEVLHFLGTDIRCCARNALGR 240
 QY 241 ECTKLFTIDLNOAQOSTLPQLFLKVGPELWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
 DB 241 ECTKLFTIDLNOAQOSTLPQLFLKVGPELWIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
 QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360

DB 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILEKGFINATSSQBEY 360
 QY 361 EIDPYEKFCFSVRKAYPRINCTWIFSOASPCORGLDGYSISKFCDHKNKPGEYIFY 420
 DB 361 EIDPYEKFCFSVRKAYPRINCTWIFSOASPCORGLDGYSISKFCDHKNKPGEYIFY 420
 QY 421 AENDDAQFTKMFTLNIRKKPOVLANASASQASCSGDPYPLSWTWKKCSKSPNCTEIP 480
 DB 421 AENDDAQFTKMFTLNIRKKPOVLANASASQASCSGDPYPLSWTWKKCSKSPNCTEIP 480
 QY 481 EGVNKKANRKFQOWVSSSTLNMSERAGLLVKCCAYNSMGTSCTETIFLNSPGPFPIQ 540
 DB 481 EGVNKKANRKFQOWVSSSTLNMSERAGLLVKCCAYNSMGTSCTETIFLNSPGPFPIQ 540
 QY 541 DNISFYATIGLCLPFIYVLIIVLICHYKKQPRYESOLOMIQVTPGLDNEYFVVDPRDYEY 600
 DB 541 DNISFYATIGLCLPFIYVLIIVLICHYKKQPRYESOLOMIQVTPGLDNEYFVVDPRDYEY 600
 QY 601 DLKWEFFRENLEFGKVLGSGAFGRVMNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
 DB 601 DLKWEFFRENLEFGKVLGSGAFGRVMNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
 QY 661 SELKQWTHLGHHDNIIVNLLGACTLSGPPVYLIFECYCGDLLNLYLSKREKPHRTWTEIFK 720
 DB 661 SELKQWTHLGHHDNIIVNLLGACTLSGPPVYLIFECYCGDLLNLYLSKREKPHRTWTEIFK 720
 QY 721 EHNFSYPTFOAHNSNSMPGSRREVQLHPPDLQSLGFGNCSIHSEDEIEYENQKRLAEBEE 780
 DB 721 EHNFSYPTFOAHNSNSMPGSRREVQLHPPDLQSLGFGNCSIHSEDEIEYENQKRLAEBEE 780
 QY 781 EDNLVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
 DB 781 EDNLVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
 QY 841 SDSSYVVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIFSLGVNYPYGPVVDAN 900
 DB 841 SDSSYVVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIFSLGVNYPYGPVVDAN 900
 QY 901 FYKLIQSGFKMEQPFYATEGYIFVMQSCWAFDSRKRPSFPNLTSPLGCOLAABEACIRT 960
 DB 901 FYKLIQSGFKMEQPFYATEGYIFVMQSCWAFDSRKRPSFPNLTSPLGCOLAABEACIRT 960
 QY 961 SIHLPKQAAPQORGGLRAQSPQOVKIHRRS 992
 DB 961 SIHLPKQAAPQORGGLRAQSPQOVKIHRRS 992

RESULT 3
 AAR67535
 ID AAR67535 standard; Protein; 992 AA.
 XX
 AC AAR67535;
 XX
 DT 04-JUL-1995 (first entry)
 XX
 DE Mouse flk-2.
 XX
 XX Fetal liver kinase-2; flk-2; protein tyrosine-kinase receptor;
 KW hematopoiesis; stem cell.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..27
 FT /label= Sig_peptide
 FT Domain 28..544
 FT /label= Extracellular_receptor_domain
 FT Region 545..564
 FT /label= Transmembrane_region
 FT Domain 565..992
 FT /label= Intracellular_catalytic_domain
 XX

PN US5367057-A.
 XX 22-NOV-1994.
 XX 02-APR-1991; 91US-0679666.
 XX 02-APR-1991; 91US-0679666.
 PR 28-JUN-1991; 91US-0728913.
 PR 15-NOV-1991; 91US-0793065.
 PR 24-DEC-1991; 91US-0813593.
 PR 26-JUN-1992; 92US-0806397.
 PR 12-NOV-1992; 92US-0975049.
 PR 19-NOV-1992; 92US-0977451.
 PR 30-APR-1993; 93US-0055269.
 XX (UYPR-) UNIV PRINCETON.
 PA Lemischka IR;
 PI WPI: 1995-005894/01.
 DR N-PSDB; AAQ79068.
 DR Murine fik-2 receptor protein tyrosine kinase - used to stimulate proliferation and/or stimulation of primitive mammalian haematopoietic stem cells in vitro or in vivo.
 XX Claim 1; Fig. 1A-1F; 69pp; English.
 XX cDNAs encoding receptor protein tyrosine-kinases, mouse fetal liver kinase-2 (fik-2), human fik-2 and mouse fik-1 are given in AAQ79068-70, CC respectively, and the deduced amino acid sequences in AAR67535-37, CC respectively.
 XX Sequence 992 AA;
 SQ

Query Match 100.0%; Score 5264; DB 16; Length 992;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALAQRDRRLLLVLSVILETVNQDLPVTKCVLISHENNGSSAGKPSRYMRVGRS 60
 DB 1 MRALAQRDRRLLLVLSVILETVNQDLPVTKCVLISHENNGSSAGKPSRYMRVGRS 60
 QY 61 PEDLOCTPRQSEGTVEAATVEAEGSITLOVQLATPGDLSCLWFKHSSLCQPHFD 120
 DB 61 PEDLOCTPRQSEGTVEAATVEAEGSITLOVQLATPGDLSCLWFKHSSLCQPHFD 120
 QY 121 LQNRGIVSMALNVTTQAGEYLLHIQSERANYTVLFTVNVNRTQLYVLRPFRKMEHQ 180
 DB 121 LQNRGIVSMALNVTTQAGEYLLHIQSERANYTVLFTVNVNRTQLYVLRPFRKMEHQ 180
 QY 181 DALLCISEGVPEPTVENVWLCSSHRESCKEKGPAVVRKEEKVHLFEGTDIRCCARNALGR 240
 DB 181 DALLCISEGVPEPTVENVWLCSSHRESCKEKGPAVVRKEEKVHLFEGTDIRCCARNALGR 240
 QY 241 ECTKLFITDLNOAPOSTLPOLFLKVGPELWIRCKAIHVNHEGFLTWLEOKALEEGSYFE 300
 DB 241 ECTKLFITDLNOAPOSTLPOLFLKVGPELWIRCKAIHVNHEGFLTWLEOKALEEGSYFE 300
 QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTSSSKHPQSQALVTILEKGFINATSSQEEY 360
 DB 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTSSSKHPQSQALVTILEKGFINATSSQEEY 360
 QY 361 EIDPYEKFCFSVRKAYPRIRCTWIFSOAGPCPQORGLDGYISIKPCDHKNKPGYIFY 420
 DB 361 EIDPYEKFCFSVRKAYPRIRCTWIFSOAGPCPQORGLDGYISIKPCDHKNKPGYIFY 420
 QY 421 AENDDAQFTKMTFLNIRKKPOVLANASQASCSGDCGYPLPSWTWKKCSKSPNCTEIP 480
 DB 421 AENDDAQFTKMTFLNIRKKPOVLANASQASCSGDCGYPLPSWTWKKCSKSPNCTEIP 480
 QY 481 EGVWNKKANRKFQGVWSSSTLNMSEAGKLLVKCCAYNSMGTSCTIFLNSPGPPFFIQ 540

Db 481 EGVWNKKANRKFQGVWSSSTLNMSEAGKLLVKCCAYNSMGTSCTIFLNSPGPPFFIQ 540
 QY 541 DNISFYATIGLCPLPFIIVLVILVILCHYKQFRYBSQIQMIOVQTGPLDNEYFYVFRDYEY 600
 Db 541 DNISFYATIGLCPLPFIIVLVILVILCHYKQFRYBSQIQMIOVQTGPLDNEYFYVFRDYEY 600
 QY 601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIOQAVKMLKEKADSCKEKALM 660
 Db 601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIOQAVKMLKEKADSCKEKALM 660
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 QY 721 EHNPFSSYPTFOAHSNSMPSGSRVQLHPPDLQSLGFGNGSIHSEDEIEYENOKRLAEEEE 780
 Db 721 EHNPFSSYPTFOAHSNSMPSGSRVQLHPPDLQSLGFGNGSIHSEDEIEYENOKRLAEEEE 780
 QY 781 EDLNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
 Db 781 EDLNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
 QY 841 SDSSYVVRGNARLPVKWMAPESLPEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
 Db 841 SDSSYVVRGNARLPVKWMAPESLPEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
 QY 901 FYKLIQSGFKMEQPFYATGEGIYFVMSQWAFDSRKPSFPNLTSLGCOLAEEACIRT 960
 Db 901 FYKLIQSGFKMEQPFYATGEGIYFVMSQWAFDSRKPSFPNLTSLGCOLAEEACIRT 960
 QY 961 SIHLPKQAAPOQRGLRAQSPQROVKIHRERS 992
 Db 961 SIHLPKQAAPOQRGLRAQSPQROVKIHRERS 992

RESULT 4
 AAR97418
 ID AAR97418 standard; Protein; 992 AA.
 XX AAR97418;
 XX 11-DEC-1996 (first entry)
 XX Human foetal liver kinase 2.
 XX Human; foetal liver kinase 2; fik-2; protein tyrosine kinase; monoclonal; antibody; extracellular domain; receptor assay; haematopoietic stem cell; ligand; stimulation; proliferation; differentiation; treatment; anaemia; bone marrow damage; cancer chemotherapy; radiation.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..27
 FT Peptide /label= sig_peptide
 FT Peptide 28..992
 FT Peptide /label= mat_peptide
 FT Domain 28..543
 FT Domain /label= extracellular_domain
 FT Domain 544..563
 FT Domain /label= transmembrane_domain
 FT Domain 564..992
 FT Domain /label= intracellular_domain
 XX US5548065-A.
 XX 20-AUG-1996.
 XX 02-APR-1991; 91US-0679666.
 XX 19-NOV-1992; 92US-0977451.
 XX 02-APR-1991; 91US-0679666.

PR 28-JUN-1991; 91US-0728913.
 PR 15-NOV-1991; 91US-0793065.
 PR 24-DEC-1991; 91US-0813593.
 PR 26-JUN-1992; 92US-0906397.
 PR 12-NOV-1992; 92US-0975049.
 PR 30-APR-1993; 93US-0055269.
 PR 31-OCT-1994; 94US-0252517.
 XX (UYPR-) UNIV PRINCETON.
 PA Lemischka IR;
 PI
 XX
 XX
 DR WPI; 1996-392678/39.
 DR N-PSDB; AAT38733.
 XX
 XX
 PT Anti-fetal liver kinase 2 (flk-2) antibodies - useful in assays,
 PT for isolating haematopoietic stem cells expressing receptor and for
 PT obtaining ligands
 XX
 PS Claim 1; Columns 27-34; 50pp; English.
 XX
 CC The present sequence is human foetal liver kinase 2 (flk-2), a
 CC protein tyrosine kinase. Isolated antibodies, pref. monoclonal,
 CC raised against the extracellular portion of flk-2 can be used to
 CC assay for flk receptors on the surface of primitive haematopoietic
 CC stem cells, and to obtain positive cells. The antibodies can also
 CC be used as, or to obtain ligands, which stimulate the proliferation
 CC and/or differentiation of stem cells. The ligands can be used, e.g.
 CC for treating anaemia, or bone marrow damage resulting from cancer
 CC chemotherapy, or radiation.
 CC
 XX Sequence 992 AA;
 SQ

Query Match 100.0%; Score 5264; DB 17; Length 992;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALQSRDRRLLLVLSVMILETTVNDLPVVKVLSHNNSSAGKPSRYRVRGS 60
 DB 1 MRALQSRDRRLLLVLSVMILETTVNDLPVVKVLSHNNSSAGKPSRYRVRGS 60
 QY 61 PEDLQTPRQSGTVEAATVEAAGSITLQVLAATPGDLSCLVFRHSSLGCPHFD 120
 DB 61 PEDLQTPRQSGTVEAATVEAAGSITLQVLAATPGDLSCLVFRHSSLGCPHFD 120
 QY 121 LQNRGIVSMALNVETQAGEYLLHIOSEANVTYVLTNNVRDTQYVLRPRYRKMENQ 180
 DB 121 LQNRGIVSMALNVETQAGEYLLHIOSEANVTYVLTNNVRDTQYVLRPRYRKMENQ 180
 QY 181 DALLCISEGVPEPTVWVLCSSHRECKEGPAVVRKEKVLHFGTDIRCCARNALGR 240
 DB 181 DALLCISEGVPEPTVWVLCSSHRECKEGPAVVRKEKVLHFGTDIRCCARNALGR 240
 QY 241 ECTKLTIDLNOAPOSTLPQFLKVGPELWIRCKAIHVNHGFGLTWELEDKALEGSYPE 300
 DB 241 ECTKLTIDLNOAPOSTLPQFLKVGPELWIRCKAIHVNHGFGLTWELEDKALEGSYPE 300
 QY 301 MSTYSNRTWIRILLAFVSVGNDTGYTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
 DB 301 MSTYSNRTWIRILLAFVSVGNDTGYTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
 QY 361 EIDPYEKFCFVRFKAYPRICRTWIFSQASFCEQGLEGGYSISKFDHKNKPGYIFY 420
 DB 361 EIDPYEKFCFVRFKAYPRICRTWIFSQASFCEQGLEGGYSISKFDHKNKPGYIFY 420
 QY 421 AENDDAQFTKMTFLNIRKPKQVLANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
 DB 421 AENDDAQFTKMTFLNIRKPKQVLANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
 QY 481 EGVNKKARKKVFQGVSSSTLNNSSAGKGLLVKCCAYNSMGTSCTIFLNSPGPPFFIQ 540
 DB 481 EGVNKKARKKVFQGVSSSTLNNSSAGKGLLVKCCAYNSMGTSCTIFLNSPGPPFFIQ 540

QY 541 DNISFYATIGLCLPFIIVLVILICHKYKQFRYESQLQMIQVTPGLDNEYFYVDFRDY 600
 DB 541 DNISFYATIGLCLPFIIVLVILICHKYKQFRYESQLQMIQVTPGLDNEYFYVDFRDY 600
 QY 601 DLKWEFPRENLEFGKVLGSCAFGRVMNATAYGISKTVSIVAVKMLKEKADSCKEALM 660
 DB 601 DLKWEFPRENLEFGKVLGSCAFGRVMNATAYGISKTVSIVAVKMLKEKADSCKEALM 660
 QY 661 SELKMMTHLGHNDINVLGACTLSGPVYLI FEYCCYGDLLNLYRSKREKPHRTWTTEIFK 720
 DB 661 SELKMMTHLGHNDINVLGACTLSGPVYLI FEYCCYGDLLNLYRSKREKPHRTWTTEIFK 720
 QY 721 EHNFSYPTFOAHSNMPGSRVQLHPPLDQLSGFNGNSIHSEDEIYEYENQKELABEEE 780
 DB 721 EHNFSYPTFOAHSNMPGSRVQLHPPLDQLSGFNGNSIHSEDEIYEYENQKELABEEE 780
 QY 781 EDLNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVVKICDFGLARDIL 840
 DB 781 EDLNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVVKICDFGLARDIL 840
 QY 841 SDSYVVRGNARLPVKWMAPESEFEGIYTIKSDVMSYGILLWEIFSLGVNVPYGPVVDAN 900
 DB 841 SDSYVVRGNARLPVKWMAPESEFEGIYTIKSDVMSYGILLWEIFSLGVNVPYGPVVDAN 900
 QY 901 FYKLIQSGFKMEQPFYATEGIYFVMQSCWAFDSKRPSFNLTSFLGCQLAEAEACIRT 960
 DB 901 FYKLIQSGFKMEQPFYATEGIYFVMQSCWAFDSKRPSFNLTSFLGCQLAEAEACIRT 960
 QY 961 SIHLPKQAAPQQRGLRAQSPQQRVQKIHRRS 992
 DB 961 SIHLPKQAAPQQRGLRAQSPQQRVQKIHRRS 992

RESULT 5
 AAW19874
 ID AAW19874 standard; Protein; 992 AA.
 XX
 AC AAW19874;
 XX
 DT 19-AUG-1997 (first entry)
 XX
 DE Murine flk-2 receptor.
 XX
 KW Human; fetal liver kinase 2; flk2; receptor protein tyrosine kinase;
 KW PTK; liver; spleen; thymus; adult; brain; bone marrow; primitive portion;
 KW haematopoietic hierarchy; extracellular domain; soluble form; ligand;
 KW proliferation; differentiation; mammalian; haematopoietic stem cell;
 KW macrocytic anaemia; aplastic anaemia; cancer; radiation; mouse.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..27
 FT /note= "Signal peptide"
 FT Domain 28..544
 FT /note= "Extracellular receptor domain"
 FT Region 545..564
 FT /note= "transmembrane region"
 FT Domain 565..992
 FT /note= "Intracellular catalytic domain"
 FT Active-site 618..623
 FT /note= "Catalytic sub-domain"
 FT Active-site 811..819
 FT /note= "Catalytic sub-domain"
 FT Active-site 832..834
 FT /note= "Catalytic sub-domain"
 FT Active-site 857..862
 FT /note= "Catalytic sub-domain"
 FT Active-site 872..878
 FT /note= "Catalytic sub-domain"
 FT Peptide 709..785
 FT /note= "Signature sequence characteristic of flk-2"
 XX

PN US5621090-A.
 XX 15-APR-1997.
 PD
 XX 02-APR-1991; 91US-0679666.
 XX
 XX 26-JUN-1992; 92US-0906397.
 PR 02-APR-1991; 91US-0679666.
 PR 28-JUN-1991; 91US-0728913.
 PR 15-NOV-1991; 91US-0793065.
 PR 24-DEC-1991; 91US-0813593.
 XX
 XX (UYPR-) UNIV PRINCETON.
 PA
 XX Lemischka IR;
 XX WPI; 1997-235228/21.
 DR N-PSDB; AAT72118.
 XX
 XX protein containing the extracellular domain of human flk-2 - used
 PT for identification of primitive haematopoietic cell proliferation
 PT and differentiation stimulatory ligands, e.g. for treating anaemia
 XX
 XX Disclosure; Fig 1A; 55pp; English.
 XX
 CC This sequence represents murine fetal liver kinase 2 (flk2). flk-2 is
 CC a receptor protein tyrosine kinase (pTK) and is important in transducing
 CC putative self-renewal signals from the environment. flk-2 is expressed
 CC in fetal liver, spleen, fetal thymus, adult brain and adult bone marrow,
 CC and it is thought that flk-2 is expressed in the entire primitive portion
 CC of the haematopoietic hierarchy. The invention concerns a recombinant
 CC nucleic acid, preferably mRNA, which encodes a protein containing only
 CC the extracellular domain of human flk-2 and lacking the flk-2 intra-
 CC cellular catalytic domain. The resultant protein represents a soluble
 CC form of flk-2 which is used to isolate specific ligands for flk-2. These
 CC ligands can be used to stimulate proliferation and/or differentiation of
 CC mammalian haematopoietic stem cells, in vivo or in vitro, e.g. for
 CC treatment of macrocytic or aplastic anaemia or bone marrow damage caused
 CC by cancer treatment or radiation.
 XX
 XX Sequence 992 AA;
 SQ

Query Match 100.0%; Score 5264; DB 18; Length 992;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALQSRDRRLLLVLSVMIETVTDLPVVKVLSHENNGSSAGKPSRYMRVRS 60
 DB 1 MRALQSRDRRLLLVLSVMIETVTDLPVVKVLSHENNGSSAGKPSRYMRVRS 60
 QY 61 PEDLOCTPRQSEGTYEATVEAVERSGSITLQVQLATPGDLSCLVWFKHSSLGCOPHPD 120
 DB 61 PEDLOCTPRQSEGTYEATVEAVERSGSITLQVQLATPGDLSCLVWFKHSSLGCOPHPD 120
 QY 121 LQNRGIVSMAILNVTQAGEYLLHQSERANVTVLFTVNRDTQLYLRRPFRKWNQ 180
 DB 121 LQNRGIVSMAILNVTQAGEYLLHQSERANVTVLFTVNRDTQLYLRRPFRKWNQ 180
 QY 181 DALLCISEGVPETVWLVCSHRESCKEKGPAVVRKEEVLHLEFGTDIRCCARNALGR 240
 DB 181 DALLCISEGVPETVWLVCSHRESCKEKGPAVVRKEEVLHLEFGTDIRCCARNALGR 240
 QY 241 ECTKLTIDINQAPQSTLPOLFLKVEPLWIRCKAIVHNHGFGLTWELEDKALEEGSYFE 300
 DB 241 ECTKLTIDINQAPQSTLPOLFLKVEPLWIRCKAIVHNHGFGLTWELEDKALEEGSYFE 300
 QY 301 MSTYSNTRMIRILLAFVSSVGRNDGYTCSSSKHPSOSALVTILEKGFINATSSQEEY 360
 DB 301 MSTYSNTRMIRILLAFVSSVGRNDGYTCSSSKHPSOSALVTILEKGFINATSSQEEY 360
 QY 361 EIDPYEKFCFSVRFKAYPRIRCTWIIFSQAQSPCEQGLEGDGYSISKFDHKNKPGYIFY 420
 DB 361 EIDPYEKFCFSVRFKAYPRIRCTWIIFSQAQSPCEQGLEGDGYSISKFDHKNKPGYIFY 420

QY 421 AENDDAQFTKMFLLNIRKKPOVLANASASQSSDGYPLPSWTWKCKSDKSPNCTEIP 480
 DB 421 AENDDAQFTKMFLLNIRKKPOVLANASASQSSDGYPLPSWTWKCKSDKSPNCTEIP 480
 QY 481 EGVNKKANRKYFGQWSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGPPFIQ 540
 DB 481 EGVNKKANRKYFGQWSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGPPFIQ 540
 QY 541 DNISFYATIGLCLPIVVLIVLICHYKKQFRYESQLOMIQVTGPDNIEYFVVDPRDIEY 600
 DB 541 DNISFYATIGLCLPIVVLIVLICHYKKQFRYESQLOMIQVTGPDNIEYFVVDPRDIEY 600
 QY 601 DLKWEFPRENLEFGVGLSGAFGRVWNNATAYGISTKTVSIQVAVKMLKEKADSCKEALM 660
 DB 601 DLKWEFPRENLEFGVGLSGAFGRVWNNATAYGISTKTVSIQVAVKMLKEKADSCKEALM 660
 QY 661 SELKWMTHLGHHDNIVNLLGACTLSGPVYLIFFEYCCYGDLLNLYRSKRKPHRTWTEIFK 720
 DB 661 SELKWMTHLGHHDNIVNLLGACTLSGPVYLIFFEYCCYGDLLNLYRSKRKPHRTWTEIFK 720
 QY 721 EHNFSYPTFOAHNSMPCSGREVQLHPDLQSGFNGNSIHSEDEIEYENOKRLAEEEE 780
 DB 721 EHNFSYPTFOAHNSMPCSGREVQLHPDLQSGFNGNSIHSEDEIEYENOKRLAEEEE 780
 QY 781 EDLNVLTPEDLCCFAYQVAKGMELEFSCVHRDLAARNVLVTHGKVKVICDFGLARDIL 840
 DB 781 EDLNVLTPEDLCCFAYQVAKGMELEFSCVHRDLAARNVLVTHGKVKVICDFGLARDIL 840
 QY 841 SDSSVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
 DB 841 SDSSVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
 QY 901 FYKLIQSGFKMQPFYATGIEYFVMSQWAFDSRKRPSFPNLTSLFLGCOLAEEACIRT 960
 DB 901 FYKLIQSGFKMQPFYATGIEYFVMSQWAFDSRKRPSFPNLTSLFLGCOLAEEACIRT 960
 QY 961 SIHLPRQAAPQORGGLRAQSPORQVKIHERS 992
 DB 961 SIHLPRQAAPQORGGLRAQSPORQVKIHERS 992

RESULT 6
 AAY08616
 ID AAY08616 standard; Protein; 992 AA.
 XX
 AC AAY08616;
 XX
 DT 05-AUG-1999 (first entry)
 XX
 DE Murine flk-2 protein.
 XX
 KW Murine; flk-2; flk-1; cell isolation; fetal liver kinase; receptor;
 KW monoclonal; polyclonal; antibody; tyrosine kinase.
 XX
 OS Mus sp.
 XX
 XX US5912133-A.
 XX
 PD 15-JUN-1999.
 XX
 PF 10-FEB-1998; 98US-0021324.
 XX
 PR 19-NOV-1992; 92US-0977451.
 PR 02-APR-1991; 91US-0679666.
 PR 28-JUN-1991; 91US-0728913.
 PR 15-NOV-1991; 91US-0793065.
 PR 24-DEC-1991; 91US-0813593.
 PR 26-JUN-1992; 92US-0906397.
 PR 12-NOV-1992; 92US-0975049.
 PR 30-APR-1993; 93US-0055269.
 PR 31-OCT-1994; 94US-0252498.
 PR 15-FEB-1996; 96US-0601891.

XX (UYPR-) UNIV PRINCETON.
PA Lemischka IR;
PI
XX
XX
DR WPI; 1999-357194/30.
DR N-PSDB; AAX77514.
XX
XX
PT Isolating hematopoietic cells expressing fetal liver kinase 1
PT receptors
XX
XX
PS Disclosure; Fig 1a; 59pp; English.
XX
CC This invention describes a novel method of isolating cells expressing
CC fetal liver kinase 1 (flk-1) receptors on their surface and comprises
CC binding the cells to a polyclonal or monoclonal antibody specific to
CC the flk-1 receptor and isolating the cells that have bound to the
CC antibody. The method can be used to isolate hematopoietic stem cells in
CC any mammal but preferably a rat, mouse, rabbit or human. The proteins of
CC the invention belong to the receptor protein family. This sequence
CC represents the murine flk-2 protein which is used in the method of
CC the invention.
XX
XX Sequence 992 AA;
SQ
Query Match 100.0%; Score 5264; DB 20; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRALAQSRDRLLLVLSWMILETVNQDLPVTKVLI SHENNGSAGKPSYRMVRGS 60
Db 1 MRALAQSRDRLLLVLSWMILETVNQDLPVTKVLI SHENNGSAGKPSYRMVRGS 60
QY 61 PEDLOCTPRQSGTYEATVAESGSI TQVQLATPGDLSCLMWFKHSLGCQPHD 120
Db 61 PEDLOCTPRQSGTYEATVAESGSI TQVQLATPGDLSCLMWFKHSLGCQPHD 120
QY 121 LQNRGIVSMALNVETQAGEYLLHQSERANYTVLFTVNVVDTQLYLRRPYFRKMENQ 180
Db 121 LQNRGIVSMALNVETQAGEYLLHQSERANYTVLFTVNVVDTQLYLRRPYFRKMENQ 180
QY 181 DALLCISEGVPEPTVEVLCSHRESCKRGPAVRKEEKVHLFGTDIRCCARNALGR 240
Db 181 DALLCISEGVPEPTVEVLCSHRESCKRGPAVRKEEKVHLFGTDIRCCARNALGR 240
QY 241 ECTKLFTIDLNAQPOSTLPQLFLKVGEP LIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
Db 241 ECTKLFTIDLNAQPOSTLPQLFLKVGEP LIRCKAIHVNHGFGLTWELEDKALEEGSYFE 300
QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSGSKHPSQSALVTILEKGFINATSSQEEY 360
Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSGSKHPSQSALVTILEKGFINATSSQEEY 360
QY 361 EIDPYEKFCFVSFKAYPRIRCTWIFSQASFPCQRGLEDGYSISKPCDHKNKPGEVIFY 420
Db 361 EIDPYEKFCFVSFKAYPRIRCTWIFSQASFPCQRGLEDGYSISKPCDHKNKPGEVIFY 420
QY 421 AENDDAQFTKMTFLNIRKKQVLANASASQASCSGDPPLPSWTWKCKSDKSPNCTEIP 480
Db 421 AENDDAQFTKMTFLNIRKKQVLANASASQASCSGDPPLPSWTWKCKSDKSPNCTEIP 480
QY 481 EGVNKKANRKFVQGVSSSTLNNSSEAGKLLVKCCAYNSMGTSCTEIFLNSPGPPFFIQ 540
Db 481 EGVNKKANRKFVQGVSSSTLNNSSEAGKLLVKCCAYNSMGTSCTEIFLNSPGPPFFIQ 540
QY 541 DNISFYATIGLCPLFFIVLVILVLI CHYKKQFRYESQLQMIQVGTGLDNEFYVDYFRDYEY 600
Db 541 DNISFYATIGLCPLFFIVLVILVLI CHYKKQFRYESQLQMIQVGTGLDNEFYVDYFRDYEY 600
QY 601 DLKWEFFPRENLEFGKVLGSAFGRVNNAATYISKTGVSQTQAVVMLEKADSCKEKALM 660
Db 601 DLKWEFFPRENLEFGKVLGSAFGRVNNAATYISKTGVSQTQAVVMLEKADSCKEKALM 660

QY 661 SELKMMTHLGHHDNI VNLGACTLSGPGVYLIFEYCCYGDLLNLYRSKREKPHRTWTIFK 720
Db 661 SELKMMTHLGHHDNI VNLGACTLSGPGVYLIFEYCCYGDLLNLYRSKREKPHRTWTIFK 720
QY 721 EHNFSYPTFOAHSNNSMPCGSRVQLHPDQLSGFGNGSIHSEDEIEYENQKLAEEEE 780
Db 721 EHNFSYPTFOAHSNNSMPCGSRVQLHPDQLSGFGNGSIHSEDEIEYENQKLAEEEE 780
QY 781 EDLNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
Db 781 EDLNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
QY 841 SDSYVVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Db 841 SDSYVVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
QY 901 FYKLIQSGFKMEQPFYATEGIYFVMQSCWAFDSKRSFNLTSFLGCOLAEAEACIRT 960
Db 901 FYKLIQSGFKMEQPFYATEGIYFVMQSCWAFDSKRSFNLTSFLGCOLAEAEACIRT 960
QY 961 SIHLPKQAAPOQRGGLRAQSPQROVKIHRERS 992
Db 961 SIHLPKQAAPOQRGGLRAQSPQROVKIHRERS 992
RESULT 7
AAR44994
ID AAR44994 standard; Protein; 992 AA.
XX AAR44994;
XX
DT 27-JUN-1994 (first entry)
XX
DE Murine flk-2 receptor protein tyrosine kinase.
XX
KW Receptor protein tyrosine kinase; pTK family; foetal liver kinase;
KW primitive; totipotent; haematopoietic cell; stem cell; proliferation;
KW mflk; stromal cell.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..27 /label= signal_peptide
FT /note= "hydrophobic leader"
FT Protein 28..992 /label= flk-2
FT /note= "mature protein"
FT Domain 28..544 /label= extracellular_domain
FT Region 545..564 /label= transmembrane_region
FT Domain 565..992 /label= intracellular_catalytic_domain
FT /note= "catalytic subdomain"
FT Domain 618..623 /note= "catalytic subdomain"
FT Domain 811..819 /note= "catalytic subdomain"
FT /note= "catalytic subdomain"
FT Domain 832..834 /note= "catalytic subdomain"
FT Domain 857..862 /note= "catalytic subdomain"
FT Domain 872..878 /note= "catalytic subdomain"
XX US270458-A.
PN
XX
XX 14-DEC-1993.
XX
PF 02-APR-1991; 91US-0679666.
XX
XX 02-APR-1991; 91US-0679666.
PR 28-JUN-1991; 91US-0728913.

XX 26-JUN-1992; 92WO-US05401.
XX 28-JUN-1991; 91US-0728913.
XX 15-NOV-1991; 91US-0793065.
XX 24-DEC-1991; 91US-0813593.
XX 02-APR-1992; 92WO-US02750.
XX (UYPR-) UNIV PRINCETON.
XX PA
XX Lemischka IR;
XX WPI; 1993-036323/04.
XX N-PSDB; AAQ45247.
XX Nucleic acid encoding receptor protein tyrosine kinase - allows
XX development of ligands to stimulate proliferation and/or
XX differentiation of mammalian haematopoietic stem cells
XX Claim 5; Fig 1a; 78pp; English.
XX This sequence represents a murine receptor protein tyrosine kinase
XX which belongs to a new functional class of protein tyrosine kinases
XX (ptks). ptks in this class are expressed in primitive mammalian
XX hematopoietic (phc) cells but not in mature hematopoietic cells (mhc).
XX This protein is an example of a receptor ptk and is called fetal liver
XX kinase 2 (flk-2). flk-2 is expressed in fetal liver, spleen and
XX thymus, and adult brain and marrow. Expression of flk-2 mRNA occurs
XX in the most primitive thymocyte subset, which is believed to be
XX uncommitted. Therefore, thymocytes expressing flk-2 may be multi-
XX potential. flk-2 is the first receptor tyrosine kinase known to be
XX expressed in the T-lymphoid lineage.
XX Sequence 992 AA;
SQ

Query Match 99.8%; Score 5256; DB 14; Length 992;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVALAQRDRRLILLVLSVMTLETVTNODLPVICKVLISHENNGSSAGKPSRYRVGRS 60
DB 1 MVALAQRDRRLILLVLSVMTLETVTNODLPVICKVLISHENNGSSAGKPSRYRVGRS 60
QY 61 PEDLOCTPRQSEGTVEATVEAASGITTLOVQLATGDLISLWFKHSSLGCOHPED 120
DB 61 PEDLOCTPRQSEGTVEATVEAASGITTLOVQLATGDLISLWFKHSSLGCOHPED 120
QY 121 LQNRGIVSMAILNVTTQAGEYLLHIQSERANYTVLFTVNVRTDQYVLRPYFRKXENQ 180
DB 121 LQNRGIVSMAILNVTTQAGEYLLHIQSERANYTVLFTVNVRTDQYVLRPYFRKXENQ 180
QY 181 DALLCISEGVPEPTVWVLCSSHRECKEGPAVVRKEKVLHELFGTDIRCCARNALGR 240
DB 181 DALLCISEGVPEPTVWVLCSSHRECKEGPAVVRKEKVLHELFGTDIRCCARNALGR 240
QY 241 ECTKLFTIDLNOAQSTLPQLFKVGEPLWIRCKALHVNHGFLTWELEDKALEEGSYFE 300
DB 241 ECTKLFTIDLNOAQSTLPQLFKVGEPLWIRCKALHVNHGFLTWELEDKALEEGSYFE 300
QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
DB 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
QY 361 EIDPYKFCFVRFKAYPRICRTWIFSQAQSPCEQRLGDEGYSISKFDHKNKPGYIFY 420
DB 361 EIDPYKFCFVRFKAYPRICRTWIFSQAQSPCEQRLGDEGYSISKFDHKNKPGYIFY 420
QY 421 AENDDAQFTKMFNLNIRKPKQVLNANASQAQSCSDGYPLPSWTWKCKSDKSNCTEETIP 480
DB 421 AENDDAQFTKMFNLNIRKPKQVLNANASQAQSCSDGYPLPSWTWKCKSDKSNCTEETIP 480
QY 481 EGVWNNKANRKFQGVQVSSSTLNMSEAGKGLLVKCCAYNSMGTSCTIFLNSPGPPFFIQ 540

Db 481 EGVWNNKANRKFQGVQVSSSTLNMSEAGKGLLVKCCAYNSMGTSCTIFLNSPGPPFFIQ 540
QY 541 DNISFYATIGLCLPFIIVLIVLICHYKQFRYESOLQMIQVTPGLDNEYFYVDFRDYEF 600
Db 541 DNISFYATIGLCLPFIIVLIVLICHYKQFRYESOLQMIQVTPGLDNEYFYVDFRDYEF 600
QY 601 DLKWEFPRENLEFGKVLGSGAFGRVNNATAYGISKTVGSIQAVKMLKEKADSCKEALM 660
Db 601 DLKWEFPRENLEFGKVLGSGAFGRVNNATAYGISKTVGSIQAVKMLKEKADSCKEALM 660
QY 661 SELKWMTHLGHHDNIIVNLGACTLSGPNVLIIEYCCYGDLLNLYRSKREKPHETWEIFK 720
Db 661 SELKWMTHLGHHDNIIVNLGACTLSGPNVLIIEYCCYGDLLNLYRSKREKPHETWEIFK 720
QY 721 ENHFSYPTFOAHSNMPGSRREVLPDLDLQSGFNGNSIHSEDEIEYENQKRLAESEE 780
Db 721 ENHFSYPTFOAHSNMPGSRREVLPDLDLQSGFNGNSIHSEDEIEYENQKRLAESEE 780
QY 781 EDLNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVVICDFGLARDIL 840
Db 781 EDLNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVVICDFGLARDIL 840
QY 841 SDSSYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPDYGPVVDAN 900
Db 841 SDSSYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPDYGPVVDAN 900
QY 901 FYKLQSGFKMEQPFYATGIIYFVMQSCWAFDSRKRPSPNLTSLFGCOLAEAEACIRT 960
Db 901 FYKLQSGFKMEQPFYATGIIYFVMQSCWAFDSRKRPSPNLTSLFGCOLAEAEACIRT 960
QY 961 SIHLPKQAAPQQRGGLRAQSPQKVIHRERS 992
Db 961 SIHLPKQAAPQQRGGLRAQSPQKVIHRERS 992

RESULT 9
AAR28038
ID AAR28038 standard; Protein; 992 AA.
XX AC AAR28038;
XX DT 15-MAR-1993 (first entry)
XX DE Murine flk-2.
XX KW Thymidine kinase; TK; haematopoietic; stem cells; proliferation;
XX OS Mus musculus.
XX FH Key Location/Qualifiers
FT Peptide 1..27 /note= "hydrophobic leader"
FT Domain 28..544 /note= "extracellular receptor domain"
FT Region 545..564 /note= "transmembrane region"
FT Domain 565..992 /note= "intracellular catalytic domain"
FT Region 709..785 /note= "signature sequence of flk-2"
XX PN W09217486-A.
XX 15-OCT-1992.
XX PF 02-APR-1992; 92WO-US02750.
XX PR 02-APR-1991; 91US-0679666.
XX PR 28-JUN-1991; 91US-0728913.
XX PR 15-NOV-1991; 91US-0793065.
XX PR 24-DEC-1991; 91US-0813593.

PA (UYPR-) UNIV PRINCETON.
 XX Lemischka IR;
 XX WPI; 1992-366185/44.
 DR N-PSDB; AAQ29954.
 XX Stimulating proliferation and/or differentiation of primitive
 PT mammalian haematopoietic stem cells - using ligand that binds
 PT thymidine kinase and flk-1 and flk-2
 XX Claim 37; Fig 1a; 94pp; English.
 XX The murine foetal liver kinase (flk) -2 sequence was deduced from
 CC that of the flk-2 clone obtd. by standard PCR techniques from stem-
 CC cell receptor-contg. tissue cDNA libraries. Suitable tissues include
 CC foetal liver, spleen or thymus cells or adult marrow or brain cells.
 CC The PCR primers used are based on known sections of the flk-2 gene.
 CC The murine flk-2 clone may be used in a vector to transform haemato-
 CC poietic cells. The thymidine kinase encoded by flk-2 is expressed in
 CC primitive but not mature haematopoietic cells. Ligand binding to the
 CC TK may be prepd. which can stimulate proliferation and/or
 CC differentiation of primitive haematopoietic cells in vivo. The ligands
 CC can stimulate the proliferation of additional primitive stem cells,
 CC differentiation into more mature progenitor cells, or both.
 CC See also AAR28039-41.
 XX Sequence 992 AA;
 SQ

Query Match 99.5%; Score 5239; DB 13; Length 992;
 Best Local Similarity 99.7%; Pred. NO. 0;
 Matches 989; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MRALQSDRRLLLVLSWILETVTNQDLPIVKVLISHENNGSSAGKSSYRMVRGS 60
 Db 1 MRALQSDRRLLLVLSWILETVTNQDLPIVKVLISHENNGSSAGKSSYRMVRGS 60
 Qy 61 PEDLOCTPRQSEGTVEAATVEAESSITLQVQLATPGDLSCLWVFKHSLGCGPHD 120
 Db 61 PEDLOCTPRQSEGTVEAATVEAESSITLQVQLATPGDLSCLWVFKHSLGCGPHD 120
 Qy 121 LQNRGIVSMALNVTETQAGEYLLHQSERANYTLFTVNVVDLTQYLVRPYPKRMENQ 180
 Db 121 LQNRGIVSMALNVTETQAGEYLLHQSERANYTLFTVNVVDLTQYLVRPYPKRMENQ 180
 Qy 181 DALLCISEGVPTVEWVLCSSHRESCKEKGPAVVRKEKVLHELFGTDIRCCARNALGR 240
 Db 181 DALLCISEGVPTVEWVLCSSHRESCKEKGPAVVRKEKVLHELFGTDIRCCARNALGR 240
 Qy 241 ECTKLFTDLNQAPOSTLPQLFKYGEPLWIRCKAIHVNHGFLTWELDKALEGSGYFE 300
 Db 241 ECTKLFTDLNQAPOSTLPQLFKYGEPLWIRCKAIHVNHGFLTWELDKALEGSGYFE 300
 Qy 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCSSSKHPSQSALVTILEKGFINATSSQREY 360
 Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCSSSKHPSQSALVTILEKGFINATSSQREY 360
 Qy 361 EIDPYEKFCSVRKAYPRIRCTWIPFQASPCBQEGLEDGYSISKFDHKNKPGYEIFY 420
 Db 361 EIDPYEKFCSVRKAYPRIRCTWIPFQASPCBQEGLEDGYSISKFDHKNKPGYEIFY 420
 Qy 421 AENDDAQFTMTNIRKKPOVLANASQASCSGDPVLPSTWTKCKSDKSPNCTEETIP 480
 Db 421 AENDDAQFTMTNIRKKPOVLANASQASCSGDPVLPSTWTKCKSDKSPNCTEETIP 480
 Qy 481 EGVWNNKANRVFGQWSSSTLNMSSAGKGLLVKCCAYNSMGTSCTETPLNSPGFPFTIQ 540
 Db 481 EGVWNNKANRVFGQWSSSTLNMSSAGKGLLVKCCAYNSMGTSCTETPLNSPGFPFTIQ 540
 Qy 541 DNISFYATIGLCLPFTIVLIVLICHYKQFYESQLOMIQVGTPLDNEFYVDFRDVEY 600
 Db 541 DNISFYATIGLCLPFTIVLIVLICHYKQFYESQLOMIQVGTPLDNEFYVDFRDVEY 600

Qy 601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIQVAVQMLKEKADSCKEKALM 660
 Db 601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIQVAVQMLKEKADSCKEKALM 660
 Qy 661 SELKQWTHLGHHDNIVNLLGACTLSGPPVYLIFEYCCYGDLLNLYLSKREKPHRTWTEIPK 720
 Db 661 SELKQWTHLGHHDNIVNLLGACTLSGPPVYLIFEYCCYGDLLNLYLSKREKPHRTWTEIPK 720
 Qy 721 EHNPFSSYPTFOAHNSNSMPGSRREVQLHPDLQSLGFGNSIHSEDEIEYENOKRLAEDEE 780
 Db 721 EHNPFSSYPTFOAHNSNSMPGSRREVQLHPDLQSLGFGNSIHSEDEIEYENOKRLAEDEE 780
 Qy 781 EDNLVLTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVICDFGLARDIL 840
 Db 781 EDNLVLTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVICDFGLARDIL 840
 Qy 841 SDSSYVVRGNARLPVKWMAPELSEFEGITIKSDWWSYGILLWEIISLGVNPPGIPVDAN 900
 Db 841 SDSSYVVRGNARLPVKWMAPELSEFEGITIKSDWWSYGILLWEIISLGVNPPGIPVDAN 900
 Qy 901 FYKLIQSGFKMEQPPYATEGYFVWQSWAFDSRKRPSFPNLTSLFGQLAEAEACIRT 960
 Db 901 FYKLIQSGFKMEQPPYATEGYFVWQSWAFDSRKRPSFPNLTSLFGQLAEAEACIRT 960
 Qy 961 SIHLPKQAAPQQRGLRAQSQRQVKIHRERS 992
 Db 961 SIHLPKQAAPQQRGLRAQSQRQVKIHRERS 992

RESULT 10
 AAR81868
 ID AAR81868 standard; Protein; 1000 AA.
 XX AAR81868;
 AC AAR81868;
 XX 29-FEB-1996 (first entry)
 DT Flk2/flt3 tyrosine kinase receptor.
 DE Tyrosine kinase receptor; flk2; flt3; agonist; monoclonal antibody;
 KW haematopoiesis; hypoplasia; anaemia; thrombocytopenia; stem cell.
 XX Mus sp.
 OS Key Location/Qualifiers
 FH Domain 1..542
 FT /label= Extracellular_domain
 XX WO9527062-A1.
 XX 12-OCT-1995.
 XX 23-MAR-1995; 95WO-US03718.
 XX 04-APR-1994; 94US-0222299.
 XX (GETH) GENENTECH INC.
 XX Bennett BD, Broz SD, Matthews W, Zeigler FC;
 PI WPI; 1995-358636/46.
 XX N-PSDB; AAT00801.
 DR Agonist antibody which binds to flk2-flt3 tyrosine kinase receptor
 XX PT - enhances proliferation of haematopoietic stem cells, in the
 PT treatment of hypoplasia, anaemia, etc.
 XX Example 1; Page 38-40; 59pp; English.
 XX Murine stem cell tyrosine kinase receptor flk2 (also called flt3)
 CC (AAR81868) is encoded DNA (AAT00801) obtd. by RT-PCR amplification of
 CC RNA isolated from mid-gestation mouse foetal livers. An flk2/flt3
 CC extracellular domain-IgG1 Fc fusion protein was used to raise

CC agonist antibodies able to bind to, and activate, flk2/flt3.
CC Such antibodies can enhance repopulation of mature blood cell
CC lineages following chemotherapy, radiotherapy, or bone marrow
CC transplantation.
XX
SQ Sequence 1000 AA;

Query Match 96.9%; Score 5102; DB 16; Length 1000;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 968; Conservative 6; Mismatches 17; Indels 10; Gaps 2;

QY	1	MRALAQSDRRLLLLVLSVILETVTNQDLPIVKVLIHENNGSSAGKPSYRMVRGS	60
DB	1	MRALAQSDRRLLLLVLSVILETVTNQDLPIVKVLIHENNGSSAGKPSYRMVRGS	60
QY	61	PEDLQCTPRQSEGVTEAATVEAEGSITLQVLAATPGDLCLVWFKHSSLCQPHD	120
DB	61	PEDLQCTPRQSEGVTEAATVEAEGSITLQVLAATPGDLCLVWFKHSSLCQPHD	120
QY	121	LQNRGIVSMALNVTTQAGELYLHIQSERANYTVLFTVNVVDTQLVLRPYPRKMEQ	180
DB	121	LQNRGIVSMALNVTTQAGELYLHIQSERANYTVLFTVNVVDTQLVLRPYPRKMEQ	180
QY	181	DALLCTSEGVPETVWVWLCSSHRESCKEKGPAVVRKEEVKVLHBLFGTDIRCCARNALGR	240
DB	181	DALLCTSEGVPETVWVWLCSSHRESCKEKGPAVVRKEEVKVLHBLFGTDIRCCARNALGR	240
QY	241	ECTKLFITDLNQAPSTLPQLFLVKGPELIRCKAIHNVHGFGLTWELEDKALEGSYFE	300
DB	241	ESTKLFITDLNQAPSTLPQLFLVKGPELIRCKAIHNVHGFGLTWELEDKALEGSYFE	300
QY	301	MSYVSTNRTMIRILLAFVSSVGRNDTGYYTCSKHPQSQALVTILEKGFINATSSOBEY	360
DB	301	MSYVSTNRTMIRILLAFVSSVGRNDTGYYTCSKHPQSQALVTILEKGFINATSSOBEY	360
QY	361	EIDPYEKFCFSVRKAYPRIRCTWIFSOAGPFCBQGLDGYSISKFDHKNKPGYIFY	420
DB	361	EIDPYEKFCFSVRKAYPRIRCTWIFSOAGPFCBQGLDGYSISKFDHKNKPGYIFY	420
QY	421	AENDDAQFTKMTNIRIKKQVLANASQSCSDGYPSPSWTKKCSKSPNCTEIP	480
DB	421	AENDDAQFTKMTNIRIKKQVLANASQSCSDGYPSPSWTKKCSKSPNCTEIP	480
QY	481	EGVWKKANRKFVQWYSSSTLNNSEAGKGLLVKCCAYNSMGTSCETIFLNSPGFPFFIQ	540
DB	481	EGVWKKANRKFVQWYSSSTLNNSEAGKGLLVKCCAYNSMGTSCETIFLNSPGFPFFIQ	540
QY	541	DNISFYATIGLCLPFIIVLVLI CHYKKQPRYESQLQMIQVTGPDLDNEYFYVDPRDYEY	600
DB	541	DNISFYATIGLCLPFIIVLVLI CHYKKQPRYESQLQMIQVTGPDLDNEYFYVDPRDYEY	600
QY	601	DLKWEFPRENLEFGKVLGSGAFGRVWMTATYISKTGYSIQVAVKMLKEKADSCKEALM	660
DB	601	DLKWEFPRENLEFGKVLGSGAFGRVWMTATYISKTGYSIQVAVKMLKEKADSCKEALM	660
QY	661	SELKQWTHLGHDDNI VNLGACTLSGPVYLIFCYCCGDLNLVRSKREKFRHTWTIFK	720
DB	661	SELKQWTHLGHDDNI VNLGACTLSGPVYLIFCYCCGDLNLVRSKREKFRHTWTIFK	720
QY	721	EHNFSSYPTTQAHSNMPGSRREYQLHPPDLQSLGFGNGSIHSEDEIEYENQKRLAESEE	780
DB	721	EHNFSSYPTTQAHSNMPGSRREYQLHPPDLQSLGFGNGSIHSEDEIEYENQKRLAESEE	780
QY	781	EDNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLARNVLVTHGKVVKICDFGLARDIL	840
DB	781	EDNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLARNVLVTHGKVVKICDFGLARDIL	840
QY	841	SDSSYVVRGNARLPKVMAPESLPEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDAN	900
DB	841	SDSSYVVRGNARLPKVMAPESLPEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDAN	900
QY	901	FYKLIQSGFKMEQPFYATGEGYFVWQSCWAFDSRKRPSPNLTSLFLGCOLAEAEACIRT	960

Db	901	FYKLIQSGFKMEQPFYATGEGYFVWQSCWAFDSRKRPSPNLTSLFLGCOLAEAEACIRT	960
QY	961	-----SIHLPKQAAPQORGLRAQSPORQVKIHRERS	992
		: : :	
Db	961	MGGNVPEHPSIYQNRRLPSREAGS-EPPSPQAQVKIHRERS	1000
RESULT 11			
AAR75961			
ID	AAR75961	standard; Protein; 993 AA.	
XX	AAR75961;		
AC	XX		
DT	29-DEC-1995	(first entry)	
XX	XX		
DE	Human STK-1.		
XX	XX		
KW	STK-1; receptor PTK; protein tyrosine kinase.		
XX	XX		
OS	Homo sapiens.		
PH	Key	Location/Qualifiers	
FT	Peptide	1..23	
FT		/label= signal	
FT		/note= "unique PTK receptor sequence"	
FT	Cleavage-site	25..26	
FT	Domain	35..524	
FT		/note= "Part of extracellular domain contg. 22 Cys residues marked on Fig. 1"	
FT	Modified-site	43..45	
FT		/label= potential N-linked glycosylation site	
FT	Modified-site	100..102	
FT		/label= see above	
FT	Modified-site	151..153	
FT		/label= see above	
FT	Modified-site	250..252	
FT		/label= see above	
FT	Modified-site	306..308	
FT		/label= see above	
FT	Modified-site	323..325	
FT		/label= see above	
FT	Modified-site	351..353	
FT		/label= see above	
FT	Modified-site	354..356	
FT		/label= see above	
FT	Modified-site	473..475	
FT		/label= see above	
FT	Modified-site	502..504	
FT		/label= see above	
FT	Region	542..562	
FT		/label= transmembrane spanning region	
FT	Region	708..782	
FT		/label= kinase insert region	
FT	Domain	617..622	
FT		/label= ATP binding domain	
FT	Domain	835..840	
FT		/label= WMAPES motifs	
FT		/note= "cytoplasmic domain"	
FT	Peptide	808..813	
FT		/note= "used to design PCR oligos"	
FT	Peptide	870..875	
FT		/note= "used to design PCR oligos"	
XX	XX		
PN	W09519175-A.		
XX	XX		
PD	20-JUL-1995.		
XX	XX		
PF	06-JAN-1995;	95WO-US00176.	
XX	XX		
PR	14-JAN-1994;	94US-0183211.	
XX	XX		
PA	(UYJO) UNIV JOHNS HOPKINS.		
PA	(UYPE-) UNIV PENNSYLVANIA.		

XX Civin CI, Gewirtz AM, Small D;
 XX WPI; 1995-263709/34.
 DR N-PSDB; AAQ91356.
 XX Artificial STK-1 gene and gene-specific anti-sense oligo: nucleotide -
 PT used to treat neoplastic diseases and as bone marrow purging agents for
 PT treating leukaemia and neoplasia
 XX Disclosure; Fig 1; 66pp; English.
 XX The STK-1 gene encodes a receptor PTK which is expressed in
 CC proliferating hematopoietic stem cells but not in quiescent stem
 CC cells. The STK-1 gene is also expressed in certain malignant cells
 CC of non-hematopoietic origin. An antisense oligo specific for STK-1
 CC is an oligo having a sequence (i) capable of forming a stable
 CC triplex with a portion of the STK-1 gene, or (ii) capable of forming
 CC a stable duplex with a portion of an mRNA transcript of the STK-1
 CC gene. Antisense oligos capable of forming a stable duplex with a
 CC portion of a STK-1 mRNA transcript are given in AAQ91536 PT and in
 CC AAQ91537 and AAQ91538. The antisense oligos of the invention are useful
 CC in the treatment of hematologic malignancies characterized by
 CC STK-1 expression. Several of the conserved domains of PTKs
 CC including the ATP binding domain and the WMAPES motifs are
 CC found in the STK-1 protein (see AAQ75961 FT).
 XX Sequence 993 AA;
 SQ

Query Match 84.3%; Score 4436.5; DB 16; Length 993;
 Best Local Similarity 84.2%; Pred. No. 0;
 Matches 837; Conservative 57; Mismatches 89; Indels 11; Gaps 4;

QY 1 MRALQRSRRRLVLLVLSWILETVNQDLPVVKVLSHENNGSSAGKPSRYRVRGS 60
 DB 1 MPALA-RDAGTVPLLVFSAIFGTITNQDLPVVKVLSHENNGSSAGKPSRYRVRGS 59
 QY 61 PEDLOCTPRQSGTYVEATVVAESGTTLOVQATPGDLSCLWVFKHSSIGCOPHFD 120
 DB 60 PEDLGALRPQSGTYVEAAVEVDVSASITLQVLDAPGNISCLWVFKHSSLNCOHFD 119
 QY 121 LQNRGVSMALNVETQAGEYLLIHQSERANYTVFTVNVROTQYLVLRPFRKXENQ 180
 DB 120 LQNRGVSMVILKQVETQAGEYLLFQSEATNYTLFTVIRNTLLYLRPFRKXENQ 179
 QY 181 DALLCISEGVPEPTVEVLCSHRESCKEKGPAVRKEKVLHFLFTDTRCCARNALGR 240
 DB 180 DALVCISEGVPEPIVEVLCDSECKESPAVVKKEKVLHFLFTDTRCCARNALGR 239
 QY 241 ECTKLTIDLNQAPQSTLPQLFLKVGEPVLRCKAIVNHGFGLTWELEDKALEEGSYPE 300
 DB 240 ECTRLFTIDLNQPTQTLPLQLFLKVGEPVLRCKAVNHGFGLTWELEDKALEEGSYPE 299
 QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCSGSKHPSQSALVTILEKGFINATSSOEY 360
 DB 300 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCSGSKHPSQSALVTILEKGFINATSSOEY 359
 QY 361 EIDPYEKFCFSVRPKAYPRIRCTWIFQASFPCCQGLEDGYSISKPCDHKNKPGVEIFY 420
 DB 360 EIDQYEEFCFSVRPKAYPQIRCTWTFSRKSPCCQKGLDNGYSISKPCDHKNKPGVEIFY 419
 QY 421 AENDDAQFTKMTFLNIRKKQVLANASQASCSDDGYPLPSWTWKCSKSPNCTEIP 480
 DB 420 AENDDAQFTKMTFLNIRKKQVLANASQASCSDDGYPLPSWTWKCSKSPNCTEIP 479
 QY 481 EGVNWKANRKFQWYSSSTLNSEAGKLLVKKCAYNMGTSCTIFLNSPGPPFFIQ 540
 DB 480 EGVNWKANRKFQWYSSSTLNSEAGKLLVKKCAYNMGTSCTIFLNSPGPPFFIQ 539
 QY 541 DNISFYATIGLCLPFIIVVLIVLICHYKQFRYESQLQMIQVGTPLDNEYFYVDFRDEY 600
 DB 540 DNISFYATIGLCLPFIIVVLIVLICHYKQFRYESQLQMIQVGTPLDNEYFYVDFRDEY 599

QY 601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSQVAVKMLKEKADSCEKALM 660
 DB 600 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSQVAVKMLKEKADSCEKALM 659
 QY 661 SELKMTLGHNDINVLGACTLSGPVYLIPEYCCYGDLLANLYRSKRKFKHRTWTEIFK 720
 DB 660 SELKMTLGHNDINVLGACTLSGPVYLIPEYCCYGDLLANLYRSKRKFKHRTWTEIFK 719
 QY 721 EHNFSYPTFOAHNSMPCGSEVQLHPPLDOLSGPNGNSIHSEDEIEYENOKRLAEE 780
 DB 720 EHNFSYPTFOAHNSMPCGSEVQLHPPLDOLSGPNGNSIHSEDEIEYENOKRLAEE 777
 QY 781 EDNLVLTFFEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVKIKCDFGLARDIL 840
 DB 778 EDNLVLTFFEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVKIKCDFGLARDIL 837
 QY 841 SSSSYVVRGNARLPVKWMAPESELFEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDAN 900
 DB 838 SSSSYVVRGNARLPVKWMAPESELFEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDAN 897
 QY 901 FYKLIQSGFMEQPPVATGIEYVMSQSWAFDSRKPSPFNLTSLFLCQLAAEAEAC--- 957
 DB 898 FYKLIQSGFMEQPPVATGIEYVMSQSWAFDSRKPSPFNLTSLFLCQLAAEAEAMYNQ 957
 QY 958 ----IRTSIHLPKQAAPOQRG-GLRAQSPQRYK 986
 DB 958 VDRGVSECPHYQNRPRPFSREMDLGLLSPOAQVE 991
 RESULT 12
 AAR67816
 ID AAR67816 standard; Protein; 993 AA.
 XX AAR67816;
 DT 18-AUG-1995 (first entry)
 XX Flk2 receptor protein-tyrosine-kinase.
 DE Human Flk2; receptor protein-tyrosine-kinase; primitive
 KW hematopoietic cell; fetal liver kinase; diagnostic ligand
 KW isolation; bone marrow disease therapy.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Peptide 1..27 /note= "signal peptide"
 FT Protein 28..993 /note= "mature protein"
 FT Domain 28..543 /note= "extracellular receptor domain"
 FT Domain 544..563 /note= "transmembrane region"
 FT Domain 564..993 /note= "intracellular catalytic domain"
 XX WO9500554-A.
 PN 05-JAN-1995.
 XX 17-JUN-1994; 94WO-US06944.
 XX 18-JUN-1993; 93US-0080244.
 PR 21-JUN-1993; 93US-0081508.
 PR 23-NOV-1993; 93US-0157490.
 XX (UYPR-) UNIV PRINCETON.
 XX Lemischka IR;
 XX WPI; 1995-052014/07.
 DR N-PSDB; AAQ81013.

XX Ligand for receptor protein tyrosine kinase - useful for the
PT stimulation of primitive haematopoietic stem cells causing
PT proliferation and/or differentiation
XX
PS Disclosure; Fig 1b; 131pp; English.
XX

CC The sequence corresponds to a human Flk2 (fetal liver kinase)
CC receptor protein-tyrosine-kinase, which is expressed in primitive
CC hematopoietic cells but not in mature hematopoietic cells. The
CC protein is useful in isolation of receptor ligands, which have
CC applications in diagnosis of bone marrow disorders and in
CC stimulating proliferation and/or differentiation of primitive
CC hematopoietic stem cells.

XX
SQ Sequence 993 AA;

Query Match 84.1%; Score 4429.5; DB 16; Length 993;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

QY 1 MRALAQRSDRLLLVLSVMILETVTQDLPVVKVILSHENNGSSAGKPSRYRMVRS 60
Db 1 MPALA-RDAGTVPLLVFSAMFGTITNQDLPVVKVILSHENNGSSAGKPSRYRMVRS 59
QY 61 PEDLCQTPRRQSEGTVEBAATVEAESGSIITQVOLATPGDLCLVWFKHSSLGCPHFD 120
Db 60 PEDLCALRQSSGTVEAAAVEVDVASITLQVLVDAPGNISCLVWFKHSSLGCPHFD 119
QY 121 LQNRGIVSMALNTVETQAGYLLIHQSERANYTVLTVNVRDOLYVLRPYFRKMNQ 180
Db 120 LQNRGVVSMVLKNTVQAGYLLIFIOSEATNYTILFTVSRNTLLYLRPYFRKMNQ 179
QY 181 DALLCISEGVPEPTVEVWVLCSSHRESCKEKPAPVVRKEKVLHFGDIRCCARNALGR 240
Db 180 DALVCISEGVPEPTVEVWVLCSSHRESCKEKPAPVVRKEKVLHFGDIRCCARNALGR 239
QY 241 ECTKLFTIDLNAQPSLTLPQLFLKVGELPWRCKAIVHNGFGLTWLEDKALEEGSYFE 300
Db 240 ECTRLFTIDLNQTPQTLTLPQLFLKVGELPWRCKAIVHNGFGLTWLEDKALEEGSYFE 299
QY 301 MSTYSTNRMTIRILLAFVSSVGRNDTGYTSSSKHPSQSALVTILEKGFNATSSQBEY 360
Db 300 MSTYSTNRMTIRILLAFVSSVGRNDTGYTSSSKHPSQSALVTIVGKGFNATSSBDY 359
QY 361 EIDYERKFCFSVRKAYPRIRCTWIFSOAPCQRGLEDGYSISKCDHKNKCEYIFY 420
Db 360 EIDYERKFCFSVRKAYPRIRCTWIFSOAPCQRGLEDGYSISKCDHKNKCEYIFY 419
QY 421 AENDDAQFTKMTNIRKPPQVLANASQASCSGSDGYPLSPWTKKCSKSPNCTEIP 480
Db 420 AENDDAQFTKMTNIRKPPQVLANASQASCSGSDGYPLSPWTKKCSKSPNCTEIP 479
QY 481 EGVNKKANRVKFCQWSSSTLANSEAGKLLVKCCAVNSGTCETIFLNSPGPPFIQ 540
Db 480 EGVNKKANRVKFCQWSSSTLANSEAGKLLVKCCAVNSGTCETIFLNSPGPPFIQ 539
QY 541 DNISFYATIGLCLEPIVVLVILCHYKKQPRYSOLOMIQVGTGLDNEYFYVDFRDEY 600
Db 540 DNISFYATIGLCLEPIVVLVILCHYKKQPRYSOLOMIQVGTGLDNEYFYVDFRDEY 599
QY 601 DLKWEFFPRENLEFGKVLGSGAFGMVNATAYIGSKTGVSIQVAVMKLKEKADSKCEKALM 660
Db 600 DLKWEFFPRENLEFGKVLGSGAFGMVNATAYIGSKTGVSIQVAVMKLKEKADSKCEKALM 659
QY 661 SELKQMTLGHHDHNVNLLGACTLSGPVILIFYCCYGGDLNLYRSKREKPHRTWTIFK 720
Db 660 SELKQMTLGHHDHNVNLLGACTLSGPVILIFYCCYGGDLNLYRSKREKPHRTWTIFK 719
QY 721 EHNFSYPTFOAHNSNMPGSRVQLHPDQLDGLGFGNNSHSEDETEYENQKRIABEE 780
Db 720 EHNFSYPTFOAHNSNMPGSRVQLHPDQLDGLGFGNNSHSEDETEYENQKRIABEE 777

QY 781 EDNLVLTEDLLCFAYQVAKGMFELEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
Db 778 EDNLVLTEDLLCFAYQVAKGMFELEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIM 837
QY 841 SDSSVVVRGNARLPVKWMAPELSEFGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Db 838 SDSSVVVRGNARLPVKWMAPELSEFGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 897
QY 901 FYKLIQSGFKMQPFYATGEGYFVWQSCWAFDSRKRKPSFPNLTSLFLGCOLAAEAEAC--- 957
Db 898 FYKLIQSGFKMQPFYATGEGYFVWQSCWAFDSRKRKPSFPNLTSLFLGCOLAAEAEAMYQN 957
QY 958 ----IRTSIHLPKQAAPQORG-GLRAQSPQK 986
Db 958 VDRVSECPHTYQNRPRFSDMDLGLLSQAQVE 991

RESULT 13
AAR67536
ID AAR67536 standard; Protein; 993 AA.
XX AAR67536;
XX
DT 04-JUL-1995 (first entry)
XX
DE Human flk-2.
XX
KW Fetal liver kinase-2; flk-2; protein tyrosine-kinase receptor;
KW hematopoiesis; stem cell.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT Domain /label= Sig_peptide 28..543
FT /label= Extracellular_receptor_domain 544..563
FT /label= Transmembrane_region 564..993
FT /label= Intracellular_catalytic_domain

XX US367057-A.
XX PN 22-NOV-1994.
XX PD 02-APR-1991; 91US-0679666.
XX PF 02-APR-1991; 91US-0679666.
XX PR 02-APR-1991; 91US-0679666.
XX PR 28-JUN-1991; 91US-0728913.
XX PR 15-NOV-1991; 91US-0730065.
XX PR 24-DEC-1991; 91US-0813593.
XX PR 26-JUN-1992; 92US-0906397.
XX PR 12-NOV-1992; 92US-0975049.
XX PR 19-NOV-1992; 92US-0977451.
XX PR 30-APR-1993; 93US-0055269.
XX (UYPR-) UNIV PRINCETON.
XX
XX Lemischka IR;
XX
XX WPI; 1995-005894/01.
XX N-PSDB; AAQ79069.

XX Murine flk-2 receptor protein tyrosine kinase - used to stimulate
XX proliferation and/or stimulation of primitive mammalian
XX haematopoietic stem cells in vitro or in vivo.
XX
XX Disclosure; Fig. 2A-1F; 69pp; English.
XX
XX cDNAs encoding receptor protein tyrosine-kinases, mouse fetal liver
XX kinase-2 (flk-2), human flk-2 and mouse flk-1 are given in AAQ79068-70,
XX respectively, and the deduced amino acid sequences in AAR67535-37,

CC respectively.

XX Sequence 993 AA;

Query Match 84.1%; Score 4429.5; DB 16; Length 993;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

Qy 1 MRALQRSRRLLLVLSVILETVNODLPVKVLISHENSSAGKPSRYRVGRS 60
Db 1 MPALA-RDAGTVPLLVFAMIFGITINQDLPVKVLINHKNDSSVGKSSYPWVSES 59

Qy 61 PEDLOCTPRQRSGITVEAATVEAEGSITLQVQLATPGDLSCLWVFXHSSLCQPHFD 120
Db 60 PEDLGCALPQSGITVEAANVEDVVSASITLQVLVDAFGNISCLWVFXHSSLCQPHFD 119

Qy 121 LQNRGIVSMALNVETQAGEYLLHTQSRANVTVLFTVNRVRTQYLVLRPFRQWENQ 180
Db 120 LQNRGVSMVILKMTQAGEYLLFTQSEATNTYTLFTVSIKNTLLYTLRRPYFRQWENQ 179

Qy 181 DALLCISEGVPEPTVEWVLCSSHRECKEGRPAVRKEKVLHELFGTDIRCCARNALGR 240
Db 180 DALVCISESVPEPIVFWVLCDSQGESCKEESPAPVVRKEKVLHELFGTDIRCCARNELGR 239

Qy 241 ECTKLFTIDINQAPQSTLPQLFKVGEPLWIRCKAIHVNHGFLGTWELEDKALEEGSYFE 300
Db 240 ECTRLFTIDINQPTQTLQLFKVGEPLWIRCKAVVNHGFLGTWELENKALEEGNYFE 299

Qy 301 MSTYSTNRTMIRILLAPVSSVGRNDTGYTTCSSKHPQSALVTILEKGFINATSSQEEY 360
Db 300 MSTYSTNRTMIRILLAPVSSVGRNDTGYTTCSSKHPQSALVTIVKGFINATSSSEY 359

Qy 361 EIDPYEKFCFVRFKAYPRCTRWISQASFPCEQGLEGDYISIKFCHKNKPGVIFY 420
Db 360 EIDQYEEFCFVRFKAYPQIRCTWTSRFSFPCEQGLONGYISIKPCNKKHQPGEYIFH 419

Qy 421 AENDDAQTKMFTLNIRKPOVLNANASQASCSQGYPLPSWTWKCKSDKSPNCTEIEP 480
Db 420 AENDDAQTKMFTLNIRKPOVLNANASQASCSQGYPLPSWTWKCKSDKSPNCTEIEIT 479

Qy 481 EGVNKKANRKFQGVQVSSSTLNSBAGKLLVKCCAYNSMGTSCTIFLNSPGPPFFIQ 540
Db 480 EGVNKKANRKFQGVQVSSSTLNSBAIKFLVKCCAYNSGLTSCETILLNSPGPPFFIQ 539

Qy 541 DNISFYATIGLCPFIWLVILCHYKQFRYESQLOMQLQVTPLDNEYVDYDRDEY 600
Db 540 DNISFYATIGVCLLFIWLVLLCHYKQFRYESQLOMQLQVTPDNEYVDYDRDEY 599

Qy 601 DLKWEPPRENLEFGKVLGSGAFGRVMNATAYGSKTGVSIQVAVKMLKERADSCKEALM 660
Db 600 DLKWEPPRENLEFGKVLGSGAFGRVMNATAYGSKTGVSIQVAVKMLKERADSSERELM 659

Qy 661 SELKMMTHLGHNDINVLGACTLSGPVYLIFCYCCYGDLLNLYLRSKREKPHRTWTBIFK 720
Db 660 SELKMMTHLGHNDINVLGACTLSGPVYLIFCYCCYGDLLNLYLRSKREKPHRTWTBIFK 719

Qy 721 EHNFSYPTTQAHNSNMPGSRVOLHPPDLQSLGFGNSIHSEDEIYEYENKELAESEE 780
Db 720 EHNFSYPTTQAHNSNMPGSRVOLHPPDLQSLGFGNSIHSEDEIYEYENKELAESEE 777

Qy 781 EDNLVLTFFELLFCFAYQVAKGMFLEPKSCVHRDLARNVLVTHGKVKVLCDFGLARDIL 840
Db 778 EDNLVLTFFELLFCFAYQVAKGMFLEPKSCVHRDLARNVLVTHGKVKVLCDFGLARDIM 837

Qy 841 SDSYVVRGNARLPVKWMAPESLFEGITYTIKSDVMSYGILLWEIFSLGVNPGIPVDAN 900
Db 838 SDSYVVRGNARLPVKWMAPESLFEGITYTIKSDVMSYGILLWEIFSLGVNPGIPVDAN 897

Qy 901 FYKLIQSGFQWQBPYATGFIYFMQSCWAFDSKRSFNLTSFLGCOLABEAC--- 957
Db 898 FYKLIQSGFQWQBPYATGFIYFMQSCWAFDSKRSFNLTSFLGCOLABEANYQN 957

Qy 958 ----IRTSIHLPKQAPQQRG-GLRAQSPQRQVK 986

Db 958 VDGVRSECPHTYQNRPPFGREMDLGLLSPOAQVE 991

RESULT 14
AAR97419

ID AAR97419 standard; Protein; 993 AA.

XX
AC AAR97419;

DT 11-DEC-1996 (first entry)

XX
DE Murine foetal liver kinase 2.XX
KW Murine; foetal liver kinase 2; flk-2; protein tyrosine kinase;
monoclonal; antibody; extracellular domain; receptor assay;
haematopoietic stem cell; ligand; stimulation; proliferation;
cancer chemotherapy; radiation.XX
OS Mus musculus.XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT Peptide /label= sig_peptide
FT Peptide 28..993
FT Domain /label= mat_peptide
FT Domain 28..544
FT Domain /label= extracellular_domain
FT Domain 545..564
FT Domain /label= transmembrane_domain
FT Domain 565..993
FT Domain /label= intracellular_domainXX
PN US5548065-A.XX
PD 20-AUG-1996.XX
PF 02-APR-1991; 91US-0679666.XX
PR 19-NOV-1992; 92US-0977451.XX
PR 02-APR-1991; 91US-0679666.XX
PR 28-JUN-1991; 91US-0728913.XX
PR 15-NOV-1991; 91US-0793065.XX
PR 24-DEC-1991; 91US-0813593.XX
PR 26-JUN-1992; 92US-0906397.XX
PR 12-NOV-1992; 92US-0975049.XX
PR 30-APR-1993; 93US-0055269.XX
PR 31-OCT-1994; 94US-0252517.XX
PA (UYPR-) UNIV PRINCETON.XX
PI Lemischka IR;XX
DR WPI; 1996-392678/39.XX
DR N-PSDB; AAT38734.XX
PT Anti-foetal liver kinase 2 (flk-2) antibodies - useful in assays,
for isolating haematopoietic stem cells expressing receptor and for
obtaining ligandsXX
PS Claim 1; Columns 39-48; 50pp; English.XX
CC The present sequence is murine foetal liver kinase 2 (flk-2),
a protein tyrosine kinase. Isolated antibodies, pref. monoclonal,
CC against the extracellular portion of flk-2 can be used to
assay for flk receptors on the surface of primitive haematopoietic
stem cells, and to isolate positive cells. The antibodies can also
be used as, or to obtain ligands, which stimulate the proliferation
and/or differentiation of stem cells. The ligands can be used, e.g.
for treating anaemia, or bone marrow damage resulting from cancer
chemotherapy, or radiation.

XX

SQ Sequence 993 AA;		Query Match Best Local Similarity 84.1%; Score 4429.5; DB 17; Length 993; Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;
Qy	1 MRALAQSRDRRLLLVLSVMILETVNQDLPVTKVLSHENNGSSAGKPSRYRMVRGS 60	
Db	1 MPALA-RDAGTVPLLVVFSAMIFGTTITQDLPVTKVLIHNKNDSSVGKSSYPVWVSES 59	
Qy	61 PEDLOCTPRROSEGTVEAATVEVAESGSTITLOVLATPGDLSCLWVFKXSSICGQPHFD 120	
Db	60 PEDLGCALPQSGTGYEAAAEVDVSASITLQVLVADPAGNISCLWVFKXSSINCPHFD 119	
Qy	121 LQNRGVSVMAILNVTTQAGEYLHIIQSERANYTVLTVNVNRDTQLYVLRRPYFRKMENQ 180	
Db	120 LQNRGVSVVILXWTTQAGEYLLFTQSEATNTILFTVSRNTLLYTLRRPYFRKMENQ 179	
Qy	181 DALLCISEGVPEPTVEWVLCSSHRESCKEGBPAVVRKEEKVLHLEFGTDIRCCARNALGR 240	
Db	180 DALVCISESVPEPIVEWVLCDSQGESCKEESPAVVRKEEKVLHLEFGTDIRCCARNELGR 239	
Qy	241 ECTKLTIDINQAPOSTLPQLFKVGEPLWIRCKAHVNHGFGLTWELEDKALEBSGYFE 300	
Db	240 ECTRLFTIDLNQPTTLPQLFLKVGEPWIRCKAVHNVHGFGLTWELENKALEEGNYFE 299	
Qy	301 MSTYSTNRTMIRILLAFVSSVGRNDGYTTCSSSKHPSQSALVTILEKGFINATSSQEEY 360	
Db	300 MSTYSTNRTMIRILLAFVSVARNDGYTTCSSSKHPSQSALVTIVKGFINATNSSEY 359	
Qy	361 EIDPYEKFCSFRKAYPRIRCTWIFSQASFPCEQRGLEDGYSISKPCDHKNKPGEIFY 420	
Db	360 EIDQYEEFCFSFRKAYPQIRCTWTSRKSFPCEQKGLDNGYISIKFCHKHQPGEIFY 419	
Qy	421 AENDDAQFTMTFTLNTRKQPVLNANASQASCSGYPPLSPWTKCKSDKSPNCTEIEP 480	
Db	420 AENDDAQFTMTFTLNTRKQPVLNANASQASCSGYPPLSPWTKCKSDKSPNCTEIEIT 479	
Qy	481 EGVNKKANKRVFGQWVSSSTLNNSAGKLLVKCAVNSMGTSCETIFLNSPQPPFIQ 540	
Db	480 EGVNKKANKRVFGQWVSSSTLNNSAIGKLVKCAVNSLGTSCETIFLNSPQPPFIQ 539	
Qy	541 DNISFYATIGLCLPFVTVLIVLICHYKKQFRYESQLOMIQVTPGLDNEYFYVDPRDYEY 600	
Db	540 DNISFYATIGVCLLFIVVLTLICHYKKQFRYESQLOMQVQVGTSSDNEYFYVDFREY 599	
Qy	601 DLKWEPPRENLEFGKVGSGAFGRVNNATAYGISTGVSTQVAVKMLKEKADSCKEALM 660	
Db	600 DLKWEPPRENLEFGKVGSGAFGRVNNATAYGISTGVSTQVAVKMLKEKADSSEREALM 659	
Qy	661 SELKMTHLGHNDIYNLLGACTLSGPVYLI FYCCYGDLLNVLRSKREKHEHTWTEIFK 720	
Db	660 SELKMTQLGSHENIYNLLGACTLSGPYLI FYCCYGDLLNVLRSKREKPHRTWTEIFK 719	
Qy	721 EHNFSSYPTFOAHSNMPGSRVQLHPDQLDLSGFNGNSIHSEDETEYENQKRLAESEE 780	
Db	720 EHNFSSYPTFOAHSNMPGSRVQLHPDSDQISGLHNSFHSDETEYENQRL--EE 777	
Qy	781 EDNLVLTFDLLCFAYQAVKMGFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840	
Db	778 EDNLVLTFDLLCFAYQAVKMGFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIM 837	
Qy	841 SDSYVVRGNARLPVKWMAPESLFEGITYITKSDVWSGILLWIFSLGVNYPGIPVDAN 900	
Db	838 SDSYVVRGNARLPVKWMAPESLFEGITYITKSDVWSGILLWIFSLGVNYPGIPVDAN 897	
Qy	901 FYKLIQSGFMQEPFYATEGIIYFWMQSCAFDSRKRPSFNNLTSFLGCOLAEAREAC-- 957	
Db	898 FYKLIQSGFMQEPFYATEGIIYIMQSCAFDSRKRPSFNNLTSFLGCOLAEAREAMQN 957	
Qy	958 ----IRTSIHLPKQAAFPQORG-GLRAQSPQORQVK 986	
Db	958 VDGVRSECPHTYQNRRFPFSREMDLGLLSPOAQVE 991	

RESULT 15
AAW19873
ID AAW19873 standard; Protein; 993 AA.
XX
AC AAW19873;
XX
DT 19-AUG-1997 (first entry)
XX
DE Human flk-2 receptor.
XX
KW Human; fetal liver kinase 2; flk2; receptor protein tyrosine kinase;
KW PTK; liver; spleen; thymus; adult; brain; bone marrow; primitive portion;
KW haematopoietic hierarchy; extracellular domain; soluble form; ligand;
KW proliferation; differentiation; mammalian; haematopoietic stem cell;
KW macrocytic anaemia; aplastic anaemia; cancer; radiation; mouse.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..27 /note= "Signal peptide"
FT Protein 28..993 /note= "Mature flk-2"
FT FT
XX US5621090-A.
XX PN
XX PD 15-APR-1997.
XX
XX 02-APR-1991; 91US-0679666.
XX PF
XX PR 26-JUN-1992; 92US-0906397.
XX PR 02-APR-1991; 91US-0679666.
XX PR 28-JUN-1991; 91US-0728913.
XX PR 15-NOV-1991; 91US-0793065.
XX PR 24-DEC-1991; 91US-0813593.
XX
XX (UYPR-) UNIV PRINCETON.
XX
XX Lemischka IR;
XX
XX WPI; 1997-235228/21.
XX N-PSDB; AAT72117.
XX
XX Protein containing the extracellular domain of human flk-2 - used
XX for identification of primitive haematopoietic cell proliferation
XX and differentiation stimulatory ligands, e.g. for treating anaemia
XX
XX Claim 1; Fig 1B; 55pp; English.
XX
XX This sequence represents human fetal liver kinase 2 (flk2). flk-2 is
XX a receptor protein tyrosine kinase (PTK) and is important in transducing
XX putative self-renewal signals from the environment. flk-2 is expressed
XX in fetal liver, spleen, fetal thymus, adult brain and adult bone marrow,
XX and it is thought that flk-2 is expressed in the entire primitive portion
XX of the haematopoietic hierarchy. The invention concerns a recombinant
XX nucleic acid, preferably mRNA, which encodes a protein containing only
XX the extracellular domain of human flk-2 and lacking the flk-2 intra-
XX cellular catalytic domain. The resultant protein represents a soluble
XX form of flk-2 which is used to isolate specific ligands for flk-2. These
XX ligands can be used to stimulate proliferation and/or differentiation of
XX mammalian haematopoietic stem cells, in vivo or in vitro, e.g. for
XX treatment of macrocytic or aplastic anaemia or bone marrow damage caused
XX by cancer treatment or radiation.
XX
XX SQ Sequence 993 AA;
Query Match 84.1%; Score 4429.5; DB 18; Length 993;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;
Qy 1 MRALAQSRDRRLLLVLSVMILETVNQDLPVTKVLSHENNGSSAGKPSRYRMVRGS 60

Db 1 MPALA-RDAGTVLLVVPISAMIFGTITNQDLVVKVNLHNKNDSSVGKSSSYPVWSES 59
Qy 61 PEDLOCTPRQSGTVYBAATVEVAESGSIITLQVQIATPGDLSCLVWVFKHSSLGCPHF 120
Db 60 PEDLGALRPQSSGTVYAAAVDVDSASITLQVLVDAFGNISCLVWVFKHSSLNCQPHF 119
Qy 121 LQNRGIVSMALNVTTQAGEYLLHQSERANYTVLTVNVRTQLYVLRPYFRKWEQ 180
Db 120 LQNRGVVSMVLKMTQAGEYLLFQSEATNYITLTVSIRNLTLYLRPYFRKWEQ 179
Qy 181 DALLCISEGVPEPTVEWVLCSSHRESCKEEGPAVVRKEKVLHELFGTDIRCCARNALGR 240
Db 180 DALVCISESYPEPIVEWVLCDSQESCKEESPAVVKKEKVLHELFGTDIRCCARNELGR 239
Qy 241 ECTKLTIDLNQAPQSTLPOLPKVGEPLWIRKALIHVNHGFGLTWELEDKALEBGSYFE 300
Db 240 ECTRLFTIDLNOTPOTTLPOLFLKVGEPWIRCKAVHVNHGFGLTWELENKALEBGNIFE 299
Qy 301 MSTYSTNRTMIRILLAFVSSVGRNDGYTTCSSSKHPSQSALVTILEKGFINATSSOEY 360
Db 300 MSTYSTNRTMIRILFAFVSSVARNDGYTTCSSSKHPSQSALVTIIVKGFINATNSEDI 359
Qy 361 EIDPYEKFCFSVRFKAYPRIRCTWIPSOASFCEQORLEGDGYSISKFDHKNKPGYIFY 420
Db 360 EIDQYEFCSVRFKAYPOIRCTWTFSRKSFCEQKGLONGYSISKFNHKGQGEYIFH 419
Qy 421 AENDDAQFTKMTLNIRKKPOVLANASASQSCSSDGYPLPSWTWKKCDKSPNCTEIP 480
Db 420 AENDDAQFTKMTLNIRKKPOVLANASASQSCFSDGYPLPSWTWKKCDKSPNCTEIT 479
Qy 481 EGVNKKANRKFQGVSSSTLANSEAGKLLVKCAVNSMGTSCETIPLNSPGPFFIQ 540
Db 480 EGVNKRANRKFQGVSSSTLANSEAIKGLVKCAVNSLGTSCETIPLNSPGPFFIQ 539
Qy 541 DNISFYATIGLCIPFIIVLILVLICHKYKQFRYESOLOMIQVGTGLDNEYFYVDFFRDY 600
Db 540 DNISFYATIGVCLLFIIVLTLCHKYKQFRYESOLOMVQVGTSSDNEYFYVDFREY 599
Qy 601 DLKWEPPRENLEFGKVLGSAFGVNMATAYGISTGVSTQAVKMLKEKADSCKEALM 660
Db 600 DLKWEPPRENLEFGKVLGSAFGVNMATAYGISTGVSTQAVKMLKEKADSSEREALM 659
Qy 661 SELKMTHLGHNDINVLGACLTSGPVYLI FEYCCVGDLLNLYRSKREKFRHTWTEIFK 720
Db 660 SELKMTQLGSHENIVNLGACLTSGPIYLI FEYCCVGDLLNLYRSKREKFRHTWTEIFK 719
Qy 721 EHNFSYPTFQAHSNSMPSREYQLHPDLDQSLGFGNSIHSEDEIEYENQKRLAESEE 780
Db 720 EHNFSYPTFQSHNSMPSREYQIHPDSDOIISGLHNSFHSEDEIEYENQKRL--EE 777
Qy 781 EDNLVLTFFEDLLCFAYQVAKGMEFLPKSCVHRDLAARNVLVTHGKVVKI CDFGLARDIL 840
Db 778 EDNLVLTFFEDLLCFAYQVAKGMEFLPKSCVHRDLAARNVLVTHGKVVKI CDFGLARDIM 837
Qy 841 SDSYVVRGNARLPVKWMAPESEFEGITTKSDVWSYGLLWEIFSLGVNPNYPCI PVDAN 900
Db 838 SDSYVVRGNARLPVKWMAPESEFEGITTKSDVWSYGLLWEIFSLGVNPNYPCI PVDAN 897
Qy 901 FYKLIQSGFKWEQPFYATEGIYFVWQSCWAFDSRKRPSFPNLTSLGCOLAEAEAC--- 957
Db 898 FYKLIQNGFKWQPFYATEIYIIMQSCWAFDSRKRPSFPNLTSLGCOLAEAEAMYQN 957
Qy 958 ----IRTSIHLPKQAAPQORG-GLRAQSPQRQVK 986
Db 958 VDGVRSECPHTYQVRPDRPFSREMDLGLLSPQAQVE 991

Search completed: May 24, 2003, 16:56:02
Job time : 59.9718 secs

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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:59:30 ; Search time 40.9793 Seconds
(without alignments)
2400.704 Million cell updates/sec

Title: US-09-919-408-2

Perfect score: 5264

Sequence: 1 MRALQRSRRLLLVLSV.....RGGLRAQSPQVKIHRRS 992

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW PUB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5264	100.0	992	10	US-09-919-408-2
2	5264	100.0	992	10	US-09-872-136-2
3	4429.5	84.1	993	10	US-09-919-408-4
4	4429.5	84.1	993	10	US-09-872-136-4
5	1223	23.2	975	9	US-10-192-867-2
6	1221.5	23.2	972	10	US-09-944-807-10
7	1196	22.7	976	9	US-10-099-895-32
8	1196	22.7	976	9	US-10-192-867-4
9	1152.5	21.9	1088	9	US-09-961-403-4
10	1152.5	21.9	1089	10	US-09-769-987-2
11	1152.5	21.9	1089	10	US-09-919-497-90
12	1152.5	21.9	1089	10	US-09-866-510-2
13	1150.5	21.9	1089	9	US-09-955-363-36
14	1149.5	21.8	1089	10	US-09-866-510-10
15	1148.5	21.8	1089	10	US-09-866-510-4
16	1147.5	21.8	1089	10	US-09-866-510-8
17	1146.5	21.8	1089	10	US-09-866-510-6
18	1078	20.5	1090	10	US-09-866-510-14
19	1078	20.5	1106	9	US-09-955-363-2

20	1078	20.5	1106	10	US-09-866-510-22	Sequence 22, Appl
21	1074	20.4	1106	10	US-09-866-510-16	Sequence 16, Appl
22	1073	20.4	1106	10	US-09-866-510-20	Sequence 20, Appl
23	1072	20.4	1106	10	US-09-866-510-18	Sequence 18, Appl
24	998.5	19.0	1338	9	US-10-059-585-44	Sequence 44, Appl
25	961.5	18.3	1356	9	US-10-022-939-2	Sequence 2, Appl
26	961.5	18.3	1356	9	US-10-100-405A-2	Sequence 2, Appl
27	960.5	18.2	1356	9	US-09-969-037-7	Sequence 7, Appl
28	954.5	18.1	1298	10	US-09-982-610-33	Sequence 33, Appl
29	954.5	18.1	1363	9	US-09-375-248-2	Sequence 34, Appl
30	952.5	18.1	1368	9	US-10-105-901-34	Sequence 19, Appl
31	952	18.1	1363	9	US-09-375-248-19	Sequence 33, Appl
32	943.5	17.9	1362	9	US-10-105-901-33	Sequence 6, Appl
33	941	17.9	386	9	US-09-939-833-6	Sequence 6, Appl
34	941	17.9	386	10	US-09-939-754-6	Sequence 6, Appl
35	941	17.9	386	10	US-09-939-832-6	Sequence 6, Appl
36	937.5	17.8	1367	10	US-09-766-678-2	Sequence 2, Appl
37	936.5	17.8	1363	9	US-10-105-901-32	Sequence 32, Appl
38	926.5	17.6	1367	10	US-09-919-408-6	Sequence 6, Appl
39	926.5	17.6	1367	10	US-09-872-136-6	Sequence 6, Appl
40	862	16.4	367	9	US-09-939-833-9	Sequence 9, Appl
41	862	16.4	367	10	US-09-939-754-9	Sequence 9, Appl
42	862	16.4	367	10	US-09-939-832-9	Sequence 9, Appl
43	856	16.3	367	9	US-09-939-833-12	Sequence 12, Appl
44	856	16.3	367	10	US-09-939-754-12	Sequence 12, Appl
45	856	16.3	367	10	US-09-939-832-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-919-408-2
; Sequence 2, Application US/09919408
; Patent No. US2002007207A1
; GENERAL INFORMATION:

APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
RECEPTORS AND THEIR LIGANDS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Imclone Systems Incorporated

STREET: 180 Varick Street

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10014

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/919,408

FILING DATE: 31-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/977,451

FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/906,397

FILING DATE: 26-JUN-1992

APPLICATION NUMBER: US PCT/US92/05401

FILING DATE: 26-JUN-1992

APPLICATION NUMBER: TW 81102961

FILING DATE: 15-APR-1992

APPLICATION NUMBER: US PCT/US92/02750

FILING DATE: 02-APR-1992

APPLICATION NUMBER: US 07/813,593

FILING DATE: 24-DEC-1991

APPLICATION NUMBER: US 07/793,065

FILING DATE: 15-NOV-1991

APPLICATION NUMBER: US 07/728,913

FILING DATE: 28-JUN-1991

APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28 601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-919-408-2

Query Match	100.0.0%;	Score 5264;	DB 10;	Length 992;
Best Local Similarity	100.0.0%;	Pred. No. 0;		
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Qy	1	MRAALQSRDRLLLLVLSVMILFETVNQDLPVTKCVLISHENNGSSAGKPSRYMVRGS	60	
Db	1	MRAALQSRDRLLLLVLSVMILFETVNQDLPVTKCVLISHENNGSSAGKPSRYMVRGS	60	
Qy	61	PEDLOCTPRRQSEGTVEAATVEVAESGISTLOVOLATPGDLSCLWPKHSSLCQPHFD	120	
Db	61	PEDLOCTPRRQSEGTVEAATVEVAESGISTLOVOLATPGDLSCLWPKHSSLCQPHFD	120	
Qy	121	LONRGIVSMALLNTETQAGEYILHIOSERANYTVLFTVNVNRTDQLVYLRPRYFRKMENQ	180	
Db	121	LONRGIVSMALLNTETQAGEYILHIOSERANYTVLFTVNVNRTDQLVYLRPRYFRKMENQ	180	
Qy	181	DALLCISEGPEPTVEWVWVLCSSHRESCKEEGPAVVRKEEKVLHFLFGTDIRCCARNALGR	240	
Db	181	DALLCISEGPEPTVEWVWVLCSSHRESCKEEGPAVVRKEEKVLHFLFGTDIRCCARNALGR	240	
Qy	241	ECTKLFTIDLNAQAPQSTLPQLFLKVGBPWLTRCKAIHVNHGFGITWELEDKALBEGSYFE	300	
Db	241	ECTKLFTIDLNAQAPQSTLPQLFLKVGBPWLTRCKAIHVNHGFGITWELEDKALBEGSYFE	300	
Qy	301	MSTYSTNRTMIRIILAFVSSVGRNDTGYYTCCSSKHPSQSALVITILEKGFNATSSQBEY	360	
Db	301	MSTYSTNRTMIRIILAFVSSVGRNDTGYYTCCSSKHPSQSALVITILEKGFNATSSQBEY	360	
Qy	361	EIDPYEFCFVSFRFKAYPRIKCTWIFSOASFPCEQRGLEDGYSISKFDHKNKPGXEYIFY	420	
Db	361	EIDPYEFCFVSFRFKAYPRIKCTWIFSOASFPCEQRGLEDGYSISKFDHKNKPGXEYIFY	420	
Qy	421	AENDDAOFTKFTLNIRKKPOVLANASASQCSDDGYPLFSWTWKKCSDKSPNCTEIP	480	
Db	421	AENDDAOFTKFTLNIRKKPOVLANASASQCSDDGYPLFSWTWKKCSDKSPNCTEIP	480	
Qy	481	EGVWNKANRKFQGVWSSSTLNKSEAGKLLVKCCAYNSMGTSCETITFLNSPGPFPIQ	540	
Db	481	EGVWNKANRKFQGVWSSSTLNKSEAGKLLVKCCAYNSMGTSCETITFLNSPGPFPIQ	540	
Qy	541	DNISFYATIGLCLPFIIVLIVLICHYKKQPRYESQLQMIQVTPGLDNEYFYVDFRDYEF	600	
Db	541	DNISFYATIGLCLPFIIVLIVLICHYKKQPRYESQLQMIQVTPGLDNEYFYVDFRDYEF	600	
Qy	601	DLKWEFPRENLEFGKVLGSGAFGRVWNNATVGISKTGVSIQVAVKMLKEKADSCKEALM	660	
Db	601	DLKWEFPRENLEFGKVLGSGAFGRVWNNATVGISKTGVSIQVAVKMLKEKADSCKEALM	660	
Qy	661	SELKMWTHLGHHDNIVNLGACTLSGPPVYLIFEYCCYGDLLNLYRSKREKPHRTWTEIFK	720	
Db	661	SELKMWTHLGHHDNIVNLGACTLSGPPVYLIFEYCCYGDLLNLYRSKREKPHRTWTEIFK	720	
Qy	721	EHNFTSSYPTFOAHNSNMPGSGREVOLHPPLDQSGFNGNSIHSEDEIYENOKRLAESEE	780	
Db	721	EHNFTSSYPTFOAHNSNMPGSGREVOLHPPLDQSGFNGNSIHSEDEIYENOKRLAESEE	780	

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781 EDNLVTFEDLLCFAYQVAKGMEFLFEKSCVHRDLAARNVLVTHGKVWIKCDFGLARDIL 840
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781 EDNLVTFEDLLCFAYQVAKGMEFLFEKSCVHRDLAARNVLVTHGKVWIKCDFGLARDIL 840
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841 SDSYVVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDAN 900
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841 SDSYVVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDAN 900
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901 FYKLIOSGFRMGEFPFYATEGIYFVMQSWAFDSRKRPSFNLTSLFLGCQLAEAEACIRT 960
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901 FYKLIOSGFRMGEFPFYATEGIYFVMQSWAFDSRKRPSFNLTSLFLGCQLAEAEACIRT 960
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961 SIHLPKOAAPOQRGGRLRAQSPQOVKIHRERS 992
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961 SIHLPKOAAPOQRGGRLRAQSPQOVKIHRERS 992
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RESULT 2
US-09-872-136-2
; Sequence 2, Application US/09872136
; Patent No. US20020119545A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ibor R.
; TITLE OF INVENTION: TOTIPOENT HEMATOPOIETIC STEM CELL
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/872,136
; FILING DATE: 01-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/208,786
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/09/021,324
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 1992-11-19
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054

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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-872-136-2

Query Match 100.0%; Score 5264; DB 10; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALAQRSDRLRLVSVMLTNTQDLPVTKVLIHSHENNGSSAGKPSYRMVRGS 60
DB 1 MRALAQRSDRLRLVSVMLTNTQDLPVTKVLIHSHENNGSSAGKPSYRMVRGS 60

QY 61 PEDLOCTPRQSEGTVEAATVEAEGSITLQVLAATPGDLSCILWPKHSLGCQPHD 120
DB 61 PEDLOCTPRQSEGTVEAATVEAEGSITLQVLAATPGDLSCILWPKHSLGCQPHD 120

QY 121 LQNRGIVSMALNVTQAGEYLHIQSERANYTVLFTVNVVDTQLYVLRPRYFRKMEQ 180
DB 121 LQNRGIVSMALNVTQAGEYLHIQSERANYTVLFTVNVVDTQLYVLRPRYFRKMEQ 180

QY 181 DALLCISEGVPEPTVWVLCSSHRESCKEKGPAVVRKEEVKLHFLFGTDIRCCARNALGR 240
DB 181 DALLCISEGVPEPTVWVLCSSHRESCKEKGPAVVRKEEVKLHFLFGTDIRCCARNALGR 240

QY 241 ECTKLFITDLNOAPOSTLPQLFLVKGPELWIRCAIHNHGFGLTWELDKALBEGSYFE 300
DB 241 ECTKLFITDLNOAPOSTLPQLFLVKGPELWIRCAIHNHGFGLTWELDKALBEGSYFE 300

QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCSKSHPSQSALVILEKGFNATSSQBEY 360
DB 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCSKSHPSQSALVILEKGFNATSSQBEY 360

QY 361 EIDPYEKFCPSVRKAYPRIRCTWIFSOAFCPCQBGLEDGYSISKPCDHKNKPGYIFY 420
DB 361 EIDPYEKFCPSVRKAYPRIRCTWIFSOAFCPCQBGLEDGYSISKPCDHKNKPGYIFY 420

QY 421 AENDDAQTKMTFNIIRKQVLANASQASCSDDGYPLPSWTWKCSKSPNCTEIP 480
DB 421 AENDDAQTKMTFNIIRKQVLANASQASCSDDGYPLPSWTWKCSKSPNCTEIP 480

QY 481 EGVNKKANRKFQGWSSSTLNMSAGKLLVKCCAYNSMGTSCTIFLNSPGPFPIQ 540
DB 481 EGVNKKANRKFQGWSSSTLNMSAGKLLVKCCAYNSMGTSCTIFLNSPGPFPIQ 540

QY 541 DNISFYATIGLCLPFIIVLVILICHYKKQFRIESQLQMIQVTPGLDNEYFYVDFRDY 600
DB 541 DNISFYATIGLCLPFIIVLVILICHYKKQFRIESQLQMIQVTPGLDNEYFYVDFRDY 600

QY 601 DLKWEPPRENLEFGKVLGSAFGFVWNAATYGIKGTGSIQVAVMKLKEKADSCEKALM 660
DB 601 DLKWEPPRENLEFGKVLGSAFGFVWNAATYGIKGTGSIQVAVMKLKEKADSCEKALM 660

QY 661 SELKMTLGHNDINVLGACTLSGPPVILIFEYCCYGGDLNLYRSKREKPHRTWTETFK 720
DB 661 SELKMTLGHNDINVLGACTLSGPPVILIFEYCCYGGDLNLYRSKREKPHRTWTETFK 720

QY 721 EHNFSYPTTQAHNSNMPGSRVQLHPPLDQLSGFNGNSIHSEDEIEYENQKRLABEEE 780
DB 721 EHNFSYPTTQAHNSNMPGSRVQLHPPLDQLSGFNGNSIHSEDEIEYENQKRLABEEE 780

QY 781 EDNLVTFEDLLCFAYQVAKGMEPLEKSCVHRDLARNVLVTHGKVVKICDPLGARDIL 840
DB 781 EDNLVTFEDLLCFAYQVAKGMEPLEKSCVHRDLARNVLVTHGKVVKICDPLGARDIL 840

QY 841 SDSSVYVRGNARLPVKWAPESLPEGIYTTKSDVWSYGLLWEIFSLGVNYPGIPVDAN 900
DB 841 SDSSVYVRGNARLPVKWAPESLPEGIYTTKSDVWSYGLLWEIFSLGVNYPGIPVDAN 900

QY 901 FYKLIQSGFKMEQPPYATGEGYFVWQSCWAFDSRKRPSFPNLTSLFGCOLAEACIRT 960
DB 901 FYKLIQSGFKMEQPPYATGEGYFVWQSCWAFDSRKRPSFPNLTSLFGCOLAEACIRT 960

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DB 961 SIHLPKQAAPQORGLRAQSPORQVKIHRERS 992

RESULT 3
US-09-919-408-4
; Sequence 4, Application US/09919408
; Patent No. US2002007207A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/919,408
; FILING DATE: 31-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,451
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-919-408-4

Query Match 84.1%; Score 4429.5; DB 10; Length 993;
Best Local Similarity 84.1%; Pred. No. 2.3e-297;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;


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Db 1 MPALA-RDAGTVPLLVVFSAMIFCTITNQDLPVTKCVLIHKNNDSSVGKSSYPMVSES 59

QY 61 PEDLOCTPRQSGTGYEAATVEAAGSITLQVLAATPGDLSCLWPKHSSLCGQPHFD 120
Db 60 PEDLGALRPOSSGTGYEAAAVEVDVSASITLQVLDVDPAGNISCLWPKHSSLCGQPHFD 119

QY 121 LQNRGIVSMALNVETQAGEYLLHIOSEANVTYVLTNNVDTOLVLRPRPKMENQ 180
Db 120 LQNRGVSMVILKMTETQAGEYLLFQSEATNTYLTFTVSRINLLTYLRRPKMENQ 179

QY 181 DALLCISEGPEPTVEVVLCSHRESCKBGPVAVRKEEVHLHELFGTDIRCCARNALGR 240
Db 180 DALVCISESPEPIVEVVLCSGESCCKESPAPVKEEVHLHELFGTDIRCCARNELGR 239

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Db 240 ECTRLFTIDLNOTPOTTLPOLFLKVGEPMLIRCKAVHNVHGFGLTWLENKALEEGNYFE 299

QY 301 MSTYSTNRTMIRILLAPVSSVGRNDTGYTCCSSSKHPSQSALVTILEKGFNATSSOEY 360
Db 300 MSTYSTNRTMIRILFAFVSSVANRDTGYTCCSSSKHPSQSALVTIVGKGFNATNSDEY 359

QY 361 EIDPYKFCFSVRFAKAYPRIRCTWIFSOASFPCEORGLDEGYISIKFCDHKNKPGYIFY 420
Db 360 EIDPYEFCFSVRFAKAYPOIRCTWTSRKFPPCEQKGLDGYISIKFCNKKHQPGYIFH 419

QY 421 AENDDAQFTKXFTLNIRKPKQVLANASASQSSDGYPLPSMTWKKCSKSPNCTBEIP 480
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QY 481 EGVNKKANRKGQWVSSSTLANNSEAGKLLVKCCAYNSMGTSCETIFLNSCPGPPFIQ 540
Db 480 EGVNKRANRKGQWSSSTLANNSEAKGLVKCCAYNSLGTSCETILNLSGPPFFFIQ 539

QY 541 DNISFYATIGLCPLFIVLVILVICHYKKQFYESQLOMIQVTPGLDNEYFYVDPRDYEY 600
Db 540 DNISFYATIGVCLLFIVLVLLICHYKKQFYESQLOMVQVGTSSDNEYFYVDPRYEY 599

QY 601 DLKWEPPRENLEFGKVLGSGAFGMVMTATYIGISKTGVSIOVAVMKLKEKADSCEKALM 660
Db 600 DLKWEPPRENLEFGKVLGSGAFGMVNATYIGISKTGVSIOVAVMKLKEKADSSEREALM 659

QY 661 SELKMTLGHNDINVLGACTLSGPVLIPEYCCYGDLLNLYLSKREKPHRTWTIEFK 720
Db 660 SELKMTQLGSHENIVNLGACTLSGPIYLIPEYCCYGDLLNLYLSKREKPHRTWTIEFK 719

QY 721 EHNFSYPTFOAHNSNMPGSRVQLHPDLSGFGNNGSIHSEDEIYEYENOKRLABEEE 780
Db 720 EHNFSYPTFOAHNSNMPGSRVQIHPDSQISGLHNSFHSDEIYEYENOKEL--EEE 777

QY 781 EDNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
Db 778 EDNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIM 837

QY 841 SDSYVVRGNARLPVKWMAPESLPEGITYTKSDYWSYGILLWEIFSLGVNPGIPVDAN 900
Db 838 SDSYVVRGNARLPVKWMAPESLPEGITYTKSDYWSYGILLWEIFSLGVNPGIPVDAN 897

QY 901 FYKLIQSGFKWQEPFYATEGIFYVMQSCWAFDSKRSPNLTSLFLGCOLAEAEAC--- 957
Db 898 FYKLIQSGFKWQEPFYATEEIIYIMQSCWAFDSKRSPNLTSLFLGCOLADAEANMYQN 957

QY 958 ----IRTSIHLPKQAAPQORG-GLRAQSPQOVK 986
Db 958 VDRGVSECPHYQNRPRFSPREMDLGLLSPOAQVE 991

RESULT 4
US-09-872-136-4
; Sequence 4, Application US/09872136
; Patent No. US20020119545A1
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GENERAL INFORMATION:
APPLICANT: Lemischka, Ibor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/872,136
FILING DATE: 01-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/208,786
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/021,324
FILING DATE: <Unknown>
APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
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APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
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APPLICATION NUMBER: US 07/813,593
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FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-872-136-4
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Query Match 84.1%; Score 4429.5; DB 10; Length 993;
Best Local Similarity 84.1%; Pred. No. 2.3e-297;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

QY 1 MRALAQRSDRRLLLVLLVLSVMILETVTNQDLPVTKCVLI SHENNGSSAGKPSYRMVRGS 60
Db 1 MPALA-RDAGTVPLLVVFSAMIFCTITNQDLPVTKCVLIHKNNDSSVGKSSYPMVSES 59

QY 61 PEDLOCTPRQSGTGYEAATVEAAGSITLQVLAATPGDLSCLWPKHSSLCGQPHFD 120
Db 60 PEDLGALRPOSSGTGYEAAAVEVDVSASITLQVLDVDPAGNISCLWPKHSSLCGQPHFD 119

QY 121 LQNRGIVSMALNVETQAGEYLLHIOSEANVTYVLTNNVDTOLVLRPRPKMENQ 180
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Db 120 LONRGVSVMLKNTETQAGSYLLFIOSEATNYTLFTVSRNTLLYLRPPYRKMENQ 179
Qy 181 DALLCISEGPEPTVWVLCSSHRESCKEGPAVVRKEEVLHFGTDIRCCARNALGR 240
Db 180 DALVCISEGPEPIVWVLCDSQESCKEESPAVVRKEEVLHFGTDIRCCARNALGR 239
Qy 241 ECTKLFTIDLNAQOSTLPQLFKVGBPLWIRCKAIHVNHGFGLTWELEKALEBGSYFE 300
Db 240 ECTRLFTIDLNOTPTTLPLFKVGBPLWIRCKAVHNVHGFGLTWELNKALEBGNFE 299
Qy 301 MSTYSTNRTMIRILAFVSSVGRNDTGYTCTSSKHPQSALVILEKGFNATSSQBEY 360
Db 300 MSTYSTNRTMIRILFAVSSVARNDTGYTCTSSKHPQSALVTIVGKGFNATSSSDY 359
Qy 361 EIDYEFKFCFSVRKAPRICTWIFSOASPPCEORGLEDGYSISKFCDHKNKPGCEIFY 420
Db 360 EIDYEFKFCFSVRKAPRICTWIFSKPCBOKGJNDGYSISKFCNHRKHPGCEIFY 419
Qy 421 AENDDAOFTKMTFLNIRKPOVLANASASQASCSGSDGYPLFSWTWKCDKSPNCTEIP 480
Db 420 AENDDAOFTKMTFLNIRKPOVLAEASASQASCSGSDGYPLFSWTWKCDKSPNCTEIT 479
Qy 481 EGVWVKANRKFVGOVSSSTLNSEAGKLLVCCAYNSMGTSCTETPLNSPGPPFIQ 540
Db 480 EGVWVKANRKFVGOVSSSTLNSEATKGFVLKCCAYNSLGTSCETILLNSPGPPFIQ 539
Qy 541 DNISFYATIGCLPFIIVLVI CHYKQKOPRYESOLOMIQVTPGLDNEYFVDPREY 600
Db 540 DNISFYATIGVCLLFIIVLTLI CHYKQKOPRYESOLOMQVQTGSSDNEYFYVDPREY 599
Qy 601 DLKWEFPRENLEFGKVLGSGAFGRVMAATAYGISKTGYSIOAVKMLKEKADSCKEALM 660
Db 600 DLKWEFPRENLEFGKVLGSGAFGRVMAATAYGISKTGYSIOAVKMLKEKADSSREALM 659
Qy 661 SELKMTHLGHHDNIVNLGACTLSGPVLIIFYCCYGBLLNVLDRSKREKHTWTETPK 720
Db 660 SELKMTQLGSHENIVNLGACTLSGPVLIIFYCCYGBLLNVLDRSKREKHTWTETPK 719
Qy 721 EHNFSYPTFOAHNSNMPGSGREVQLHPDLQSLGFGNSHSEDEIEYENOKRLAEE 780
Db 720 EHNFSYPTFOHNSNMPGSGREVQIHPDQIOLGFGNSHSEDEIEYENOKRLAEE 777
Qy 781 EDNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
Db 778 EDNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIM 837
Qy 841 SDSYVVRGNARLPVKWMAPESLFPGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Db 838 SDSNVVRGNARLPVKWMAPESLFPGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 897
Qy 901 FYKLIOSGPKMEOPYATGEGYFVMSQWAPDSRKRSPFNLTSLGCOLAEEAEAC--- 957
Db 898 FYKLIQNGFRKQDPYATEEYIYIMOSQWAFDSRKRSPFNLTSLGCOLAEEAEAMQYON 957
Qy 958 ---IRTSIHLPKQAAPOORG-GLRAQSPQROVK 986
Db 958 VDRGVECPHYTQNRPPSRREMDLGLLSPQAQVE 991
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RESULT 5

US-10-192-867-2

; Sequence 2, Application US/10192867

; Publication No. US2003008466A1

; GENERAL INFORMATION:

; APPLICANT: BLUME-JENSEN, Peter

; APPLICANT: HUNTER, Tony

; TITLE OF INVENTION: SYSTEM AND METHOD FOR CONTROLLING MALE FERTILITY

; FILE REFERENCE: SALKINS.002C1

; CURRENT APPLICATION NUMBER: US/10/192,867

; CURRENT FILING DATE: 2002-07-08

; PRIOR APPLICATION NUMBER: US 60/175,625

; 2000-01-11

; PRIOR APPLICATION NUMBER: PCT/US01/00573

; 2001-01-08

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 975

; TYPE: PRT

; ORGANISM: MUS MUSCULUS

US-10-192-867-2

Query Match 23.2%; Score 1223; DB 9; Length 975;

Best Local Similarity 32.1%; Pred. No. 4.3e-76;

Matches 324; Conservative 172; Mismatches 331; Indels 182; Gaps 39;

Qy 36 CVLISHENNGSAGKPPSSYRMVRGSPEDLQCTPRQSEGTVVEAATVEVAESGSLTLQVQ 95

Db 12 CVLLVLLRGQTATPSA-----SPGSPSPSHPAQSELIVEAGD-TL--- 54

Qy 96 LATPGDLSCL-----WVFKHSSLCQPHF-----DLQNRGIVSMAILNVTTQAGEYLL 144

Db 55 -----SLTCIDPDFVRWTFK-----TYFNMVKNKNEWIOEKA-----EATRTGTTC 98

Qy 145 HIQSERANYTVLFTVVRD-TQLYVLRPPYPRKMNQDALL-----CIS 187

Db 99 ---SNSNGLTSSYYVVRDPAKFLVGLPLFGK-EDSDALVRCPLTDPQVSNYSLIECDG 154

Qy 188 EG-----VPEPTVWVLCSSHRESCKEEGPAVVRKEEVLHFGTDIRCCARNALGR 240

Db 155 KSLPTDILTFVNP-----KAGITIKNVKRAYH-----RLCVRCAOR 191

Qy 241 ECTKL-----FTIDLNOA-----POSTLPQ---FLKVGEPILWIRCKAIHVNHGFGLTW--- 286

Db 192 DGTWLHSDKFTLKVREAIKAIIPVSVSPETSHLLKKGDTFTVVCTIKDVSTSVNMLKKN 251

Qy 287 -----ELEKALBEGSYFEMSTYSTNRTMIRILAFVSSVGRNDTGYTCTSSKHPQ 339

Db 252 PQQHIAQVKNHSHRGDF-----NYERQETLT-----ISSARVDDSGVFCMYANNFTGS 301

Qy 340 SALVT---ILEKGFNATS-SOEVEIDPYEKFCFVRPKAYPR-IRCTWIFSOASFPCE 394

Db 302 ANVTTLKVKVEGFNIPVKNVTVFVDGENVDLVEYEAYPEHQHQQWIYNRT--SA 359

Qy 395 ORGLE---DGYSISKFCDH-----KNKPGEIFYAEENDDAQFTKMTFLNIRKPKQVL 443

Db 360 NKGKDYVRSNDKSNIRYVNLRLTLKGTGEGTYTFLVSNSDASASVTENVVNTKPEIL 419

Qy 444 A--NASASQASCSGYPPLPSWTWKCDKSPNCTEEL-PEGWVKANRKFVGOVSS 500

Db 420 TYDRLLINGMLQCVARGPEPTIDWYFCTGAEQRCITTPSPVDVQVQNVSVSPGKLWVS 479

Qy 501 TLNMSEAGKLLVKKCCAYNSMGTSCTETFLNSPGPPFPFIQDNI SFVATIGLCLPFIIV--- 557

Db 480 SIDSSVFRHNGTVECKASNDVGKS--SAFFN----FAKBEQIOAHTLFTPLIGFVVAAG 533

Qy 558 ---VLIVLICHYKQKOPRYESOLOMI-QVTGPLDNEYFYVDPRDYEDLKWFFPRENLEF 613

Db 534 AMGIIVMLVLYTKYLOKPMYEVQWKVVEING---NNYVVIDTQLPYDHKWEFPNRLSF 590

Qy 614 GKVLGSGAFGRVMNATAYGISKTGYSIOAVKMLKEKADSCKEALMSLKMVTHLGHHD 673

Db 591 GKTGLGAGAFGKVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSLKVLSYLGNIH 650

Qy 674 NIVNLGACTLSGPVLIIFYCCYGBLLNVLDRSKREKPF-----HRTWTEIKHEINFSY 727

Db 651 NIVNLGACTVGGPTLVITEYCCYGBLLNVLDRSKRSDSFIFSKQBEQAEAAALYNLHSTE 710

Qy 728 PTFQAHNSNM---PGSREVOLHPPLDOLSGFGNSHSEDEIEYENOKRLAEEBEDLN 784

Db 711 PSCDS-SNEYMDMKGVSYV-VPTKTDK-----RSARIDSIVERTVDTVAIHEDDELD 763

Qy 785 VLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDILSDSS 844

Db 764 L---DDLLSFSYQVAKAMAFASKNCIHRDLAARNILLTHGRITKICDFGLARDIRDSN 820

QY 845 YVGRNARLPVKWAPSLPBGIVTIKSDVMSYGILLWEIFSLGWNYPGIPVDANFYKL 904
Db 821 YVWGNARLPVKWAPSLPBGIVTIKSDVMSYGILLWEIFSLGWNYPGIPVDANFYKL 880
QY 905 IQSGFKMEQPPYATEGIFVFMQSWAFDSRKRPFNLTSLFGLQLABA 953
Db 881 IKGFRMVSPEHAPAEYDVNMTCDADPLKPTFKQVQVQVQVQVQVQVQVQV 929
RESULT 6
US-09-944-807-10
; Sequence 10, Application US/09944807
; Patent No. US20020119494A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082.00n
; CURRENT APPLICATION NUMBER: US/09/944, 807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-944-807-10

Query Match 23.2%; Score 1221.5; DB 10; Length 972;
Best Local Similarity 32.5%; Pred. No. 5.4e-76;
Matches 330; Conservative 152; Mismatches 331; Indels 201; Gaps 33;
QY 76 VYEAATVEAESGSIITLQVQATPGDLSCLWVFKHSSLGCPHFDLQNRGIVSMAIL--- 132
Db 22 VIEPSVELVVKPAT--VTLRCVNGSVENDGPPS-----PHTLYSDG--SSSILSTN 72
QY 133 NVETQAGEYLLHQSBRANTVTLTVNVRTQTLVLRPPY-----FRKMNQDALL-C 185
Db 73 NATQNTGTGRCTEPCGPGPLGSSAHLVYKDP-----ARPMNVLAQEVVPEQDQALLPC 127
QY 186 ISEGVPEPTVEWLCSHRECKEKGAVVRKEK-----VLHE--LF 226
Db 128 L---LTDPLV-----BAGVSLVRGRPLMRHTNYSFSPWHGTHIRAKFIQ 171
QY 227 GTDIRCARNALGRECTKLTIDLNOAPQSTLP-----QLFLKVGEPFLWIRCKAI 276
Db 172 SDYQCSALMG-GR---KWSISIRLKVQKVPFPALTLPALVIRGEAAQIVCSAS 227
QY 277 HVNKGFLTWELDEKALEEGSYFEMSTYTNRTWIRILLAFVSVGRNDTGYTTCSSS-- 334
Db 228 SDVNVDFVFLQHNNTKL---AIPQSDPHNNRYQ-KVLTNLNDQVDFQHAGNYSVASNV 283
QY 335 ---KHPQSALVTILEKGFNATSSQE-EYEDPYEKECFVRKAYPRIR-CTWIFSOAS 390
Db 284 QGKH-STSMFRVVEYSAIYLNLSSEQNLIQEVTVGEGNLKVMVEAYPCLOGFNWY---- 338
QY 391 PFCBQGLDGYSTSKFCDHKNP-----GEVIFYAEN 423
Db 339 -----LQPSDHPQEPKLANATTKTYRHTFTLSLPLKPSAGRSFLARN 385
QY 424 DDAQFTKMTNIRKKPOV-----LANASQASCSGSDGYPLPSWTWKKCKSDKPNCTEE 478
Db 386 PGNWALTFELTLVPPRVSIVTWFINGSGT-LLCAASGYPPQNVVTLQCSGHTDRDEA 444
QY 479 LPEGVWN-----KKNRKYVQGWVSSSTLNMSEAGKLLVKKCANSMGTSCTETFLNSPG 534
Db 445 QVLQVDDDPYVELVSEPPFHKVTYQSLTLVETLEHNTYECRAHNSVSGSGSWAFIPISAG 504
QY 535 PFPFIQDNISFYATIGLC---LPTIVVILVLI CHYKKQPRYESQLQMIQVGTGLDNEYF 591

Db 505 AHTHPBOBFLTPVWVACMSIMALLLLLLLLLLLYKKQPKYQVRWKIIE--SYEGNSYT 562
QY 592 YVDFRDYEDLKWEPRENLEFGVGLSGAGFGRVWMTATYGISKTGVSIOAVAKMLKEKA 651
Db 563 FIDFTQLPYNEKWEFFPRNNLQFGKTLGAGAPKVVVEATAFGLGKEDAVLKVAVKMLKSTA 622
QY 652 DSCKEALMSLKMTHLGHHDNIWNLGACTLSGPPVLIFFEYCCYGDLLNLYLSKRKRF 711
Db 623 HADEKEALMSLKMTHLGHHDNIWNLGACTLSGPPVLIFFEYCCYGDLLNLYLSKRKRF 680
QY 712 HRTWTEIFKEHNFSSYPTFOAHNSNMPGSRREVOLHPLDLSGFGNSIHSDE----- 766
Db 681 -----AMLGP-----SLSPQDPEGGVDYKNIHLEKKYVRD 712
QY 767 -----IYENQKELAE--EEDLNVLTFEDLLCFAYQVAKGMELEFK 808
Db 713 SGFSSQGVDTYVEMRPVSTSNDSFSEODLDKEDGRPLEURDLHLFSQVAGMAFLASK 772
QY 809 SCVHRDLAARNVLTGHKVKIKCDFGLARDILSDSSVYVGRNARLPVKWMAPESEFEGY 868
Db 773 NCIRDVAAARNVLTGHKVKIKCDFGLARDILSDSSVYVGRNARLPVKWMAPESEFEGY 832
QY 869 TIKSDVMSYGILLWEIFSLGWNYPGIPVDANFYKLQSGFKMEQPPYATEGIFVFMQSC 928
Db 833 TVQSDVMSYGILLWEIFSLGWNYPGIPVDANFYKLQSGFKMEQPPYATEGIFVFMQSC 892
QY 929 WAFDSRKRPFNLTSLFGLQLABAEBACITSLHLPKQAPQORGLRAQSPQ 982
Db 893 WALEPHTHRTFQIQCSFL--OEQAQEDRRERDYNLFPSS---RSGGSGSSSE 941

RESULT 7
US-10-099-895-32
; Sequence 32, Application US/10099895
; Patent No. US20020177166A1
; GENERAL INFORMATION:
; APPLICANT: BERNDT, Michael C
; APPLICANT: STOMSKI, Frank C
; APPLICANT: LOPEZ, Angel F
; APPLICANT: GUTHRIE, Mark A
; TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR
; FILE REFERENCE: 3991/0K379
; CURRENT APPLICATION NUMBER: US/10/099, 895
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/AU00/01118
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 32
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-099-895-32

Query Match 22.7%; Score 1196; DB 9; Length 976;
Best Local Similarity 31.4%; Pred. No. 3.1e-74;
Matches 312; Conservative 172; Mismatches 361; Indels 148; Gaps 32;
QY 36 CVLISHENNGSSAGKPSRYMVRGSPEDLOCTPRRQSGTVYEAATVEAESGSIITLQVQ 95
Db 12 CVLLLLLRVQTSSQPS-----VSPGEPSPSIHPGKSDLIVRVD-EIRLL 57
QY 96 LATPGDLSCLWVFKHSSLGCPHFDLQNRGIVSMAILNVETQAGEYLLHQSBRANTV 155
Db 58 CTDPGFVK--WTFE---ILDETENKQNEWITEKA-----EATNTKYCTCTNKHGSLNSIY 108
QY 156 LFTVNVVD--TOLYVLRPRYFVKMENQDALLCI-----SEG-----VPE 192
Db 109 VF---VRDPAKFLVDRSLYKEDNDTLVRCLPTDPEVTNYSKGCQCKPLPKDLRFIPD 165
QY 193 PTVEWVLCSSHRE-----SCKEGPAVVRKEKVLHLEFGTDIRCCARNALGRECTK 244

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Db 166 PKAGIMIKSVKRAVHRLCHLHCSVDQEG-----KSVLSEKFIKVRPAFK-----A 210
Qy 245 LFTIDLNAQPOSTLPQLFLKVGEPILWIRCKAIHNVHGFGLTWELEDK--ALEE----- 295
Db 211 VPVVSUSKA-----SYLLREGEBEFTVCTIKDVSSSVYSTWKRENSOTKLOEKYNSWHH 264
Qy 296 GSYFEMSTYSTNRIMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILE---KGFIN 352
Db 265 GDF-----NYERQATLT-----ISSARVNDSGVFCYANNTFGSANVTITLLEVVVDKGFIN 314
Qy 353 A-TSSQBEYEIDPYEKFCSVRFKAYPR-IRCTWIFSQASE--PCEQRGLEDDGYISKFC 408
Db 315 IFPMINTTVFVNDGENVDLIVEYEAFFPKPEHQOQIYMRFTTDKWDYEPKSENEINRIV 374
Qy 409 DHKN-----KPGEYIFYAENDDAQFTKMFNLIRKPKQVLA--NASASQASCSDDGYP 459
Db 375 SELHLTRLKGTGGTYTFLVNSDVNAIAFNVYVNTKPEILTYDRLVNGMLQCVAAAGFP 434
Qy 460 LPSWTWKCSKSPNCTEEI-PEGVWKKANKRVQGWSSSTLNMSEAGKGLLVKCCAY 518
Db 435 EPTIDWYFCPTQRCSCASVLPVDVQTLNNSGPPFGKLVVQSSIDSSAFKHNGTVECKAY 494
Qy 519 NSMGTSCETIFLNSPGPPFTQDN-----ISFYATIGLCLPFIVLVILIC 564
Db 495 NDVGKT---SAYFN-----FAFGNNKEQIHPHTLFTPLLIGFVIVAGM---MCIIVMLIT 544
Qy 565 HKYKQFRIESQLOMI-QVTGPLDNEYFYVDPRDYEYDLKWEFFPRENLEFGKVLGSGAFG 623
Db 545 YKYLQKPMYEQWKVVEING---NNYVYIDPTQLPYDHKWEFFPRNRLSFGKTLGAGAFG 601
Qy 624 RVMNATAYGISKTGVSIOAVVMKKEKADSCKEKALMSELKMWTHLGHHDNIVNLGACT 683
Db 602 KVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELKVLVSLGNHNMIVNLGACT 661
Qy 684 LSGPVYLIFCYCCYGDLLNLYLRSREKPHRTWTETFEKHNFSSYPTFOAHNSNMPGSR 743
Db 662 IGGTFLVITEYCCYGDLLNLYLRRKRDSPICSKQEDHAAALYKNLLHSSKSSCSDSTNEY 721
Qy 744 VOLHPPDLQOL---SGFNNGSIHSEDEIEYENQKRLAEEDLNLVLTPEDLLCFAYQVAK 800
Db 722 MDMPKGVSVVPTKADKERSVRIGSYIERDVTPTAIMEDELALDL---EDLLSFSYQVAK 778
Qy 801 GMEFLEPKSCVHRDLAARNLVTHGKVKIKCDFGLARDILSDSSVYVRGNARLPVKWMAP 860
Db 779 GMAFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIKNDNSYVVKGNARLPVKWMAP 838
Qy 861 ESLPEGIYTIKSDVMSYGIILLWEIFSLGVNYPGIPVDANFYKLIQSGFKMEQPPYATEG 920
Db 839 ESIFNCVYTFESDVMSYGIUWELFSLGSSYPGMPVDKSFYKMIKEGFRMLSPHAPAE 898
Qy 921 IYFVWQSCWAFDSRKRPSFNLTSFLGQLAE 953
Db 899 MYDIMKTCDADPLKRPFTFKQIVOLIEKQISES 931

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RESULT 8

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US-10-192-867-4
; Sequence 4, Application US/10192867
; Publication No. US2003008446A1
; GENERAL INFORMATION:
; APPLICANT: BLUME-JENSEN, Peter
; TITLE OF INVENTION: SYSTEM AND METHOD FOR CONTROLLING MALE FERTILITY
; FILE REFERENCE: SALKINS.002C1
; CURRENT APPLICATION NUMBER: US/10/192,867
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: US 60/175,625
; 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US01/00573
; 2001-01-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 4

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; LENGTH: 976
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-192-867-4

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Query Match 22.7%; Score 1196; DB 9; Length 976;

Best Local Similarity 31.4%; Pred. No. 3.1e-74;
Matches 312; Conservative 172; Mismatches 361; Indels 148; Gaps 32;

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Qy 36 CVLISHENNGSAGKPSYRMVGRSGPEDLQCTPRQSRGTVEAATVEVAESGSIITLQVQ 95
Db 12 CVLLLLLRVQTSSQPS-----VSPGEPSPSHPGKSDLIIVRGD-EIRLL 57
Qy 96 LATPGLSCLVFKHSLGCGPHDLQNRGIVSMAILNVTTQAGEYLHIIOSERANYTV 155
Db 58 CTDPGFVK--WTFE---ILDENENKQEWITEKA---EATNTGKYCTCNKHGLSNSIY 108
Qy 156 LFTVNVVRD-TQLYVLRPRYFRKMNQDALLCI-----SEG-----VPE 192
Db 109 VF---VRDPAKFLVDRSLYKEDNDTLVRCPLTDPEVTNYSKGCQKPLPKDLRFIPD 165
Qy 193 PTVEVLWCSSHRE-----SCKEGPAVVRKEBKVHLHELFGTDIRCCARNALGRECTK 244
Db 166 PKAGIMIKSVKRAVHRLCHLHCSVDQEG-----KSVLSEKFIKVRPAFK-----A 210
Qy 245 LFTIDLNAQPOSTLPQLFLKVGEPILWIRCKAIHNVHGFGLTWELEDK--ALEE----- 295
Db 211 VPVVSUSKA-----SYLLREGEBEFTVCTIKDVSSSVYSTWKRENSOTKLOEKYNSWHH 264
Qy 296 GSYFEMSTYSTNRIMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILE---KGFIN 352
Db 265 GDF-----NYERQATLT-----ISSARVNDSGVFCYANNTFGSANVTITLLEVVVDKGFIN 314
Qy 353 A-TSSQBEYEIDPYEKFCSVRFKAYPR-IRCTWIFSQASE--PCEQRGLEDDGYISKFC 408
Db 315 IFPMINTTVFVNDGENVDLIVEYEAFFPKPEHQOQIYMRFTTDKWDYEPKSENEINRIV 374
Qy 409 DHKN-----KPGEYIFYAENDDAQFTKMFNLIRKPKQVLA--NASASQASCSDDGYP 459
Db 375 SELHLTRLKGTGGTYTFLVNSDVNAIAFNVYVNTKPEILTYDRLVNGMLQCVAAAGFP 434
Qy 460 LPSWTWKCSKSPNCTEEI-PEGVWKKANKRVQGWSSSTLNMSEAGKGLLVKCCAY 518
Db 435 EPTIDWYFCPTQRCSCASVLPVDVQTLNNSGPPFGKLVVQSSIDSSAFKHNGTVECKAY 494
Qy 519 NSMGTSCETIFLNSPGPPFTQDN-----ISFYATIGLCLPFIVLVILIC 564
Db 495 NDVGKT---SAYFN-----FAFGNNKEQIHPHTLFTPLLIGFVIVAGM---MCIIVMLIT 544
Qy 565 HKYKQFRIESQLOMI-QVTGPLDNEYFYVDPRDYEYDLKWEFFPRENLEFGKVLGSGAFG 623
Db 545 YKYLQKPMYEQWKVVEING---NNYVYIDPTQLPYDHKWEFFPRNRLSFGKTLGAGAFG 601
Qy 624 RVMNATAYGISKTGVSIOAVVMKKEKADSCKEKALMSELKMWTHLGHHDNIVNLGACT 683
Db 602 KVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELKVLVSLGNHNMIVNLGACT 661
Qy 684 LSGPVYLIFCYCCYGDLLNLYLRSREKPHRTWTETFEKHNFSSYPTFOAHNSNMPGSR 743
Db 662 IGGTFLVITEYCCYGDLLNLYLRRKRDSPICSKQEDHAAALYKNLLHSSKSSCSDSTNEY 721
Qy 744 VOLHPPDLQOL---SGFNNGSIHSEDEIEYENQKRLAEEDLNLVLTPEDLLCFAYQVAK 800
Db 722 MDMPKGVSVVPTKADKERSVRIGSYIERDVTPTAIMEDELALDL---EDLLSFSYQVAK 778
Qy 801 GMEFLEPKSCVHRDLAARNLVTHGKVKIKCDFGLARDILSDSSVYVRGNARLPVKWMAP 860
Db 779 GMAFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIKNDNSYVVKGNARLPVKWMAP 838
Qy 861 ESLPEGIYTIKSDVMSYGIILLWEIFSLGVNYPGIPVDANFYKLIQSGFKMEQPPYATEG 920
Db 839 ESIFNCVYTFESDVMSYGIUWELFSLGSSYPGMPVDKSFYKMIKEGFRMLSPHAPAE 898

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QY 921 IYFMOSWAFDSKRPSPFNLSFLGCOLAEA 953
Db 899 MYDMKTCWDADPLKPTFKQIVQLIEKQISES 931

RESULT 9

US-09-961-403-4
; Sequence 4, Application US/09961403
; Publication No. US20030077589A1
; GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLT
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTTI, SIMONE
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: SCH-1789
; CURRENT APPLICATION NUMBER: US/09/961,403
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-403-4

Query Match 21.9%; Score 1152.5; DB 9; Length 1088;
Best Local Similarity 32.1%; Pred. No. 3.6e-71;
Matches 314; Conservative 154; Mismatches 320; Indels 189; Gaps 33;

QY 94 VOLATPGDLSCLWVFKHSSLCGCPHFDLQNRGIVSMALNTVETQAGEY--LLHIQERA 151
Db 39 VOLNSSFSLR--FGSEVSWQ--YPMSEESSDVEIRN--EENNSGLFVTVLEVSSASA 92
QY 152 NYTVLFTVNVDRDQLYVLRPFYRKMNODALLCISEG-----VPEPTV-----EW 197
Db 93 AHTGLTYCYNNHTQ-----TEENE-----LEGRHIYVVPDPAFVPLGMDTY 136
QY 198 VLCSHRES-----CK---EEGPAVVRKEEVL-----HFLFGTDIRCCARNALGR 240
Db 137 LVIVEDDSDAIIPCRTTDPFTVTLHNSGVVPSYDSRQGFNGFTTVPVCEATVKGK 196
QY 241 ECTKLFIDINQAQPOSTLPQLF-----KVGBPLWTRCKAIHNVHNGFLTW-----E 287
Db 197 ---KFQIPFNVAALKATSELDLEMEALKTVYKSGETIVVTC-AVFNNVVDLQWTPGE 252
QY 288 LEDKALEEGSYFEMSTYSTNRMTIR-----ILLAFVSSVGR-----NDTGYTCSSK-- 335
Db 253 VKGKI-----TMLBEIKVPSIKLVTLTVPEATVKOSGDYECARQATR 297
QY 336 --HPSQALVTILEKGF--INATSSQBEYEIDPYEKFCSVRFKAYPRIRCTWIFSOASF 391
Db 298 EVKEMKVTISVHEKGFIEIKPTSOLE-AVNLHVKHFVVEVRAYPPRISLWLNLT 356
QY 392 PCEORGLDGYISKFCO-----HKNK-----PGYIIFYAENDDAQFTMFTLN 435
Db 357 -----IENLTEITTDVEKIQEIRYRSKLIRAKEEDSGHYTTVAQNEADAVKSYTFELL 410
QY 436 IRKXPQVL-----ANASASQACSSDGYPLPSWTWKCKSDKSPNCTEETIEPEGVWKK 488
Db 411 TQVPSSTILDVDDHHGGTGGTACTAGTLPDIEMWICKD-IKCKNNETS-----WTILA 466
QY 489 NRKVFQGWSS-----STLNMSEAGKGLLVKCCAVNSMGTSCETIFLNSPG 534
Db 467 NN-----VSMIITEHSRDRSTVEGRVTFPAKVETIAVRCLAKNLLGAENRELKIVA-- 518
QY 535 PFPPIQDNISFYATIGLCPFIVLVILCHIKYKQKPEYSQLOMQVOTGPDLDNEYFYVD 594
Db 519 --PTLRSELTVAAVLVLLVIVILSLIVLVVWVKQKPYEIRWRVIESISPDGHEYIYVD 576

QY 595 FRDYEDLKWEFFRENLEFGKVLGSGAFGRVMNATAYGISKTVSIOAVVMLEKADSC 654
Db 577 PMQLPYDSRWEEFRDGLVLRGVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSS 636
QY 655 EKEALMSELQWTHLGHHDNIVNLLGACTLSGPPYLIFFECCYCCGDLNLYLSRKEKF--- 711
Db 637 EKOALMSELKIMTHLGHPLNIVNLLGACTKSGPIYIITEYCFYGDLYNLYLHKNDSDFLSH 696
QY 712 -----HRTWTEIFKBHNFSSYPTFOAHNSNSMP--GSREVQLHPP 749
Db 697 HPEKPKKELDIFGLNPADESTRSVILSPENNGDYMMDKQADTTQYVPMLEKVESKYS 756
QY 750 LDQLSGFNGNSIHSEDEIYEYENQKRLAEEDDEDLNLTFFEDLLCFAYQVAKGMEFLFKFS 809
Db 757 IQRSLYDRPASYYKKKMLDSEVKNLLSDNSEGLTLL--DLSFTTYQVARGMEFLASKN 813
QY 810 CVHRDLAARNVLVTHGKVKICDFGLARDILSDSSYVVRGNARLPVKWMAPESEIFEGIYT 869
Db 814 CVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYSYVSKGSTFLPVKWMAPESEIFDNLYT 873
QY 870 IKSDVWSYGIILLWEIFSLGIVNYPGIPVDANFYKLIOSGFKMEOPFYATEGIYFVMOQSCW 929
Db 874 TLDVWSYGIILLWEIFSLGTPYGMVMDSTFYNKISGRMARPDHATSEVYIIMVKCW 933
QY 930 AFDSCRKPSFPNLTSL 946
Db 934 NSEPEKPSFVHLSEIV 950

RESULT 10

US-09-769-987-2
; Sequence 2, Application US/09769987
; Patent No. US20020055129A1
; GENERAL INFORMATION:
; APPLICANT: Matsui, Toshimitsu
; APPLICANT: Aaronson, Stuart A.
; APPLICANT: Pierce, Jacalyn H.
; TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor
; FILE REFERENCE: 14014, 026602
; CURRENT APPLICATION NUMBER: US/09/769,987
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 08/460,656
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: US 08/439,095
; PRIOR FILING DATE: 1995-05-11
; PRIOR APPLICATION NUMBER: US 07/915,884
; PRIOR FILING DATE: 1992-07-20
; PRIOR APPLICATION NUMBER: US 07/308,282
; PRIOR FILING DATE: 1989-02-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. US20020055129A1e =
; OTHER INFORMATION: synthetic construct
US-09-769-987-2

Query Match 21.9%; Score 1152.5; DB 10; Length 1089;
Best Local Similarity 32.1%; Pred. No. 3.6e-71;
Matches 314; Conservative 154; Mismatches 320; Indels 189; Gaps 33;
QY 94 VOLATPGDLSCLWVFKHSSLCGCPHFDLQNRGIVSMALNTVETQAGEY--LLHIQESRA 151
Db 39 VOLNSSFSLR--FGSEVSWQ--YPMSEESSDVEIRN--EENNSGLFVTVLEVSSASA 92
QY 152 NYTVLFTVNVDRDQLYVLRPFYRKMNODALLCISEG-----VPEPTV-----EW 197
Db 93 AHTGLTYCYNNHTQ-----TEENE-----LEGRHIYVVPDPAFVPLGMDTY 136
QY 198 VLCSHRES-----CK---EEGPAVVRKEEVL-----HFLFGTDIRCCARNALGR 240

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Db 137 LVIVEDDDSAIIPCKTTDPETPVTLHNSGVVPASYSRQGFNGTFTVGPYICEATVKGK 196
Qy 241 ECTKLFTIDLNAQAPOSTLPQLFL-----KUGEPLWIRCKAIHVNHGFLTW---E 287
Db 197 ---KFQITPFNVYALKATSELDLEALKTVYKSETIVTTC-AVFNNVVDLQWTYGE 252
Qy 288 LEDKALEEGSYFEMSTYSTNRTMIR-----ILLAFVSVGR---NDTGYTCSKK--- 335
Db 253 VKGKI-----TMLKEIKVPSIKLVYTLTVPEATVKDGDYECARQATR 297
Qy 336 --HFSQSALVTILEKGF--INATSSOEYEIDPYEKFCSVRFKAYPRIRCTWIFSQASF 391
Db 298 EVKEMKKVTISVHEKGFIEIKPTFSOLE-AVNLHVKHFVVEVRAYPPRISWLKNLTL 356
Qy 392 PCEQGLGDYSGISKPCD-----HKNK-----PGEYIFAENDDAQFTKMTFLN 435
Db 357 -----TENLTETITDVEKIQEIRYSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELL 410
Qy 436 IRKPKQVL-----ANASASQASCSDGYPLPSWTWKCKDKSPNCTEETIEPEGVWNKKA 488
Db 411 TQVPSSILDLVDDHHGSGGTGCTABGTPLPDIEWMICKD-IKKCNNETS---WTILA 466
Qy 489 NRKVPQWVSS-----STLNMSEAGKLLVKCCAYNSMGTSCTETIFLNSPG 534
Db 467 NN-----VSNITTEIHSRDRSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKVA-- 518
Qy 535 PFPTIQDNISFYATIGLCLPFIVLVILVILCHYKQKQRYESOLOMIQVTPGLDNEFYVD 594
Db 519 --PILRSELTVAAAVLVLLVILVILVILVILVILVILVILVILVILVILVILVILV 576
Qy 595 PRDYEYDLKWEFPRENLEFGKVLGSGAFGRVNNATAYGISKTGVSIOQAVXMKLEKADSC 654
Db 577 PMQLPYDSRWEFFPRDGLVLRVLSGAFGVVEGTAYGLSRSQPVMKVAVMKLPTARSS 636
Qy 655 EKEALMSELKMTWHLGHHDNIVNLLGACTLSGPVYLIFEYCYGDLLNLYLSKREKF--- 711
Db 637 EQALMSELKMTWHLGPHLNVNLLGACTKSGPIIITEYCYGDVNVLYLHKNRDSFLSH 696
Qy 712 -----HRTWTEIFKHNFSYPTFOAHSSNMP--GSRVEQLHPP 749
Db 697 HPEKPKKELDIFGLNPADESTRSVIUSFENNMDYMDKQADTQYVPMLEKVEKYSKD 756
Qy 750 LDQLSGFNGNSIHSEDEIEYENQKRLAEEDLNLVTFEDLLCFAYQVAKGMEFLFEPKS 809
Db 757 IORSLYDRPASYYKKKMLDSEVNKLLSDNSEGLTLL---DLLSFTYQVARGMEFLASKN 813
Qy 810 CVHRDLAARNVLTGHKVKVVICDFGLARDILSDSYVVRGNARLPVKWMAPESEFEGYIT 869
Db 814 CVHRDLAARNVLLAQGVKIVKICDFGLARDIMHDSNVYSKGSTFLPLVKWMAPESEFDNLYT 873
Qy 870 IKSDVWSYGILLWEIFSLGVNPPYGPIDANFYKLIQSGFKMEOPFYATEGIYFMQSCW 929
Db 874 TLDVWSYGILLWEIFSLGGTPYGMWVDSTFYNNKISGYRMAKPDHATSEVYEIMVKCW 933
Qy 930 AFDSRKPSFPNLTSLF 946
Db 934 NSRPEKPSFVHLSEIV 950
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RESULT 11

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US-09-919-497-90
; Sequence 90, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
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; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 90

; LENGTH: 1089

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-919-497-90

Query Match 21.9%; Score 1152.5; DB 10; Length 1089;

Best Local Similarity 32.1%; Pred. No. 3.6e-71;

Matches 314; Conservative 154; Mismatches 320; Indels 189; Gaps 33;

Qy 94 VOLATPGDLSCLVKPHSHSLGCPHFIDLQNRGIVSNAILNVTTETQAGEY--LLHIQSERA 151

Db 39 VOLNSSFSLRC---PGESEVSNQ--YPMSEBESSDVEIRN--ENNNSGLFVTVLEVSSASA 92

Qy 152 NYTVLFTVNRDQLYLVLRPPYFRKMNQDALLCISEG-----VPEPTV-----EW 197

Db 93 AHTGLTYCYNNHTQ-----TEENE-----LEGRHIYIYVPPDPDVAFVPLGMTDY 136

Qy 198 VLGSSHRES---CK---EEGPAVVRKEEKL-----HELFGTDIRCCARNALGR 240

Db 137 LVIVEDDDSAIIPCKTTDPETPVTLHNSGVVPASYSRQGFNGTFTVGPYICEATVKGK 196

Qy 241 ECTKLFTIDLNAQAPOSTLPQLFL-----KUGEPLWIRCKAIHVNHGFLTW---E 287

Db 197 ---KFQITPFNVYALKATSELDLEALKTVYKSETIVTTC-AVFNNVVDLQWTYGE 252

Qy 288 LEDKALEEGSYFEMSTYSTNRTMIR-----ILLAFVSVGR---NDTGYTCSKK--- 335

Db 253 VKGKI-----TMLKEIKVPSIKLVYTLTVPEATVKDGDYECARQATR 297

Qy 336 --HFSQSALVTILEKGF--INATSSOEYEIDPYEKFCSVRFKAYPRIRCTWIFSQASF 391

Db 298 EVKEMKKVTISVHEKGFIEIKPTFSOLE-AVNLHVKHFVVEVRAYPPRISWLKNLTL 356

Qy 392 PCEQGLGDYSGISKPCD-----HKNK-----PGEYIFAENDDAQFTKMTFLN 435

Db 357 -----IENLTETITDVEKIQEIRYSKLIIRAKEEDSGHYTIVAQNEDAVKSYTFELL 410

Qy 436 IRKPKQVL-----ANASASQASCSDGYPLPSWTWKCKDKSPNCTEETIEPEGVWNKKA 488

Db 411 TQVPSSILDLVDDHHGSGGTGCTABGTPLPDIEWMICKD-IKKCNNETS---WTILA 466

Qy 489 NRKVPQWVSS-----STLNMSEAGKLLVKCCAYNSMGTSCTETIFLNSPG 534

Db 467 NN-----VSNITTEIHSRDRSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKVA-- 518

Qy 535 PFPTIQDNISFYATIGLCLPFIVLVILVILCHYKQKQRYESOLOMIQVTPGLDNEFYVD 594

Db 519 --PILRSELTVAAAVLVLLVILVILVILVILVILVILVILVILVILVILVILVILV 576

Qy 595 PRDYEYDLKWEFPRENLEFGKVLGSGAFGRVNNATAYGISKTGVSIOQAVXMKLEKADSC 654

Db 577 PMQLPYDSRWEFFPRDGLVLRVLSGAFGVVEGTAYGLSRSQPVMKVAVMKLPTARSS 636

Qy 655 EKEALMSELKMTWHLGHHDNIVNLLGACTLSGPVYLIFEYCYGDLLNLYLSKREKF--- 711

Db 637 EQALMSELKMTWHLGPHLNVNLLGACTKSGPIIITEYCYGDVNVLYLHKNRDSFLSH 696

Qy 712 -----HRTWTEIFKHNFSYPTFOAHSSNMP--GSRVEQLHPP 749

Db 697 HPEKPKKELDIFGLNPADESTRSVIUSFENNMDYMDKQADTQYVPMLEKVEKYSKD 756

Qy 750 LDQLSGFNGNSIHSEDEIEYENQKRLAEEDLNLVTFEDLLCFAYQVAKGMEFLFEPKS 809

Db 757 IORSLYDRPASYYKKKMLDSEVNKLLSDNSEGLTLL---DLLSFTYQVARGMEFLASKN 813

Qy 810 CVHRDLAARNVLTGHKVKVVICDFGLARDILSDSYVVRGNARLPVKWMAPESEFEGYIT 869

Db 814 CVHRDLAARNVLLAQGVKIVKICDFGLARDIMHDSNVYSKGSTFLPLVKWMAPESEFDNLYT 873

Qy 870 IKSDVWSYGILLWEIFSLGVNPPYGPIDANFYKLIQSGFKMEOPFYATEGIYFMQSCW 929

Db 874 TLDVMSYGILLWEIFSLGTPYGMVMDSTFYNNKIKSGYRMKAPDHATSEVVEIMVKCW 933
QY 930 AFDSPKPSFNLTSFL 946
Db 934 NSEPEKPSFYHLSEIV 950
RESULT 12
US-09-866-510-2
; Sequence 2, Application US/09866510
; Patent No. US2002011304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-2
Query Match 21.9%; Score 1152.5; DB 10; Length 1089;
Best Local Similarity 32.1%; Pred No. 3.6e-71;
Matches 314; Conservative 154; Mismatches 320; Indels 189; Gaps 33;
QY 94 VQLATPGDLSCLWFKHSLGCPHFDLQNRGIVSMAILNVTETQAGEY--LLHIQSER 151
Db 39 VQLNSSPFLRC--FGESEVSWQ--YPMSEBESSDVEIRN--EENNSGLFVTVLEVSSASA 92
QY 152 NYVLFTVNRDQTLVLRPRYFRKMNQDALLCISEG-----VPEPTV-----EW 197
Db 93 AHTGLTYCYNNHTQ-----TEENE-----LEGRHYIYVDPDPAFVPLGMDTY 136
QY 198 VLCSSHRES---CK---EEGPAVVRKEEVL-----HELFGTDIRCCARNALGR 240
Db 137 LVIVEDDDSAIIPCKTTPDTPVTLHNSGVVPAASYDRQGFNGTFTVGPVCEATVKGK 196
QY 241 ECTKLFTDLNQAQOSTLPQLFL-----KVGELMIRCKAIHNVHGFGLTW-----E 287
Db 197 ---KFQTFPNNYALKATSELDLEMEALKTVYKSGETIVVTC-AVFNNVVDLQWTPGE 252
QY 288 LEDKALEBSYFEMSTYNTNTRIR-----ILLAFVSVGR---NDGYTCSSK--- 335
Db 253 VKKGI-----TMLBEIKVPSIKLYTLTVPEATVKSDGYDECAARQATR 297
QY 336 --HPSQSALVTILEKGF--INATSSQEEYEDPYEKFCSVRFKAYPRIRCTWIFSQASF 391
Db 298 EVKEMKVTISVHEKGFTEIKFTFSQLE-AVNLHEVKHFVVEVRAYPPIRISWLKNLTL 356
QY 392 PCEQGLDGYSISKFCF-----HNK-----PGEYIFYAENDDAQFTKMTLN 435
Db 357 -----IENLTETTDVEKIQEIRYRSKLLIRAKEEDSGHYTIVAQNEADAVKSYTFELL 410
QY 436 IRKKQVIL-----ANASASQSCSDGYPLPSWTWKCKSDKSNCTEETPEGVWNKA 488
Db 411 TQVPSISLDLVDHHRGSGGTVRCTAEGTPLPDETWEMICKD-INKKCNETS---WTLILA 466
QY 489 NRKVFQWVSS-----STLNMSEAGKGLVKKCAVNSMGTSCETIFLNSPG 534
Db 467 NN-----VSNITITHSRDRSTVEGRVTFKAVETIARCLAKNLGAENRELKLV 518
QY 535 PPFITQDNISFYATIGLCPFTWLVILVILCHYKQFRYESQLQIQTGTPLDNEYFYVD 594
Db 519 --PTLRSELTVAANVLVLLVLIISLVILVWVKQKPRVEIRWRVIESIPDGHEYIYD 576

QY 595 FRDEYDLKWEPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIOAVKMLKEKADSC 654
Db 577 PMQLPYDSRWEFRDGLVLRVLSGAFKVGVEGTAGLSRSQPMKVAVMKLPKPTARSS 636
QY 655 EKEALMSLKQMTHLGHHDNIVNLGACTLSGPPYLIFFCYCCYGDLLNLYLRSKREKF--- 711
Db 637 EKQALMSLKIMTHLGHPLNIVNLGACTKSGPIYIITEYCFYGDVNLHKNRDSFLSH 696
QY 712 -----HRTWTEIFKEHNFSSYPTFOAHNSNMP--GSRREVQLHPP 749
Db 697 HPEKPKKELDIFGLNPADESTRSYVLSFENNNGYMDMKQADTTQYVPMLEKREVSFYSD 756
QY 750 LDOLSGFNGNSIHSEDEIEYENOKLAEBEEDLNVLTFEDLLCFAYQVAKMGFFLRFKS 809
Db 757 IQRSLYDRPASYKKSMLESDNNSGLTLL--DLSFTYQVARGMEFLASKN 813
QY 810 CVHRDLAARNVLTGHGVKVICDFGLARDILSDSSSYVVRGNARLPVKWMAPESLFEGIYT 869
Db 814 CVHRDLAARNVLLAOGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKMAPESLFDNLYT 873
QY 870 IKSDVMSYGILLWEIFSLGVPYGPIDANFYKLIOSGFKMEQPFYATEGIYFVMQSCW 929
Db 874 TLDVMSYGILLWEIFSLGTPYGMVMDSTFYNNKIKSGYRMKAPDHATSEVVEIMVKCW 933
QY 930 AFDSPKPSFNLTSFL 946
Db 934 NSEPEKPSFYHLSEIV 950

RESULT 13

US-09-955-363-36
; Sequence 36, Application US/09955363
; Patent No. US20020173621A1
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; Kindvogel Ph.D., Wayne R.
; Bell, Lillian A.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/955,363
; FILING DATE: 18-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELE: 3723836
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:


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/ ; LENGTH: 1089 amino acids
/ ; TYPE: amino acid
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: protein
/ ; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-955-363-36

Query Match      21.9%; Score 1150.5; DB 9; Length 1089;
Best Local Similarity 32.2%; Pred. No. 5e-71;
Matches 313; Conservative 154; Mismatches 327; Indels 177; Gaps 32;

QY 94 VOLATPGDLSLWFKSSLCGCPHFDLONRGIVSMALNVTETQAGEY--LLHIQSERA 151
DB 39 VOLNSSFSRLC---FGSEVSMQ--YPMSEBESSDVEIRN--EENNSGLFVTVLEVSSASA 92
QY 152 NYTVLFTVNRDQTLVYLRFRPKMENODALLCISEG-----VPEPTV-----EW 197
DB 93 AHTGLTYCYNNHTQ-----TEENE-----LEGRHIYIYVDPDVAFVPLGMDTY 136
QY 198 VLSCHSHRES-----CK---EEGPAVVRKEEKVL-----HELFGTDIRCCARNALGR 240
DB 137 LVIVEDDDSAIIPCKTTDPETPTVLHNSGVVPASYDSRQGFNGFTVGPVYCEATVKGK 196
QY 241 ECTKLFITDLNOAPOSTLPQLFL-----KVGEPLWIRCKAIHVNHGFLTW-----E 287
DB 197 ---KFQTIPTFNVYALKATSELDLEMEALKTVYKSGETIVVTC-AVFNNNEVDLQWTPGE 252
QY 288 LEDKALEEGSYFEMSTYSTNRTMIR-----TLIAFVSSVGR---NDTCGYTCSSSK--- 335
DB 253 VKGKI-----TMLBEIKVPSIKLVYTLTVPATVKDSDGYECAARQATR 297
QY 336 --HPQSQALVTILEKGF--INATSSQEEYIDPYKFCFSVRFKAYPRIRCTWIFSOASF 391
DB 298 EVKEMKVTISVHEKGFIEIKPTFSQLE-AVNLHEVKHFVVEVRAYPPIRISLWKNLTL 356
QY 392 PCEQRGLSDGVYSISKPCD-----HNK-----PGEYIFVAENDDAQTKMFTLN 435
DB 357 -----IENLTETTDVEKIQEIRYRSKLIRAKEDSGHYTIVAQNEDEVKSYTFELL 410
QY 436 IRKKPQVL-----ANASASQASCSDDGYPLPSWTWKCKSDKSPNCTEIEPEGVWNKKA 488
DB 411 TQVPSISLDLVDHGHGSGTGQVRCRTAEGTPLPDIEWMICKD-IKKCNNETS---WTILA 466
QY 489 NRKVGQWVSS-----STLNMSEAGGLLVKCCAYNSMGTSCTETIFLNSPG 534
DB 467 NN-----VSNIIIEHSRDRSTVEGRVTFKVEETIAVCLAKNLLGAENRELKVA-- 518
QY 535 PPPFIQDNISFYATIGLCLPFIVLIVLICHKYKQFRYESQLQMIQVTPGLDNEYFYVD 594
DB 519 --PTLSELTAVALVLLVIVIIISLIVLVVWKQKPRYEIRWRVIESISPDGHEIYVD 576

/ ; LENGTH: 1089 amino acids
/ ; TYPE: amino acid
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: protein
/ ; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-955-363-36

Query Match      21.9%; Score 1150.5; DB 9; Length 1089;
Best Local Similarity 32.2%; Pred. No. 5e-71;
Matches 313; Conservative 154; Mismatches 327; Indels 177; Gaps 32;

QY 94 VOLATPGDLSLWFKSSLCGCPHFDLONRGIVSMALNVTETQAGEY--LLHIQSERA 151
DB 39 VOLNSSFSRLC---FGSEVSMQ--YPMSEBESSDVEIRN--EENNSGLFVTVLEVSSASA 92
QY 152 NYTVLFTVNRDQTLVYLRFRPKMENODALLCISEG-----VPEPTV-----EW 197
DB 93 AHTGLTYCYNNHTQ-----TEENE-----LEGRHIYIYVDPDVAFVPLGMDTY 136
QY 198 VLSCHSHRES-----CK---EEGPAVVRKEEKVL-----HELFGTDIRCCARNALGR 240
DB 137 LVIVEDDDSAIIPCKTTDPETPTVLHNSGVVPASYDSRQGFNGFTVGPVYCEATVKGK 196
QY 241 ECTKLFITDLNOAPOSTLPQLFL-----KVGEPLWIRCKAIHVNHGFLTW-----E 287
DB 197 ---KFQTIPTFNVYALKATSELDLEMEALKTVYKSGETIVVTC-AVFNNNEVDLQWTPGE 252
QY 288 LEDKALEEGSYFEMSTYSTNRTMIR-----TLIAFVSSVGR---NDTCGYTCSSSK--- 335
DB 253 VKGKI-----TMLBEIKVPSIKLVYTLTVPATVKDSDGYECAARQATR 297
QY 336 --HPQSQALVTILEKGF--INATSSQEEYIDPYKFCFSVRFKAYPRIRCTWIFSOASF 391
DB 298 EVKEMKVTISVHEKGFIEIKPTFSQLE-AVNLHEVKHFVVEVRAYPPIRISLWKNLTL 356
QY 392 PCEQRGLSDGVYSISKPCD-----HNK-----PGEYIFVAENDDAQTKMFTLN 435
DB 357 -----IENLTETTDVEKIQEIRYRSKLIRAKEDSGHYTIVAQNEDEVKSYTFELL 410
QY 436 IRKKPQVL-----ANASASQASCSDDGYPLPSWTWKCKSDKSPNCTEIEPEGVWNKKA 488
DB 411 TQVPSISLDLVDHGHGSGTGQVRCRTAEGTPLPDIEWMICKD-IKKCNNETS---WTILA 466
QY 489 NRKVGQWVSS-----STLNMSEAGGLLVKCCAYNSMGTSCTETIFLNSPG 534
DB 467 NN-----VSNIIIEHSRDRSTVEGRVTFKVEETIAVCLAKNLLGAENRELKVA-- 518
QY 535 PPPFIQDNISFYATIGLCLPFIVLIVLICHKYKQFRYESQLQMIQVTPGLDNEYFYVD 594
DB 519 --PTLSELTAVALVLLVIVIIISLIVLVVWKQKPRYEIRWRVIESISPDGHEIYVD 576
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QY 595 FRDYEDLKWEPFRENLEFGKVLGSGAFGRVMNATAYGISTGVSIOVAVKMLKEKADSC 654
Db 577 PMQLPYDSRWKFRDGLVGLGSGAFKVGVEGTAYGLRSQPMKVAVKMLKPTARSS 636
QY 655 EKEALMSELKMTHLGHHDHNIIVNLLGACTLSGPVLYFPCYCCYGDLLNLYLRSKREKF--- 711
Db 637 EKOALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDVLYLHKNRDSFLSH 696
QY 712 -----HRTWTEIFKEHNFSSYPTFOAHNSMP--GSREVQLHPP 749
Db 697 HPEKPKKELDIFGLNPADESTRSYVILSFENNMDYMDKQADTTQYVPMLEKEVSYSD 756
QY 750 LDQLSGFNGNSIHSEDEIEYENOKRLAEEDLNVLTFFDLFCAYQVAKGMEFLFKS 809
Db 757 IORSLYDRPASYYKKKMLDSEVKNLLSDNSEGTL---DLLSFTYQVARGMEFLASKN 813
QY 810 CVHRDLAARNVVLVTHGKVKIKCDPLGARDILSDSSYVVRGNARLPVKWMAPESELEGIYT 869
Db 814 CVHRDLAARNVLLAOGKIVKICDFGLARDIMHDSNYVSKGSTFLPLVKWMAPESEIFDNLTY 873
QY 870 IKSDVWSYGILLWEIFSLGVPYGPIDVDFYKLIQSGFKWEPFYATEGIFYVMQSCW 929
Db 874 TLDVWSYGILLWEIFSLGTPYFGMMVDSTFYNNKIKSGYRMAKPDHATSEVYIIMVKCW 933
QY 930 AFDSRKRPSPNLTSTFL 946
Db 934 NSEPEKRPSPFVHLSEIV 950

RESULT 15
US-09-866-510-4
; Sequence 4, Application US/09866510
; Patent No. US2002011304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: EP-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-866-510-4

Query Match 21.8%; Score 1148.5; DB 10; Length 1089;
Best Local Similarity 32.0%; Pred. No. 6.8e-71;
Matches 313; Conservative 155; Mismatches 320; Indels 189; Gaps 33;
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Db 39 VOLNSSFSLRC---FGSEVSWQ--YPMSEBESSDVEIRN--EENNSGLFVTVLEVSSASA 92
QY 152 NYTVLFTVNVDRDOLYVLRFRYFRKMNODALLCISEG-----VPEPTV-----EW 197
Db 93 AHTGLYTCYNNHTQ-----TEENE-----LEGRHIYIVDPDPAFVPLGMDTY 136
QY 198 VLSCHRES-----CK---EEGPAVVRKEEKVL-----HELFGTDIRCCARNALGR 240
Db 137 LVIVEDDDSAIIPCRITDPTETVTLHNSGVVPASYDSRQGFNGFTTVPYICEATVKG 196
QY 241 ECTKLFTIDLNOAPOSTLPQLFL-----KVGEPLWIRCKAIHVNHGGLTW----E 287
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Search completed: May 24, 2003, 17:10:16
Job time : 46.9793 secs

QY 288 LEDKALEBEGSFEMSTYSTNRTMIR-----ILLAFVSSVGR---NDTGYVTCSSK--- 335
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QY 436 IRKQPVL-----ANASASQASCSGDPYLPSPWTKKCDKSPNCTEETEEIPEGVWKA 488
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QY 489 NRKVPFGWSS-----STLNMSEAGKGLLVKCCAYNSMGTSCTETFLNPSG 534
Db 467 NN-----VSNITEIHSRDRSTVEGRVTFKVEETIAVRCLAKNLLGAENRELKLA-- 518
QY 535 PFPPIODNISFYATIGLCPLFIIVLIVLICHYKQKPRYESOLOMIQVOTGPLDNEYFYVD 594
Db 519 --PFLSELVAAAALVLLVILVILVILVILVILVILVILVILVILVILVILVILVILV 576
QY 595 FRDYEDLKWEPFRENLEFGKVLGSGAFGRVMNATAYGISTGVSIOVAVKMLKEKADSC 654
Db 577 PMQLPYDSRWKFRDGLVGLGSGAFKVGVEGTAYGLRSQPMKVAVKMLKPTARSS 636
QY 655 EKEALMSELKMTHLGHHDHNIIVNLLGACTLSGPVLYFPCYCCYGDLLNLYLRSKREKF--- 711
Db 637 EKOALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDVLYLHKNRDSFLSH 696
QY 712 -----HRTWTEIFKEHNFSSYPTFOAHNSMP--GSREVQLHPP 749
Db 697 HPEKPKKELDIFGLNPADESTRSYVILSFENNMDYMDKQADTTQYVPMLEKEVSYSD 756
QY 750 LDQLSGFNGNSIHSEDEIEYENOKRLAEEDLNVLTFFDLFCAYQVAKGMEFLFKS 809
Db 757 IORSLYDRPASYYKKKMLDSEVKNLLSDNSEGTL---DLLSFTYQVARGMEFLASKN 813
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GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:54:10 ; Search time 13.9929 Seconds
(without alignments)
2085.875 Million cell updates/sec

Title: US-09-919-408-2

Perfect score: 5264

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Scoring table: BLOSUM62

Gapop 10.0., Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5264	100.0	992	1 US-07-813-593-2	Sequence 2, Appli
2	5264	100.0	992	1 US-07-977-451-2	Sequence 2, Appli
3	5264	100.0	992	1 US-07-946-507-2	Sequence 2, Appli
4	5264	100.0	992	1 US-08-252-517-2	Sequence 2, Appli
5	5264	100.0	992	1 US-07-906-397A-2	Sequence 2, Appli
6	5264	100.0	992	1 US-08-601-891-2	Sequence 2, Appli
7	5264	100.0	992	2 US-03-021-324-2	Sequence 2, Appli
8	5264	100.0	992	5 PCT-US92-02750-2	Sequence 2, Appli
9	5264	100.0	992	5 PCT-US92-05401-2	Sequence 2, Appli
10	5264	100.0	992	5 PCT-US92-09893-2	Sequence 2, Appli
11	5102	96.9	1000	1 US-08-222-299-2	Sequence 2, Appli
12	5102	96.9	1000	2 US-08-434-878-2	Sequence 2, Appli
13	5102	96.9	1000	5 PCT-US95-03718-2	Sequence 2, Appli
14	4436.5	84.3	993	1 US-08-222-299-4	Sequence 4, Appli
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20	4429.5	84.1	993	1 US-07-906-397A-4	Sequence 4, Appli
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24	4408.5	83.7	993	1 US-08-183-211-2	Sequence 2, Appli
25	4408.5	83.7	993	5 PCT-US95-00176A-2	Sequence 2, Appli
26	2240.5	42.6	481	4 US-07-912-122-4	Sequence 4, Appli
27	2240.5	42.6	481	5 PCT-US93-06404-4	Sequence 4, Appli

28 1221.5 23.2 972 3 US-08-750-141A-2 Sequence 2, Appli
29 1196 22.7 976 3 US-08-750-141A-1 Sequence 1, Appli
30 1152.5 21.9 1089 1 US-08-168-917-4 Sequence 4, Appli
31 1152.5 21.9 1089 2 US-08-460-510-4 Sequence 4, Appli
32 1152.5 21.9 1089 2 US-08-460-490-4 Sequence 4, Appli
33 1152.5 21.9 1089 3 US-08-462-728-2 Sequence 2, Appli
34 1152.5 21.9 1089 4 US-08-461-917-2 Sequence 2, Appli
35 1152.5 21.9 1089 5 PCT-US92-00730-4 Sequence 4, Appli
36 1152.5 21.9 1089 5 PCT-US92-00862-4 Sequence 4, Appli
37 1150.5 21.9 1089 1 US-08-180-195-36 Sequence 36, Appli
38 1150.5 21.9 1089 1 US-08-477-329-36 Sequence 36, Appli
39 1150.5 21.9 1089 2 US-08-475-458-36 Sequence 36, Appli
40 1150.5 21.9 1089 3 US-08-980-400-36 Sequence 36, Appli
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43 1150.5 21.9 1089 4 US-09-583-449A-36 Sequence 36, Appli
44 1150.5 21.9 1089 4 US-09-435-059-36 Sequence 36, Appli
45 1078 20.5 1106 1 US-08-180-195-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-07-813-593-2
; Sequence 2, Application US/07813593
; Patent No. 5185438
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/813,593
; FILING DATE: 19920415
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-813-593-2

Query Match 100.0%; Score 5264; DB 1; Length 992;

		Best Local Similarity 100.0%; Pred. No. 0;				Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Qy	121	LQNGRIVSMALNVTTQAGEYLHIIQSERANYTVLTVNVNVDVQLVLRPYPKRMENQ	180						
Db	121	LQNGRIVSMALNVTTQAGEYLHIIQSERANYTVLTVNVNVDVQLVLRPYPKRMENQ	180						
Qy	181	DALLCISEGPEPTVEVVLCSHRESCKECPAVVRKEEVKHLFGTDIRCCARNALGR	240						
Db	181	DALLCISEGPEPTVEVVLCSHRESCKECPAVVRKEEVKHLFGTDIRCCARNALGR	240						
Qy	241	ECTKLFIDLNQAPQSTLPOLFLKVGEPWLIRCKAIHVNHGFGLTWELEDKALEGSGYFE	300						
Db	241	ECTKLFIDLNQAPQSTLPOLFLKVGEPWLIRCKAIHVNHGFGLTWELEDKALEGSGYFE	300						
Qy	301	MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILKGFNATSSQEEY	360						
Db	301	MSTYSTNRTMIRILLAFVSSVGRNDTGYTCTSSSKHPSQSALVTILKGFNATSSQEEY	360						
Qy	361	EIDPYEKFCFSVRKAYPRIRCTWIFSOASPCORGLDGYISKPCDHKNKGEYIFY	420						
Db	361	EIDPYEKFCFSVRKAYPRIRCTWIFSOASPCORGLDGYISKPCDHKNKGEYIFY	420						
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Qy	541	DNISFYATIGLCLPFIVLVILVILCHYKKQPRYESOLOMIQVTPLDNEYFYVDFRDY	600						
Db	541	DNISFYATIGLCLPFIVLVILVILCHYKKQPRYESOLOMIQVTPLDNEYFYVDFRDY	600						
Qy	601	DLKWEFFRENLEFGKVLGSGAFGRVWNTATYISKTGVSIOVAVKMLKEKADSKCEKALM	660						
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Qy	721	EHNFSSTPTFOAHNSNMPGSRVQLHPPLDQSGFNGNSIHSDETEIYENQKRLAEBEE	780						
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Qy	781	EDLNVLFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL	840						
Db	781	EDLNVLFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL	840						
Qy	841	SDSSYVVRGNARLPVKWMAPELSEFEGYITIKSDVMSYGILLWEIFSLGVNYPGIPVDAN	900						
Db	841	SDSSYVVRGNARLPVKWMAPELSEFEGYITIKSDVMSYGILLWEIFSLGVNYPGIPVDAN	900						
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RESULT 2

US-07-977-451-2
; Sequence 2, Application US/07977451
; Patent No. 5270458
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 19921119
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US UNASSIGNED
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-977-451-2

Query Match 100.0%; Score 5264; DB 1; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 841 SDSSYVVRGNARLPVKWMAPELFEIYTIKSDVMSYGILLWEIFSLGWNYPGIPVDAN 900
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RESULT 3

US-07-946-507-2
; Sequence 2, Application US/07946507
; Patent No. 5283354
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL

; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,507
; FILING DATE: 19920917
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-946-507-2

Query Match 100.0%; Score 5264; DB 1; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALAQRDRRLLLLVLSVMILETVTNQDLPVVKCVLISHENNGSSAGKPSRYMRVRS 60
DB 1 MRALAQRDRRLLLLVLSVMILETVTNQDLPVVKCVLISHENNGSSAGKPSRYMRVRS 60
QY 61 PEDLQCTPRQSEGVYEAATVEAEGSIITLQVLAATPGDLSPGLVFKHSLGCGQPHFD 120
DB 61 PEDLQCTPRQSEGVYEAATVEAEGSIITLQVLAATPGDLSPGLVFKHSLGCGQPHFD 120
QY 121 LQNRGIVSMALINVTQAGYLLHIQSERANYTVLFTVNVDRDTQLYVLRPPYFRKMNQ 180
DB 121 LQNRGIVSMALINVTQAGYLLHIQSERANYTVLFTVNVDRDTQLYVLRPPYFRKMNQ 180
QY 181 DALLCISGVPPEPTVEWVLCSSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
DB 181 DALLCISGVPPEPTVEWVLCSSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
QY 241 ECTKLFITIDLNAQPOSTLPQLFLKVGPELWIRCKAIHVNHGFGLTWELEDKALEGSGYFE 300
DB 241 ECTKLFITIDLNAQPOSTLPQLFLKVGPELWIRCKAIHVNHGFGLTWELEDKALEGSGYFE 300
QY 301 MSTYSTNTRTMRIRILLAFVSSVGRNDTGYTCTSSKHPSQSALVTILEKGFINATSSQBEY 360
DB 301 MSTYSTNTRTMRIRILLAFVSSVGRNDTGYTCTSSKHPSQSALVTILEKGFINATSSQBEY 360

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QY 361 EIDPYEKFCSVRKAYPRIRCTWIFSOAGFPCCBQGLEGDYSGSKFCDHKNKPGYIFY 420
Db 361 EIDPYEKFCSVRKAYPRIRCTWIFSOAGFPCCBQGLEGDYSGSKFCDHKNKPGYIFY 420
QY 421 AENDDAQFTKMTNIRKKPOVLANASASQASCSDDGYPLPSWTWKCSKSPNCTBEIP 480
Db 421 AENDDAQFTKMTNIRKKPOVLANASASQASCSDDGYPLPSWTWKCSKSPNCTBEIP 480
QY 481 EGVNWKANRKFQOWVSSSTLNNSEAGKLLVKCCAYNSNGTSCETIFLNSRGPFFPIQ 540
Db 481 EGVNWKANRKFQOWVSSSTLNNSEAGKLLVKCCAYNSNGTSCETIFLNSRGPFFPIQ 540
QY 541 DNISFYATIGLCLPFIVVLIIVLICHYKKQPRYESQLOMIQVOTGFLDNEYFYVDFRDY 600
Db 541 DNISFYATIGLCLPFIVVLIIVLICHYKKQPRYESQLOMIQVOTGFLDNEYFYVDFRDY 600
QY 601 DLKWEFFRENLEFGKVLGSGAGFGRVNMATAYGSKTGVSIQVAVKMLKEKADSCKEALM 660
Db 601 DLKWEFFRENLEFGKVLGSGAGFGRVNMATAYGSKTGVSIQVAVKMLKEKADSCKEALM 660
QY 661 SELKQMTLGHHDNIVNLLGACTLSGPVYLIFPCYCCYGDLLNLYLSRKREKPHRTWTEIFK 720
Db 661 SELKQMTLGHHDNIVNLLGACTLSGPVYLIFPCYCCYGDLLNLYLSRKREKPHRTWTEIFK 720
QY 721 EHNFSYPTFOAHNSNMPGSGREVQLHPDLQLSGFNGNSIHSDEIYENOKRLAELEE 780
Db 721 EHNFSYPTFOAHNSNMPGSGREVQLHPDLQLSGFNGNSIHSDEIYENOKRLAELEE 780
QY 781 EDLNVLFEDLLCFAYQVAKMEFLPKSCVHRDLAARNVLVTHGVKVKICDFGLARDIL 840
Db 781 EDLNVLFEDLLCFAYQVAKMEFLPKSCVHRDLAARNVLVTHGVKVKICDFGLARDIL 840
QY 841 SDSSVYVRGNARLPVKVMAPESLPEGIYTIKSDVMSYGILLWEIPLSLGVNYPYGPVVDAN 900
Db 841 SDSSVYVRGNARLPVKVMAPESLPEGIYTIKSDVMSYGILLWEIPLSLGVNYPYGPVVDAN 900
QY 901 FYKLIQSGFKMEQPPYATGEGYFVWQSCWAFDSRKRPSFPNLTSLFGCOLAEAEACIRT 960
Db 901 FYKLIQSGFKMEQPPYATGEGYFVWQSCWAFDSRKRPSFPNLTSLFGCOLAEAEACIRT 960
QY 961 SIHLPKQAAPQORGGLRAQSPQKVIHRERS 992
Db 961 SIHLPKQAAPQORGGLRAQSPQKVIHRERS 992

RESULT 4
US-08-252-517-2
; Sequence 2, Application US/08252517
; Patent No. 5548065
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,517
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,451
; FILING DATE: 19-NOV-1992
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-252-517-2
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Query Match 100.0%; Score 5264; DB 1; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRAIAQSRDRLLLLVLSVMILETVTNQDLPVKCVLISHENNGSSACKPSRYMRVGRS 60
QY 61 PEDLQCTPRQSEGTVEAATVEVAESGSITLQVQLATPGDLSCLVWFKHSSLGCPHPD 120
Db 61 PEDLQCTPRQSEGTVEAATVEVAESGSITLQVQLATPGDLSCLVWFKHSSLGCPHPD 120
QY 121 LQNRGIVSMALNVTQAGBYLLHIQSERANYTVLFTVNVDRDTQLYVLRPRYPRKMNQ 180
Db 121 LQNRGIVSMALNVTQAGBYLLHIQSERANYTVLFTVNVDRDTQLYVLRPRYPRKMNQ 180
QY 181 DALLCISEGVPEPTVEWVLCSSHRESCKEKPVRVKEKVLHELFGTDIRCCARNALGR 240
Db 181 DALLCISEGVPEPTVEWVLCSSHRESCKEKPVRVKEKVLHELFGTDIRCCARNALGR 240
QY 241 ECTKLTFTDLNQAQSTLPQLFKVGEPLWIRCKAIHYNHGFGLTWELEDKALEEGSYFE 300
Db 241 ECTKLTFTDLNQAQSTLPQLFKVGEPLWIRCKAIHYNHGFGLTWELEDKALEEGSYFE 300
QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTSSSKHPSQSALVTILEKGFINATSSQBEY 360
Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTSSSKHPSQSALVTILEKGFINATSSQBEY 360
QY 361 EIDPYEKFCSVRKAYPRIRCTWIFSOAGFPCCBQGLEGDYSGSKFCDHKNKPGYIFY 420
Db 361 EIDPYEKFCSVRKAYPRIRCTWIFSOAGFPCCBQGLEGDYSGSKFCDHKNKPGYIFY 420
QY 421 AENDDAQFTKMTNIRKKPOVLANASASQASCSDDGYPLPSWTWKCSKSPNCTBEIP 480
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Db 421 AENDDAQFTKMTLNIRKKPQVLANASQASCSDDGYPLPSWTWKKCDKSPNCTEIP 480
Qy 481 EGVNKKANRKFVQGWSSSTLNSEAGKLLVKCCAYNSMGTSCTETIFLNSPGPFPIQ 540
Db 481 EGVNKKANRKFVQGWSSSTLNSEAGKLLVKCCAYNSMGTSCTETIFLNSPGPFPIQ 540
Qy 541 DNISFYATIGLCLPIVIVLILCHYKQKQRYESQLOMIQVTPGLDNEYFYVDFRDY 600
Db 541 DNISFYATIGLCLPIVIVLILCHYKQKQRYESQLOMIQVTPGLDNEYFYVDFRDY 600
Qy 601 DLKWEFFPRENLEFGKVLGSGAFGRVNNATAYGISKTGYSIQVAVKMLKEKADSCKEALM 660
Db 601 DLKWEFFPRENLEFGKVLGSGAFGRVNNATAYGISKTGYSIQVAVKMLKEKADSCKEALM 660
Qy 661 SELKXMTLGHHDNIVNLLGACTLSGPPVLI FEYCCYGDLLNLRKREKHFRTWTEIFK 720
Db 661 SELKXMTLGHHDNIVNLLGACTLSGPPVLI FEYCCYGDLLNLRKREKHFRTWTEIFK 720
Qy 721 EHNFSYPTFOAHNSNMPGSGREVQLHPPLDQSGFNCSIHSEDEIEYENQKRLAESEE 780
Db 721 EHNFSYPTFOAHNSNMPGSGREVQLHPPLDQSGFNCSIHSEDEIEYENQKRLAESEE 780
Qy 781 EDNLVTFEDLLCFAYQVAKMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
Db 781 EDNLVTFEDLLCFAYQVAKMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
Qy 841 SDSSVYVRGNARLPVKWAPESLFEIYTIKSDVMSYGILLWEIPLSGVNPYPGIPVDAN 900
Db 841 SDSSVYVRGNARLPVKWAPESLFEIYTIKSDVMSYGILLWEIPLSGVNPYPGIPVDAN 900
Qy 901 FYKLIQSGFMEQPFYATGEGYIFWQSCWAFDSRKRPSFPNLTSLFGQLAEAEACIRT 960
Db 901 FYKLIQSGFMEQPFYATGEGYIFWQSCWAFDSRKRPSFPNLTSLFGQLAEAEACIRT 960
Qy 961 SIHLPKQAAPQOGLRAQSPQROVKIHRERS 992
Db 961 SIHLPKQAAPQOGLRAQSPQROVKIHRERS 992

RESULT 5
US-09-919-408-2
; Sequence 2, Application US/07906397A
; Patent No. 5621090
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOINT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/906,397A
; FILING DATE: 19920626
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPPPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-906-397A-2

Query Match 100.0%; Score 5264; DB 1; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALAQRSDRRLILLVLSVMILETTVNODLPVVKCVLISHENNGSSACKPSSYRMVRGS 60
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Db 61 PEDLOCTPRROSEGTVEAATVEVAESGSI TLQVOLATPGDLSCLWFKHSLGCGPHFD 120
Qy 121 LQNRGIVSMALNVTETQAGEYLLHIQSERANYTLFTVNVVDTOLYVLRPFYFRMENQ 180
Db 121 LQNRGIVSMALNVTETQAGEYLLHIQSERANYTLFTVNVVDTOLYVLRPFYFRMENQ 180
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Db 181 DALLICISGVPEPTVEWVLCSSHRESCKEGBPAVVRKEKULHELFGTDIRCCARNALGR 240
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Db 241 ECTKLTIDLNOAPOSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEGSGYFE 300
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Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTCSSSKHPSQSALVTILEKGFINATSSQEEY 360
Qy 361 EIDPYEKFCFSVRKAYPRIRCTWIFSOASFPCEORGLDGYISKFCDHKNKPGEYIFY 420
Db 361 EIDPYEKFCFSVRKAYPRIRCTWIFSOASFPCEORGLDGYISKFCDHKNKPGEYIFY 420
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Db 421 AENDDAQFTKMTLNIRKKPQVLANASQASCSDDGYPLPSWTWKKCDKSPNCTEIP 480
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Db 541 DNISFYATIGLCLPIVIVLILCHYKQKQRYESQLOMIQVTPGLDNEYFYVDFRDY 600
Qy 601 DLKWEFFPRENLEFGKVLGSGAFGRVNNATAYGISKTGYSIQVAVKMLKEKADSCKEALM 660
Db 601 DLKWEFFPRENLEFGKVLGSGAFGRVNNATAYGISKTGYSIQVAVKMLKEKADSCKEALM 660
Qy 661 SELKXMTLGHHDNIVNLLGACTLSGPPVLI FEYCCYGDLLNLRKREKHFRTWTEIFK 720
Db 661 SELKXMTLGHHDNIVNLLGACTLSGPPVLI FEYCCYGDLLNLRKREKHFRTWTEIFK 720
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Db 721 EHNFSYPTFOAHNSNMPGSGREVQLHPPLDQSGFNCSIHSEDEIEYENQKRLAESEE 780

QY 781 EDNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
DB 781 EDNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
QY 841 SDSYVVRGNARLPVKWMAPELSEFEGYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
DB 841 SDSYVVRGNARLPVKWMAPELSEFEGYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
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DB 901 FYKLIQSGFKMEQPFYATEGYIFVMSQWAPDSRKRSPFNLTSLFGCOLAEAEACIRT 960
QY 961 SIHLPKQAAPQOORGLRAQSPQOVKIHRS 992
DB 961 SIHLPKQAAPQOORGLRAQSPQOVKIHRS 992

RESULT 6

US-08-601-891-2
Sequence 2, Application US/08601891
Patent No. 5747651
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,891
FILING DATE: 15-FEB-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601

REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-601-891-2
Query Match 100.0%; Score 5264; DB 1; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRALAQRSDRRLLLLVLSVMILETVTNQDLPIVKCVLISHENNGSSAGKPSRYMRVRS 60
DB 1 MRALAQRSDRRLLLLVLSVMILETVTNQDLPIVKCVLISHENNGSSAGKPSRYMRVRS 60
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DB 61 PEDLOCTPRROSEGTVEAATVEAEGSITLQVQLATPGDLSCLVWFKHSLGCGPHFD 120
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DB 181 DALLCISEGVEPTEVWVLCSSHRESCKEKGPAVVRKEKVLHELFGTDIRCCARNALGR 240
QY 241 ECTKLFTIDLNOAQSTLPQLFKVGEPLWIRCKAIHVNHGFLTWELDKALEGSYPE 300
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DB 301 MSTYSTNRMTIRILLAFVSSVGRNDGYTCTSSSKHPQSALVTILEKGFINATSSQBEY 360
QY 361 EIDPYEKFCSVRPKAYPRICTWIFSOAPFCEQGLEDSYISKPCDHKNKPGYIFY 420
DB 361 EIDPYEKFCSVRPKAYPRICTWIFSOAPFCEQGLEDSYISKPCDHKNKPGYIFY 420
QY 421 AENDDAQFTKMTLNIRKKPOVLANASASQSSDGYPLPSWTWKCSKSPNCTEIP 480
DB 421 AENDDAQFTKMTLNIRKKPOVLANASASQSSDGYPLPSWTWKCSKSPNCTEIP 480
QY 481 EGVNKKANRVFGQWVSSSTLNKSEAGKLLVKCAVNSMGTSCTETFLNSPGPPFFIQ 540
DB 481 EGVNKKANRVFGQWVSSSTLNKSEAGKLLVKCAVNSMGTSCTETFLNSPGPPFFIQ 540
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DB 541 DNISFYATIGLCLPFIIVLILCHYKQKQRYESQLQMIQVTPLDNEYFYVDFRDY 600
QY 601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYISKTGYSIQVAVKMLKEKADSCKEALM 660
DB 601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYISKTGYSIQVAVKMLKEKADSCKEALM 660
QY 661 SELKWMTHLGHHDNIVNLGACTLSGPVLIIFYCYGDLNLYRSKREKPHRTWTEIFK 720
DB 661 SELKWMTHLGHHDNIVNLGACTLSGPVLIIFYCYGDLNLYRSKREKPHRTWTEIFK 720
QY 721 EHNFSYPTFOAHNSNMPGSRVQLHPDLQSLGFGNCSIHSEDEIEYENKRLAEES 780
DB 721 EHNFSYPTFOAHNSNMPGSRVQLHPDLQSLGFGNCSIHSEDEIEYENKRLAEES 780
QY 781 EDNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
DB 781 EDNLVTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
QY 841 SDSYVVRGNARLPVKWMAPELSEFEGYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900

Db 841 SSSSVVVRGNARLPVKWMAPESEFEGYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Qy 901 FYKLIQSGFKMEQPPFYATEGIVFMQSWAFDSRKRPSFPNLTSLFLGCOLABAEAEACIRT 960
Db 901 FYKLIQSGFKMEQPPFYATEGIVFMQSWAFDSRKRPSFPNLTSLFLGCOLABAEAEACIRT 960
Qy 961 SHLHPKQAPQORGLRAQSPORQVKIHRERS 992
Db 961 SHLHPKQAPQORGLRAQSPORQVKIHRERS 992

RESULT 7

US-09-021-324-2
; Sequence 2, Application US/09021324
; Patent No. 5912133
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOPIOTENT HEMATOPOIETIC STEM CELL
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/021,324
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 1992-11-19
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feic, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 992 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-021-324-2
Query Match 100.0%; Score 5264; DB 2; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRALAQRSDRRLLLVLSVMILETVTNQDLVPIKCVLISHENNSSAGKPSRYRVGRS 60
Db 1 MRALAQRSDRRLLLVLSVMILETVTNQDLVPIKCVLISHENNSSAGKPSRYRVGRS 60
Qy 61 PEDLOCTPRRQSEGTYEAAATVEAESGSTITIQVQLATPGDLSCLVWFKHSSLGCCPHFD 120
Db 61 PEDLOCTPRRQSEGTYEAAATVEAESGSTITIQVQLATPGDLSCLVWFKHSSLGCCPHFD 120
Qy 121 LQNRGIVSMAILNVTTQAGEYLLHIQSERANYTVLFTVNVRTQLYVLRPYFRKVENQ 180
Db 121 LQNRGIVSMAILNVTTQAGEYLLHIQSERANYTVLFTVNVRTQLYVLRPYFRKVENQ 180
Qy 181 DALLCISEGVPEPTVEWVLCSSHRESCKEKGPAVWRKEEVLHELFGTDIRCCARNALGR 240
Db 181 DALLCISEGVPEPTVEWVLCSSHRESCKEKGPAVWRKEEVLHELFGTDIRCCARNALGR 240
Qy 241 ECTKLTIDLNQAPQSTLPQLFLKVGEPWIRCKATHVNHGFLTWELDKALEEGSYFE 300
Db 241 ECTKLTIDLNQAPQSTLPQLFLKVGEPWIRCKATHVNHGFLTWELDKALEEGSYFE 300
Qy 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYVTCSSSKHPSQALVTILEKGFINATSSQEEY 360
Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYVTCSSSKHPSQALVTILEKGFINATSSQEEY 360
Qy 361 EIDPYEKFCSVRFKAYPRIRCTWIFSQASFCEQRLGLEDGYSISKFDHKNKPGYIFY 420
Db 361 EIDPYEKFCSVRFKAYPRIRCTWIFSQASFCEQRLGLEDGYSISKFDHKNKPGYIFY 420
Qy 421 AENDDAQFTKMTLNIRKKPQVLANASASQSCSDGYPLPSMTWKKCDKSPNCTEIP 480
Db 421 AENDDAQFTKMTLNIRKKPQVLANASASQSCSDGYPLPSMTWKKCDKSPNCTEIP 480
Qy 481 EGVNKKANRKYFGQWVSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETILNSGPPFFIQ 540
Db 481 EGVNKKANRKYFGQWVSSSTLNMSEAGKGLLVKCCAYNSMGTSCTETILNSGPPFFIQ 540
Qy 541 DNISFYATIGLCLPFIIVLILCHIKYKQFYESOLQMIQVTPGLDNEYFYVDFRDY 600
Db 541 DNISFYATIGLCLPFIIVLILCHIKYKQFYESOLQMIQVTPGLDNEYFYVDFRDY 600
Qy 601 DLKWEPPRENLEFGVLGSGAFGRVNNATAYGISKTGVSIQVAVKMLKEKADSCKEALM 660
Db 601 DLKWEPPRENLEFGVLGSGAFGRVNNATAYGISKTGVSIQVAVKMLKEKADSCKEALM 660
Qy 661 SELKMMTHLGHHDNIVNLLGACTLSGPVYLI FEYCCYGDLLNLYRSKRKFHRTWTETFK 720
Db 661 SELKMMTHLGHHDNIVNLLGACTLSGPVYLI FEYCCYGDLLNLYRSKRKFHRTWTETFK 720
Qy 721 EHNFSYPTFOAHNSNMPGSRVQLHPPLDQLSGPNNGSIHSEDEIEYENQKRLAEBEE 780
Db 721 EHNFSYPTFOAHNSNMPGSRVQLHPPLDQLSGPNNGSIHSEDEIEYENQKRLAEBEE 780
Qy 781 EDNLVLTREDLLCFAYQVAKGMEFEFKSCVHRDLAARNVLTGHGVKVICDFGLARDIL 840
Db 781 EDNLVLTREDLLCFAYQVAKGMEFEFKSCVHRDLAARNVLTGHGVKVICDFGLARDIL 840
Qy 841 SDSSVYVRGNARLPVKWMAPESEFEGYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Db 841 SDSSVYVRGNARLPVKWMAPESEFEGYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Qy 901 FYKLIQSGFKMEQPPFYATEGIVFMQSWAFDSRKRPSFPNLTSLFLGCOLABAEAEACIRT 960
Db 901 FYKLIQSGFKMEQPPFYATEGIVFMQSWAFDSRKRPSFPNLTSLFLGCOLABAEAEACIRT 960


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Qy 961 SIHLPKQAAPQOQGLRAQSPQOQVQKIHRS 992
Db 961 SIHLPKQAAPQOQGLRAQSPQOQVQKIHRS 992

RESULT 8
PCT-US92-02750-2
; Sequence 2, Application PC/TUS9202750
; GENERAL INFORMATION:
; APPLICANT: LEMISCHKA, IHOR R.
; TITLE OF INVENTION: Totipotent Hematopoietic Stem Cell
; TITLE OF INVENTION: Receptors And Their Ligands
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: US
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02750
; FILING DATE: 19920402
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FEIT, IRVING N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-02750-2

Query Match 100.0%; Score 5264; DB 5; Length 992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALAQRSDRRLLLVLSVMIETVTDLPVVKCVLISHENNGSSACKPSRYMRVRS 60
Db 1 MRALAQRSDRRLLLVLSVMIETVTDLPVVKCVLISHENNGSSACKPSRYMRVRS 60

Qy 61 PEDLQCTPRQSEGTVEAATVEVAESGSIITQVQLATPGDLSCLVFKHSLGCOPHD 120
Db 61 PEDLQCTPRQSEGTVEAATVEVAESGSIITQVQLATPGDLSCLVFKHSLGCOPHD 120

Qy 121 LQNRGIVSMALINVTQAGEVLIHQSERANYTVLFTVNVVDQTLVLRPRYFRKMNQ 180
Db 121 LQNRGIVSMALINVTQAGEVLIHQSERANYTVLFTVNVVDQTLVLRPRYFRKMNQ 180

Qy 181 DALLCISEGVPPTVEWVLCSSHRSCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
Db 181 DALLCISEGVPPTVEWVLCSSHRSCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240

Qy 241 ECTKLFTIDLNAQOSTLPQLFLKVGEPILWIRCKAIHVNHGFLTWELDKALEGSYFE 300
Db 241 ECTKLFTIDLNAQOSTLPQLFLKVGEPILWIRCKAIHVNHGFLTWELDKALEGSYFE 300

Qy 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCCSSKHPQSALVTILEKGFINATSSQEBY 360
Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCCSSKHPQSALVTILEKGFINATSSQEBY 360

361 EIDPYEKFCFSVRKAYPRIRCTWIFSOASPPCQORGLDGYISISKFDHKNKPGEYIFY 420
361 EIDPYEKFCFSVRKAYPRIRCTWIFSOASPPCQORGLDGYISISKFDHKNKPGEYIFY 420
421 AENDDAQFTKMTNIRKKPOVLANASASOASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
421 AENDDAQFTKMTNIRKKPOVLANASASOASCSDDGYPLPSWTWKCKSDKSPNCTEIP 480
481 EGVNKKANRKFVQWSSSTLNMSSEAGKLLVRCCAYNSMGTSCTIFLNSPGPFPIQ 540
481 EGVNKKANRKFVQWSSSTLNMSSEAGKLLVRCCAYNSMGTSCTIFLNSPGPFPIQ 540
541 DNISFYATIGLCLPPIVVLIVLICHYKKQPRYSQLOMIQVTPGLDNEYFVVDPRDVEY 600
541 DNISFYATIGLCLPPIVVLIVLICHYKKQPRYSQLOMIQVTPGLDNEYFVVDPRDVEY 600
601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISTGTYSIQVAVKMKKADSCKEALM 660
601 DLKWEFFPRENLEFGKVLGSGAFGRVMNATAYGISTGTYSIQVAVKMKKADSCKEALM 660
661 SELKQWTHLGHHDNIVNLGACTLGGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTEIFK 720
661 SELKQWTHLGHHDNIVNLGACTLGGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTEIFK 720
721 EHNFSYPTFOAHNSNMPGSRVQLHPDLQSLGFGNNSIHSEDEIEYENQKRLAESEE 780
721 EHNFSYPTFOAHNSNMPGSRVQLHPDLQSLGFGNNSIHSEDEIEYENQKRLAESEE 780
781 EDLNVLTTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVLCDFGLARDIL 840
781 EDLNVLTTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVLCDFGLARDIL 840
841 SDSSVVRGNARLPVKWMAPESLPEGIYTIKSDVMSYGILLWEIFSLGVNPPYGPVDAN 900
841 SDSSVVRGNARLPVKWMAPESLPEGIYTIKSDVMSYGILLWEIFSLGVNPPYGPVDAN 900
901 FYKLIQSGFKMEQPFYATEGIVFVMSQWAFDSRKRPSFPNLTSLFGCOLABAEACIRT 960
901 FYKLIQSGFKMEQPFYATEGIVFVMSQWAFDSRKRPSFPNLTSLFGCOLABAEACIRT 960
961 SIHLPKQAAPQOQGLRAQSPQOQVQKIHRS 992
961 SIHLPKQAAPQOQGLRAQSPQOQVQKIHRS 992

RESULT 9
PCT-US92-05401-2
; Sequence 2, Application PC/TUS9205401
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05401
; FILING DATE: 19920626
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPT
```

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-05401-2

Query Match 100.0%; Score 5264; DB 5; Length 992;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALAQRSDRRLLLVLSVMIETVNTQDLPIVKCVLISHENNGSSAGKPSRYMRVRS 60
DB 1 MRALAQRSDRRLLLVLSVMIETVNTQDLPIVKCVLISHENNGSSAGKPSRYMRVRS 60
QY 61 PEDLQCTPRRQSEGTVEAATVEVAESGITLQVQLATPGDLSCLWVKHSLGCGPHFD 120
DB 61 PEDLQCTPRRQSEGTVEAATVEVAESGITLQVQLATPGDLSCLWVKHSLGCGPHFD 120
QY 121 LQNRGIVSMALNVTTQAGEYLLHIQSERANYTVLFTVNVDRDTQLYVLRPRYFRMENO 180
DB 121 LQNRGIVSMALNVTTQAGEYLLHIQSERANYTVLFTVNVDRDTQLYVLRPRYFRMENO 180
QY 181 DALLCISGVPEPTVEVWVLCSSHRSCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
DB 181 DALLCISGVPEPTVEVWVLCSSHRSCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
QY 241 ECTKLFTIDLNOAPOSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEGSYFE 300
DB 241 ECTKLFTIDLNOAPOSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEGSYFE 300
QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSKHPSQSALVTILEKGFINATSSQBEY 360
DB 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSKHPSQSALVTILEKGFINATSSQBEY 360
QY 361 EIDPYEKFCFVRKAYPRIRCTWTFISOASPCOEORGEDGYSISKFDHKNKPGEYIFY 420
DB 361 EIDPYEKFCFVRKAYPRIRCTWTFISOASPCOEORGEDGYSISKFDHKNKPGEYIFY 420
QY 421 AENDDAQFTKMTNIRKKPQVLANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIRP 480
DB 421 AENDDAQFTKMTNIRKKPQVLANASQASCSDDGYPLPSWTWKCKSDKSPNCTEIRP 480
QY 481 EGVWNNKANRKFQGWVSSSTLNMSEAGKLLVKCAVNSMGTSCTETIFLNSPGPFPIQ 540
DB 481 EGVWNNKANRKFQGWVSSSTLNMSEAGKLLVKCAVNSMGTSCTETIFLNSPGPFPIQ 540
QY 541 DNIIFYATIGLCLPIVVLIVLICHYKKOPRYESQLOMIQVTGPDNNEYFYVDRDY 600
DB 541 DNIIFYATIGLCLPIVVLIVLICHYKKOPRYESQLOMIQVTGPDNNEYFYVDRDY 600
QY 601 DLKWEFFRENLEFQKVLGSGAFGRVNNATAYGISKTGYSIOAVKMLKEKADSCKEALM 660
DB 601 DLKWEFFRENLEFQKVLGSGAFGRVNNATAYGISKTGYSIOAVKMLKEKADSCKEALM 660
QY 661 SELKQMTHLGHHDNIVNLLGACTLGGPYLIFYECCYGDLLNVLRSKREKPHRTWTEIFK 720
DB 661 SELKQMTHLGHHDNIVNLLGACTLGGPYLIFYECCYGDLLNVLRSKREKPHRTWTEIFK 720
QY 721 EHNFSSTPFOAHNSNMPGSRVQLHPLDQLSFGNCSIHSEDEIYEYQKRLAESEE 780
DB 721 EHNFSSTPFOAHNSNMPGSRVQLHPLDQLSFGNCSIHSEDEIYEYQKRLAESEE 780
QY 781 EDNLVLTPEDLCLCFAYQVAKGMEFLEPKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
DB 781 EDNLVLTPEDLCLCFAYQVAKGMEFLEPKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
QY 841 SDSSTVVRGNARLPVKWMAPESLFEGITYIKSDVNSYGILLWEIFSLGWNYPGIPVDAN 900

DB 841 SDSSTVVRGNARLPVKWMAPESLFEGITYIKSDVNSYGILLWEIFSLGWNYPGIPVDAN 900
QY 901 FYKLIQSGFMQEPFYATEGIYFVMSQWAFDSRKRPSFPNLTSTFLGCOLAEAEACIRT 960
DB 901 FYKLIQSGFMQEPFYATEGIYFVMSQWAFDSRKRPSFPNLTSTFLGCOLAEAEACIRT 960
QY 961 SIHLPKQAAPQORGGRLAQRASPORQVKIHRERS 992
DB 961 SIHLPKQAAPQORGGRLAQRASPORQVKIHRERS 992

RESULT 10

PCT-US92-09893-2

Sequence 2, Application PC/TUS9209893
GENERAL INFORMATION:

APPLICANT: Lemischka, Ithor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09893
FILING DATE: 19921116
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7PT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-09893-2

Query Match 100.0%; Score 5264; DB 5; Length 992;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALAQRSDRRLLLVLSVMIETVNTQDLPIVKCVLISHENNGSSAGKPSRYMRVRS 60
DB 1 MRALAQRSDRRLLLVLSVMIETVNTQDLPIVKCVLISHENNGSSAGKPSRYMRVRS 60
QY 61 PEDLQCTPRRQSEGTVEAATVEVAESGITLQVQLATPGDLSCLWVKHSLGCGPHFD 120
DB 61 PEDLQCTPRRQSEGTVEAATVEVAESGITLQVQLATPGDLSCLWVKHSLGCGPHFD 120
QY 121 LQNRGIVSMALNVTTQAGEYLLHIQSERANYTVLFTVNVDRDTQLYVLRPRYFRMENO 180
DB 121 LQNRGIVSMALNVTTQAGEYLLHIQSERANYTVLFTVNVDRDTQLYVLRPRYFRMENO 180
QY 181 DALLCISGVPEPTVEVWVLCSSHRSCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
DB 181 DALLCISGVPEPTVEVWVLCSSHRSCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
QY 241 ECTKLFTIDLNOAPOSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEGSYFE 300
DB 241 ECTKLFTIDLNOAPOSTLPQLFKVGEPLWIRCKAIHVNHGFGLTWELEDKALEGSYFE 300

301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFINATSSOBEY 360
301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFINATSSOBEY 360
361 EIDPYEKFCSVRKAYPRIRCTWIFSOAFPCBORGLEDGYISKFCDHKNKPGGEYIFY 420
361 EIDPYEKFCSVRKAYPRIRCTWIFSOAFPCBORGLEDGYISKFCDHKNKPGGEYIFY 420
421 AENDDAOFTKMTNIRKKPOVLANASQASCSDDGYPLPSWTWKCDKSPNCTEIP 480
421 AENDDAOFTKMTNIRKKPOVLANASQASCSDDGYPLPSWTWKCDKSPNCTEIP 480
481 EGVNKKANRKFQOWVSSSTLNSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGFPFIQ 540
481 EGVNKKANRKFQOWVSSSTLNSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGFPFIQ 540
541 DNISFYATIGLCLPFIIVLIVLI CHYKKQPRYESQLOMIQVTPGLDNEYFVDFRDEY 600
541 DNISFYATIGLCLPFIIVLIVLI CHYKKQPRYESQLOMIQVTPGLDNEYFVDFRDEY 600
601 DLKWEFFRENLEFGKVLGSGAFGRVNNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
601 DLKWEFFRENLEFGKVLGSGAFGRVNNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
661 SELKQWTHLGHHDNI VNLGACTLSGPPVLI FEYCCYGDLLNLSRKREKPHRTWTETFK 720
661 SELKQWTHLGHHDNI VNLGACTLSGPPVLI FEYCCYGDLLNLSRKREKPHRTWTETFK 720
721 EHNFSYPTFOAHNSMPSGREGVOLHPPDLQSLGFGNSIHSEDEIEYENOKLAEBEE 780
721 EHNFSYPTFOAHNSMPSGREGVOLHPPDLQSLGFGNSIHSEDEIEYENOKLAEBEE 780
781 EDNLVTFEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
781 EDNLVTFEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
841 SDSSVVRGNARLPVKWMAPELSEGIYTIKSDVMSYGILLWEIFSLGWNYPGIPVDAN 900
841 SDSSVVRGNARLPVKWMAPELSEGIYTIKSDVMSYGILLWEIFSLGWNYPGIPVDAN 900
901 FYKLIQSGFKMEQFPYATIGYFVMSQWAFDSRKRPFPNLT3FLGCOLAEBEACIRT 960
901 FYKLIQSGFKMEQFPYATIGYFVMSQWAFDSRKRPFPNLT3FLGCOLAEBEACIRT 960
961 SIHLPKQAAPQORGGLRAQSPQOVKIHRRS 992
961 SIHLPKQAAPQORGGLRAQSPQOVKIHRRS 992

RESULT 11
US-08-222-299-2
; Sequence 2, Application US/08222299
; Patent No. 5635388
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Broz, Susan D.
; APPLICANT: Matthews, William
; APPLICANT: Zeigler, Francis C.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222.299
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 879
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-222-299-2

Query Match 96.9%; Score 5102; DB 1; Length 1000;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 968; Conservative 6; Mismatches 17; Indels 10; Gaps 2;

Qy 1 MRALAQRSDRRLLLVLSVMILETTVNQDLPVTKVLI SHENNGSSAGKFPSSYRMVRGS 60
Db 1 MRALAQRSDRRLLLVLSVMILETTVNQDLPVTKVLI SHENNGSSAGKFPSSYRMVRGS 60
Qy 61 PEDLQCTPRQSEGTVEAATVEAEGSITLQVQLATPGDLSCLWVFKHSSLGCPHF 120
Db 61 PEDLQCTPRQSEGTVEAATVEAEGSITLQVQLATPGDLSCLWVFKHSSLGCPHF 120
Qy 121 LONRGIVSMALNVTETQAGEYLLHIQSERANYTVLFTVNRDQTLVLRPPYFRKMEQ 180
Db 121 LONRGIVSMALNVTETQAGEYLLHIQSERANYTVLFTVNRDQTLVLRPPYFRKMEQ 180
Qy 181 DALLCISEGPEPTVEWVLCSSHRESCKECPAVVRKEEVLHFGTDIRCCARNALGR 240
Db 181 DALLCISEGPEPTVEWVLCSSHRESCKECPAVVRKEEVLHFGTDIRCCARNALGR 240
Qy 241 ECTKLFITDLNQAQSTLPQLFLKVGEPILWIRCKAIHVNHGFGLTWELEDALEBSYFE 300
Db 241 ESTKLFITDLNQAQSTLPQLFLKVGEPILWIRCKAIHVNHGFGLTWELEDALEBSYFE 300
Qy 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFINATSSOBEY 360
Db 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYYTCSSSKHPSQSALVTILEKGFINATSSOBEY 360
Qy 361 EIDPYEKFCSVRKAYPRIRCTWIFSOAFPCBORGLEDGYISKFCDHKNKPGGEYIFY 420
Db 361 EIDPYEKFCSVRKAYPRIRCTWIFSOAFPCBORGLEDGYISKFCDHKNKPGGEYIFY 420
Qy 421 AENDDAOFTKMTNIRKKPOVLANASQASCSDDGYPLPSWTWKCDKSPNCTEIP 480
Db 421 AENDDAOFTKMTNIRKKPOVLANASQASCSDDGYPLPSWTWKCDKSPNCTEIP 480
Qy 481 EGVNKKANRKFQOWVSSSTLNSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGFPFIQ 540
Db 481 EGVNKKANRKFQOWVSSSTLNSEAGKGLLVKCCAYNSMGTSCTETIFLNSPGFPFIQ 540
Qy 541 DNISFYATIGLCLPFIIVLIVLI CHYKKQPRYESQLOMIQVTPGLDNEYFVDFRDEY 600
Db 541 DNISFYATIGLCLPFIIVLIVLI CHYKKQPRYESQLOMIQVTPGLDNEYFVDFRDEY 600
Qy 601 DLKWEFFRENLEFGKVLGSGAFGRVNNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
Db 601 DLKWEFFRENLEFGKVLGSGAFGRVNNATAYGISTGVSIQVAVKMLKEKADSCKEALM 660
Qy 661 SELKQWTHLGHHDNI VNLGACTLSGPPVLI FEYCCYGDLLNLSRKREKPHRTWTETFK 720
Db 661 SELKQWTHLGHHDNI VNLGACTLSGPPVLI FEYCCYGDLLNLSRKREKPHRTWTETFK 720

QY 721 EHNFSYPTFOAHNSNMPGSRREVOLHPPLDQSLGFGNGSIHSEDEIEYENOKRLAESEE 780
DB 721 EHNFSYPTFOAHNSNMPGSRREVOLHPPLDQSLGFGNGSIHSEDEIEYENOKRLAESEE 780
QY 781 EDNLVLTPELDCFAQYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVVICDFGLARDIL 840
DB 781 EDNLVLTPELDCFAQYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVVICDFGLARDIL 840
QY 841 SDSSVVRGNARLPVKWMAPELSEFEGYTIKSDVMSYGILLWEIFSLGVNPPGIPVDAN 900
DB 841 SDSSVVRGNARLPVKWMAPELSEFEGYTIKSDVMSYGILLWEIFSLGVNPPGIPVDAN 900
QY 901 FYKLIQSGFKMEQPFYATEGIFVWQSCWAFDSRKRPSPNLTSLFGCOLAEAEACIRT 960
DB 901 FYKLIQSGFKMEQPFYATEGIFVWQSCWAFDSRKRPSPNLTSLFGCOLAEAEAMYNQ 960
QY 961 -----SIHLPKQAPQORGLRAQSPORQVKIHRERS 992
DB 961 MGNVPEHPSIYQNRPLSREAGS-EPPSPOAQVKIHRERS 1000

RESULT 12

US-08-434-878-2

; Sequence 2, Application US/08434878

; Patent No. 5997865

; GENERAL INFORMATION:

; APPLICANT: Bennett, Brian D.

; APPLICANT: Broz, Susan D.

; APPLICANT: Matthews, William

; APPLICANT: Zeigler, Francis C.

; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES THE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5-25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/434,878

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Hasak, Janet E.

; REGISTRATION NUMBER: 28,616

; REFERENCE/DOCKET NUMBER: 879

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1896

; TELEFAX: 415/952-9881

; TELETYPE: 910/371-7168

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1000 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-434-878-2

Query Match 96.9%; Score 5102; DB 2; Length 1000;

Best Local Similarity 96.7%; Pred. No. 0;

Matches 968; Conservative 6; Mismatches 17; Indels 10; Gaps 2;

QY 1 MRALAQRDRRLLLLVLSWMILETVTNQDLPVTKCVLISHENNGSSAGKPSRYMRVRS 60

|||||

DB 1 MRALAQRDRRLLLLVLSWMILETVTNQDLPVTKCVLISHENNGSSAGKPSRYMRVRS 60
QY 61 PEDLOCTPRRQSEGTVEAATVEVAESGSIITLQVOLATPGDLSCLWVFKHSSILGQCPHED 120
DB 61 PEDLOCTPRRQSEGTVEAATVEVAESGSIITLQVOLATPGDLSCLWVFKHSSILGQCPHED 120
QY 121 LQNRGIVSMALINVTETQAGEYLLHIQSERANYTVLFTVNVVDTQLYVLRPRYFRKMNQ 180
DB 121 LQNRGIVSMALINVTETQAGEYLLHIQSEAAANYTVLFTVNVVDTQLYVLRPRYFRKMNQ 180
QY 181 DALLCISGVPPEPTVEWVLCSSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
DB 181 DALLCISGVPPEPTVEWVLCSSHRESCKEKGPAVVRKEKVLHFGTDIRCCARNALGR 240
QY 241 ECTKLTFTDLNQAPOSTLPQLFKVGEPLWIRCKAIHVNHGFLTWELDKALEGSEYFE 300
DB 241 ESTKLTFTDLNQAPOSTLPQLFKVGEPLWIRCKAIHVNHGFLTWELDKALEGSEYFE 300
QY 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSSQSALVTILEKGFINATSSQEEY 360
DB 301 MSTYSTNRTMIRILLAFVSSVGRNDTGYTTCSSSKHPSSQSALVTILEKGFINATSSQEEY 360
QY 361 EIDPYEKECFSVRFKAYPRIRCTWIFSOASPPCEORGLDGYISIKPCDHKNKPGEYIFY 420
DB 361 EIDPYEKECFSVRFKAYPRIRCTWIFSOASPPCEORGLDGYISIKPCDHKNKPGEYIFY 420
QY 421 AENDDAQFTKMTLNIKKPOVLANASQASCSDDGYPPLSWTWKCKSDKSPNCTEETIP 480
DB 421 AENDDAQFTKMTLNIKKPOVLANASQASCSDDGYPPLSWTWKCKSDKSPNCTEETIP 480
QY 481 EGVNKKANRKFVFGQWSSSTLNSEAGKGLLVKCCAYNSMGTSCTETFLNSPGFPFPIQ 540
DB 481 EGVNKKANRKFVFGQWSSSTLNSEAGKGLLVKCCAYNSMGTSCTETFLNSPGFPFPIQ 540
QY 541 DNISFYATIGLCLPIVVLIVLI CHYKQKQRYESQLOMIQVTPGLDNEYFYVDFRDVEY 600
DB 541 DNISFYATIGLCLPIVVLIVLI CHYKQKQRYESQLOMIQVTPGLDNEYFYVDFRDVEY 600
QY 601 DLKWEFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIQVAVKMLKEKADSCKEALM 660
DB 601 DLKWEFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIQVAVKMLKEKADSCKEALM 660
QY 661 SELKXMTLGHHDNIVNLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTETPK 720
DB 661 SELKXMTLGHHDNIVNLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTETPK 720
QY 721 EHNFSYPTFOAHNSNMPGSRREVOLHPPLDQSLGFGNGSIHSEDEIEYENOKRLAESEE 780
DB 721 EHNFSYPTFOAHNSNMPGSRREVOLHPPLDQSLGFGNGSIHSEDEIEYENOKRLAESEE 780
QY 781 EDNLVLTPELDCFAQYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVVICDFGLARDIL 840
DB 781 EDNLVLTPELDCFAQYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVVICDFGLARDIL 840
QY 841 SDSSVVRGNARLPVKWMAPELSEFEGYTIKSDVMSYGILLWEIFSLGVNPPGIPVDAN 900
DB 841 SDSSVVRGNARLPVKWMAPELSEFEGYTIKSDVMSYGILLWEIFSLGVNPPGIPVDAN 900
QY 901 FYKLIQSGFKMEQPFYATEGIFVWQSCWAFDSRKRPSPNLTSLFGCOLAEAEACIRT 960
DB 901 FYKLIQSGFKMEQPFYATEGIFVWQSCWAFDSRKRPSPNLTSLFGCOLAEAEAMYNQ 960
QY 961 -----SIHLPKQAPQORGLRAQSPORQVKIHRERS 992
DB 961 MGNVPEHPSIYQNRPLSREAGS-EPPSPOAQVKIHRERS 1000

RESULT 13

PCT-US95-03718-2

; Sequence 2, Application PC/TUS9503718

; GENERAL INFORMATION:

; APPLICANT: GENENTECH, INC.

; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES T

;
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/03718
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wendy M. Lee
 ; REGISTRATION NUMBER: 00,000
 ; REFERENCE/DOCKET NUMBER: 879PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-1994
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1000 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; PCT-US95-03718-2

Query Match 96.9%; Score 5102; DB 5; Length 1000;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 968; Conservative 6; Mismatches 17; Indels 10; Gaps 2;

QY	1	MRALAQRDRRLLLVLSVILETVNODLPVVKVLI SHENNGSAGKPSRYMVRGS	60
DB	1	MRALAQRDRRLLLVLSVILETVNODLPVVKVLI SHENNGSAGKPSRYMVRGS	60
QY	61	PEDLOCTPRQSEGVYEAATVEVAESGSIITLQVLA TPGLDGLCLWVFKHSLCCQPHFD	120
DB	61	PEDLOCTPRQSEGVYEAATVEVAESGSIITLQVLA TPGLDGLCLWVFKHSLCCQPHFD	120
QY	121	LQNRGIVSMALNVTTQAGEYLLHIOSE RANYTVLFTVNVVDTQLYLRPRYPRKVMNQ	180
DB	121	LQNRGIVSMALNVTTQAGEYLLHIOSE RANYTVLFTVNVVDTQLYLRPRYPRKVMNQ	180
QY	181	DALLCISEGVPEPTVEVWLCSHRESCKEKGPAVRKEEVLHFLGTDIRCCARNALGR	240
DB	181	DALLCISEGVPEPTVEVWLCSHRESCKEKGPAVRKEEVLHFLGTDIRCCARNALGR	240
QY	241	ECTKLFTIDLNQAPQSTLPOLFLKVGPELWIRCKAIHVNHGFGLTWELEDALEEGSYFE	300
DB	241	ESTKLFTIDLNQAPQSTLPOLFLKVGPELWIRCKAIHVNHGFGLTWELEDALEEGSYFE	300
QY	301	MSYVSTNRTMIRILLAFVSSVGRNDTGYTCSGSKHPSQSALVTILEKGFNATSSQEEY	360
DB	301	MSYVSTNRTMIRILLAFVSSVGRNDTGYTCSGSKHPSQSALVTILEKGFNATSSQEEY	360
QY	361	EIDPYEKFCSVRPKAYPRIRCTWIFSOASPCCQRLGEGYSISKFDHKNKPGGEVIFY	420
DB	361	EIDPYEKFCSVRPKAYPRIRCTWIFSOASPCCQRLGEGYSISKFDHKNKPGGEVIFY	420
QY	421	AENDDAQFTKMTFLINIRKKPOVLNANASQASCSGDPPLPSMTWTKCSKSPNCTEIP	480
DB	421	AENDDAQFTKMTFLINIRKKPOVLNANASQASCSGDPPLPSMTWTKCSKSPNCTEIP	480
QY	481	EGVMNKKANRKFQGWSSSTLNMSEAGKGLLVKCCAYNSMGTSCTIFLNSPGFPFFFIQ	540

DB	481	EGVMNKKANRKFQGWSSSTLNMSEAGKGLLVKCCAYNSMGTSCTIFLNSPGFPFFFIQ	540
QY	541	DNISFYATIGLCLPFIWLVILVILCHYKQFRYESOLOMQVTQPLDNEFYVDPRDYEY	600
DB	541	DNISFYATIGLCLPFIWLVILVILCHYKQFRYESOLOMQVTQPLDNEFYVDPRDYEY	600
QY	601	DLKWEFPRENLEFGKVLGSGAFGRVMNATAYGISTGVSIQAVKMLKEKADSCKEKALM	660
DB	601	DLKWEFPRENLEFGKVLGSGAFGRVMNATAYGISTGVSIQAVKMLKEKADSCKEKALM	660
QY	661	SELKMMTHLGHNDINVLIGACTLSGVPVLIPEYCCYGDLLNLRSKREKPHRTWTIFK	720
DB	661	SELKMMTHLGHNDINVLIGACTLSGVPVLIPEYCCYGDLLNLRSKREKPHRTWTIFK	720
QY	721	EHNFSSYPTFOAHSNNSMPSGSRVQLHPPDLQSLSGFNNGSIHSEDETEYENQKLAEEEE	780
DB	721	EHNFSSYPTFOAHSNNSMPSGSRVQLHPPDLQSLSGFNNGSIHSEDETEYENQKLAEEEE	780
QY	781	EDLNVLTFEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL	840
DB	781	EDLNVLTFEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL	840
QY	841	SDSSYVVRGNARLPVKWMAPESLPEGIYTIKSDVWSYGILLWEIFSLGVNPPYGPVVDAN	900
DB	841	SDSSYVVRGNARLPVKWMAPESLPEGIYTIKSDVWSYGILLWEIFSLGVNPPYGPVVDAN	900
QY	901	FYKLIOSGFKWEOPFYVATEGIYFVMOSWAFDSRKRPSFNLSFLGCOLAEAEACIRT	960
DB	901	FYKLIOSGFKWEOPFYVATEGIYFVMOSWAFDSRKRPSFNLSFLGCOLAEAEACIRT	960
QY	961	-----SIHLPKQAAPQOGRGLRAQSPQROVKIHRERS 992	
DB	961	MCGNVPEHPHSIQNRRLPSREAGS-BPPSPQAQVKIHRERS 1000	

RESULT 14
 US-08-222-299-4
 ; Sequence 4, Application US/08222299
 ; Patent No. 5635388
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, Brian D.
 ; APPLICANT: Broz, Susan D.
 ; APPLICANT: Matthews, William
 ; APPLICANT: Zeigler, Francis C.
 ; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES T
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/222,299
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hasak, Janet E.
 ; REGISTRATION NUMBER: 28,616
 ; REFERENCE/DOCKET NUMBER: 879
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-1896
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 993 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-222-299-4

Query Match 84.3%; Score 4436.5; DB 1; Length 993;
Best Local Similarity 84.0%; Pred. NO. 0;
Matches 836; Conservative 59; Mismatches 87; Indels 13; Gaps 4;

Qy 1 MEALAQRDRRLILLVLSVMTLEVTNODLPVVKVLSHENNGSSACKPSRYMVRGS 60
Db 1 MPALA-RDGGQPLLLVFSAMIFGTITNODLPVVKVLSHENNGSSACKPSRYMVRGS 59
Qy 61 PEDLOCTPRRQSEGVYEAATVEAEGSITLQVOLATPGDLSCLWVFKHSSLGCPHF 120
Db 60 PEDLGCALRPQSGGVYEAATAVEVDVSITLQVLDPAGNLSCLWVFKHSSLNCPHF 119
Qy 121 LQNRGIVSMALNVTTQAGEYLLHIQSERANYTLFTVNVDRDTQLYLRRPYFRKMNQ 180
Db 120 LQNRGWSMVLKMTETQAGEYLLFIQSEATNYTLFTVSIINTLLYLRRPYFRKMNQ 179
Qy 181 DALLCISEGVPEPTVEWVLCSSHRSCKEESPAVVKKEKVLHFLPGTDIRCCARNALGR 240
Db 180 DALVCISESVPEPIVEWVLCDSQGESCKEESPAVVKKEKVLHFLPGMDIRCCARNELGR 239
Qy 241 ECTKLFTIDLNOAPOSTLPOLFLKGEPLWIRCKAIVHNHGFGLTWELDKALEBSYFE 300
Db 240 ECTRLFTIDLNOTPOTLPOLFLKGEPLWIRCKAIVHNHGFGLTWELDKALEBSYFE 299
Qy 301 MSTYSTNRMTIRILAFVSSVGRNDTGYTSCSSKHPQSALVTILEKGFINATSSQBEY 360
Db 300 MSTYSTNRMTIRILAFVSSVARNDTGYTSCSSKHPQSALVTIVEKGFINATSSDEY 359
Qy 361 EIDPYEKECFSVRFKAYPRICWTWIFSQASPCBQBLEGHSISKFCDHKNKPGYEIPY 420
Db 360 EIDQYEEFCFSVRFKAYPQIRCTWTWIFSRKSPFCEQGLDNGYSISKFCNHKQPGYEIPH 419
Qy 421 AENDDAQTKMPTLNIRKPKVLANASQASCSGDPVLPSTWTKCSKSPNCTEIP 480
Db 420 AENDDAQTKMPTLNIRKPKVLANASQASCSGDPVLPSTWTKCSKSPNCTEIT 479
Qy 481 EGVNKKANRVFGQWSSSTLNMSEAGKLLVKCAVNSMGTSCETPLNSPGFPFPIQ 540
Db 480 EGVNKKANRVFGQWSSSTLNMSEAIKGLVKCAVNSMGTSCETPLNSPGFPFPIQ 539
Qy 541 DNISFYATIGCLPIVILVILCHIKYKQRYESQLOM QVTGPDNEFYFVDFREY 600
Db 540 DNISFYATIGVCLLPIVILVILCHIKYKQRYESQLOM QVTGPDNEFYFVDFREY 599
Qy 601 DLKWEFFRENLEFGVKGAGFVWVNTAYGISTGVSIQVAVKMKKADSCKEALM 660
Db 600 DLKWEFFRENLEFGVKGAGFVWVNTAYGISTGVSIQVAVKMKKADSCKEALM 659
Qy 661 SELKMTLGHHDNIVNLGACTLSGPVYLPIEYCYGDLNLYRSKREKPHRTWTIEFK 720
Db 660 SELKMTQLGSHENIVNLGACTLSGPVYLPIEYCYGDLNLYRSKREKPHRTWTIEFK 719
Qy 721 EHNFSYPTFOAHSSNMPGSEVOLHPLDLSGFNGNSHSEDEIEYENOKRLAESEE 780
Db 720 EHNFSYPTFOAHSSNMPGSEVOLHPLDLSGFNGNSHSEDEIEYENOKRLAESEE 777
Qy 781 EDLNVLTPEDLCCFAYQVAKGMEFLFSCVHRDLAARNVLTGKVKVLCDFGLARDIL 840
Db 778 EDLNVLTPEDLCCFAYQVAKGMEFLFSCVHRDLAARNVLTGKVKVLCDFGLARDIM 837
Qy 841 SDSSVVRGNARLPVKWMAPESLFEGITIKSDVMSYGLLWEIFSLGNVPYGPVVDAN 900
Db 838 SDSSVVRGNARLPVKWMAPESLFEGITIKSDVMSYGLLWEIFSLGNVPYGPVVDAN 897
Qy 901 FYKLIQSGFKMEQPYATEGYIFVWQSWAFDRSRKPSFPNLTSLFGCOLABEAEACIRT 960
Db 900 FYKLIQSGFKMEQPYATEGYIFVWQSWAFDRSRKPSFPNLTSLFGCOLABEAEACIR 956

Db 898 FYKLIQSGFKMEQPYATEGYIFVWQSWAFDRSRKPSFPNLTSLFGCOLABEAEAMY- 956
Qy 961 SIHLPKQAAP-----QORGGRAQSPQROVK 986
Db 957 NVDPGVSECPHTYQNRPRPFSREMDLGLLSPOAQVE 991

RESULT 15
US-08-434-878-4
Sequence 4, Application US/08434878
Patent No. 5997855
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Broz, Susan D.
APPLICANT: Matthews, William
APPLICANT: Zeigler, Francis C.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/434,878

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Hasak, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: 879

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1896

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 993 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-434-878-4

Query Match 84.3%; Score 4436.5; DB 2; Length 993;

Best Local Similarity 84.0%; Pred. NO. 0;

Matches 836; Conservative 59; Mismatches 87; Indels 13; Gaps 4;

Qy 1 MEALAQRDRRLILLVLSVMTLEVTNODLPVVKVLSHENNGSSACKPSRYMVRGS 60
Db 1 MPALA-RDGGQPLLLVFSAMIFGTITNODLPVVKVLSHENNGSSACKPSRYMVRGS 59
Qy 61 PEDLOCTPRRQSEGVYEAATVEAEGSITLQVOLATPGDLSCLWVFKHSSLGCPHF 120
Db 60 PEDLGCALRPQSGGVYEAATAVEVDVSITLQVLDPAGNLSCLWVFKHSSLNCPHF 119
Qy 121 LQNRGIVSMALNVTTQAGEYLLHIQSERANYTLFTVNVDRDTQLYLRRPYFRKMNQ 180
Db 120 LQNRGWSMVLKMTETQAGEYLLFIQSEATNYTLFTVSIINTLLYLRRPYFRKMNQ 179
Qy 181 DALLCISEGVPEPTVEWVLCSSHRSCKEESPAVVKKEKVLHFLPGTDIRCCARNALGR 240
Db 180 DALVCISESVPEPIVEWVLCDSQGESCKEESPAVVKKEKVLHFLPGMDIRCCARNELGR 239
Qy 241 ECTKLFTIDLNOAPOSTLPOLFLKGEPLWIRCKAIVHNHGFGLTWELDKALEBSYFE 300

```
Db 240 ECTRLFTIDLNOTPOTTLPOLFLKVBPLWIRCKAVHNRGFLTWELNKALEEGNYFE 299
Qy 301 MSTYSTNRWTIRILLAAVSSVGRNDTCYTCSSSKHPSQSALVTILEKGFINATSSOEY 360
Db 300 MSTYSTNRWTIRILLAFVSSVARNDTCYTCSSSKHPSQSALVTIVEKGFINATSSB 359
Qy 361 EIDPYEKFCFSVRPKAYPRIRCTWIFSOAGFPCCQRGLDGYISIKFCDHKNKPGYIFY 420
Db 360 EIDPYEFCFSVRPKAYPQIRCTWTFSRKFPCEQKGLDNGYSISKFCNKHQGEYIFH 419
Qy 421 AENDDAQFTKMTLNIRKXQVLANASASQASCSDDGYPLPSWTWKKCSKSPNCTEIP 480
Db 420 AENDDAQFTKMTLNIRKXQVLAASASQASCSDDGYPLPSWTWKKCSKSPNCTEIT 479
Qy 481 EGVNWKANRKFQOWTSSSTLNMSBAGLLVKCCAYNSMTSCTIFLNSPGPPFIQ 540
Db 480 EGVNWRKANRKFQOWTSSSTLNMSBAGLLVKCCAYNSLGTSETILLNSPGPPFIQ 539
Qy 541 DNISFYATIGLCLPFIIVLIVLICHKYKOPRYESQLOMIQVOTGPDNEYFYVDFRDY 600
Db 540 DNISFYATIGVCLLFIIVLILILICHKYKOPRYESQLOMIQVOTGSSDNEYFYVDFREY 599
Qy 601 DLKWEPPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIOQAVKMLKEXKADSCKEALM 660
Db 600 DLKWEPPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIOQAVKMLKEXKADSSEREALM 659
Qy 661 SELKOWTHLGHNDINVLGACTLSGPVYLIFEYCCYGDLLNLYRSKREKPHRTWTIFK 720
Db 660 SELKOWTQLGSHENIVNLLGACTLSGPYILIFEYCCYGDLLNLYRSKREKPHRTWTIFK 719
Qy 721 EHNFSYPTFOAHNSNMPGSRVQLHPPLDOLSGFNGNSHSEDEIYEYENOKELABEEE 780
Db 720 EHNFSYPTFOAHNSNMPGSRVQLHPDSDQISGLHNSPHSEDEIYEYENOKEL--EEE 777
Qy 781 EDLNLVTFEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840
Db 778 EDLNLVTFEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIM 837
Qy 841 SDSSYVVRGNARLPVKWAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
Db 838 SDSSYVVRGNARLPVKWAPESLFEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 897
Qy 901 FYKLIQSGFKMEOPFYATEGIYFVMSQWAFDSRKRPSFPNLTSLGCOLAAEAEACIRT 960
Db 898 FYKLIQSGFKMEOPFYATEEYIYIIMQSCWAFDSRKRPSFPNLTSLGCOLAAEAEAMYQ- 956
Qy 961 SIHLPKQAAP-----QORGGRLAQSPORQVK 986
Db 957 NVDGVSCEPHTYQNRPRFSPREMDLGLLSPOAQVE 991
```

Search completed: May 24, 2003, 17:01:06
Job time : 18.9929 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:53:00 ; Search time 34.5174 Seconds
(without alignments)
2765.606 Million cell updates/sec

Title: US-09-919-408-4

Perfect score: 5274

Sequence: 1 MPALARDAGTVPLLVVFSAM.....PFSREMDLGLLSPOAQVEDS 993

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5238	99.3	993	2 A36873	protein-tyrosine k
2	4533.5	86.0	1000	2 S18827	Flt3 protein - mou
3	4429.5	84.0	992	2 A39931	protein-tyrosine k
4	1286	24.4	977	2 I45877	protein-tyrosine k
5	1266	24.0	975	1 TWMSKT	protein-tyrosine k
6	1263.5	24.0	978	1 A49814	protein-tyrosine k
7	1251	23.7	976	1 TVHUKT	protein-tyrosine k
8	1226	23.2	954	2 I51703	C-kit-related kina
9	1225.5	23.2	980	1 TVCTMD	macrophage colony-
10	1218	23.1	941	1 TVMMD	protein-tyrosine k
11	1216.5	23.1	972	1 TVHUMD	macrophage colony-
12	1215	23.0	960	1 JN0677	protein-tyrosine k
13	1213	23.0	975	2 T30816	macrophage colony-
14	1194	22.6	978	2 S16385	macrophage colony-
15	1183.5	22.4	976	1 TVMSMD	macrophage colony-
16	1176	22.3	1088	1 PRTGA	platelet-derived g
17	1166	22.1	1089	1 PFHUGA	platelet-derived g
18	1146	21.7	1089	1 S33727	platelet-derived g
19	1128	21.4	1087	2 I51552	platelet-derived g
20	1105.5	21.0	1098	1 PWSRRB	platelet-derived g
21	1086.5	20.6	1106	1 PFHUGB	platelet-derived g
22	1080	20.5	1048	2 T30815	platelet-derived g
23	992	18.8	790	1 FOMVHZ	gag-kit polypepti
24	990	18.8	1338	2 S09982	protein-tyrosine k
25	959.5	18.2	1333	2 I78875	receptor tyrosine
26	956	18.1	1336	2 I60598	Fit-1 tyrosine kin
27	944.5	17.9	1356	2 JC1402	protein-tyrosine k
28	939.5	17.8	1330	2 S49010	embryonic receptor
29	935	17.7	1348	2 S51656	vascular endotheli

ALIGNMENTS

RESULT 1

A36873

protein-tyrosine kinase (EC 2.7.1.112) STK-1 precursor - human

N:Alternate names: stem cell tyrosine kinase 1

C:Species: Homo sapiens (man)

C>Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 04-Feb-2000

C:Accession: A36873

R:Small, D.; Levenstein, M.; Kim, E.; Carow, C.; Amin, S.; Rockwell, P.; Witte, L.; F

Proc. Natl. Acad. Sci. U.S.A. 91, 459-463, 1994

A:Title: STK-1, the human homolog of Flk-2/Flt-3, is selectively expressed in CD34 (+)

A:Reference number: A36873; MUID:94119906; PMID:7507245

A:Accession: A36873

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-993 <SMA>

A:Cross-references: GB:U02687

A>Note: in the authors translation, an additional residue Ala is shown after 420-Ala

C:Genetics:

A:Map position: 13q12

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hon

C:Keywords: ATP; glycoprotein; phosphotransferase; transmembrane protein; tyrosine-Sg

F:608-950/Domain: protein kinase homology <KIN>

F:616-624/Region: protein kinase ATP-binding motif

Query Match 99.3%; Score 5238; DB 2; Length 993;

Best Local Similarity 99.7%; Pred. No. 2.3e-247;

Matches 991; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVTKCVLINHKNDSSVGKSSSYPMVSESP 60

Db 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVTKCVLINHKNDSSVGKSSSYPMVSESP 60

QY 61 EDLGCALRQSSGTVYAAAEVDVSASITLQVLDPAGNISCLVYFKHSSLCQPHFDL 120

Db 61 EDLGCALRQSSGTVYAAAEVDVSASITLQVLDPAGNISCLVYFKHSSLCQPHFDL 120

QY 121 QNRGVVSVILKMTETQAGEYLLFTQSEATNYTILFTVSRITLLTLRPPYRKMEQD 180

Db 121 QNRGVVSVILKMTETQAGEYLLFTQSEATNYTILFTVSRITLLTLRPPYRKMEQD 180

QY 181 ALVCISESVPFIVEVNLCDQSGCKEESPAVVKKEKVLHFLGTDIRCCARNEGRE 240

Db 181 ALVCISESVPFIVEVNLCDQSGCKEESPAVVKKEKVLHFLGTDIRCCARNEGRE 240

QY 241 CTRLFITDLNQPTQTLPOLFLKVGEPILWIRCKAVHNHFGTLWELENKALEEGNYFEM 300

Db 241 CTRLFITDLNQPTQTLPOLFLKVGEPILWIRCKAVHNHFGTLWELENKALEEGNYFEM 300

QY 301 STYSTNRTMIRILFAFVSSVARNDGYTCSSSKHPQSQALVTIVGKFINATNSSEDEYE 360

Db 301 STYSTNRTMIRILFAFVSSVARNDGYTCSSSKHPQSQALVTIVGKFINATNSSEDEYE 360

QY 361 IDQYEEFCFSVRKAYPOIRCTWTSRKSFPCEQKGLDNGYSISKFNHKKHQPGEYIFH- 419
 DB 361 IDQYEEFCFSVRKAYPOIRCTWTSRKSFPCEQKGLDNGYSISKFNHKKHQPGEYIFH- 420
 QY 420 AENDDAQFTKMTFLNIRRKPOVLAEASASQASCFSDGYPLPSWTWKCSKSPNCTEIT 479
 DB 421 AENDDAQFTKMTFLNIRRKPOVLAEASASQASCFSDGYPL-SWTWKCSKSPNCTEIT 479
 QY 480 EGVWNRKANRVKFGQWSSSTLNMSEAIGFLVKCCAYNSLGTSCETILLNSPGPPFIQ 539
 DB 480 EGVWNRKANRVKFGQWSSSTLNMSEAIGFLVKCCAYNSLGTSCETILLNSPGPPFIQ 539
 QY 540 DNISVATIGVCLLFIIVLTLIHKYKQFVYESQLOQVQVTSDDNEFYFVDFREY 599
 DB 540 DNISVATIGVCLLFIIVLTLIHKYKQFVYESQLOQVQVTSDDNEFYFVDFREY 599
 QY 600 DLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLKEKADSSEREALM 659
 DB 600 DLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLKEKADSSEREALM 659
 QY 660 SELKMTQLGSHENIVNLLGACTLSGPIYLIPEYCCYGLLNLVLRSKRKFHRTWTETIFK 719
 DB 660 SELKMTQLGSHENIVNLLGACTLSGPIYLIPEYCCYGLLNLVLRSKRKFHRTWTETIFK 719
 QY 720 EHNFSFYPTFQSHPNSSMPGSRVQIHDPDSDOI SGLHGNFSHSEDEIEYENOKRLEEBED 779
 DB 720 EHNFSFYPTFQSHPNSSMPGSRVQIHDPDSDOI SGLHGNFSHSEDEIEYENOKRLEEBED 779
 QY 780 LNVLTFFEDLLCFAYQVAKMEFLFKSCVHRDLAARNVLVTHGKVKIKCDFGLARDIMSD 839
 DB 780 LNVLTFFEDLLCFAYQVAKMEFLFKSCVHRDLAARNVLVTHGKVKIKCDFGLARDIMSD 839
 QY 840 SNYVVRGNARLPVKWMAPELFEIYIKSDVMSYGILLWEIFSLGVNYPGIPVDANFY 899
 DB 840 SNYVVRGNARLPVKWMAPELFEIYIKSDVMSYGILLWEIFSLGVNYPGIPVDANFY 899
 QY 900 KLQNGFKMDQPPYATEEIIYIMOSCAWFDNRKRPFNLTSLFLGCOLADAEAMYNQVD 959
 DB 900 KLQNGFKMDQPPYATEEIIYIMOSCAWFDNRKRPFNLTSLFLGCOLADAEAMYNQVD 959
 QY 960 GRVSECPHYQNRPPFSREMDLGLLSPOAQVEDS 993
 DB 960 GRVSECPHYQNRPPFSREMDLGLLSPOAQVEDS 993
 RESULT 2
 S18827
 Flt3 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
 C:Accession: S18827
 R:Rosnet, O.; Marchetto, S.; deLapeyriere, O.; Birnbaum, D.
 Oncogene 6, 1641-1650, 1991
 A:Title: Murine Flt3, a gene encoding a novel tyrosine kinase receptor of the PDGFR/CSF1
 A:Reference number: S18827; PMID:92019834; PMID:1656368
 A:Accession: S18827
 A:Molecule type: mRNA
 A:Residues: 1-1000 <ROS>
 A:Cross-references: EMBL:X59398; NID:g50978; PID:CAA42041.1; PID:g50979
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C:Keywords: ATP
 F:609-953/Domain: protein kinase homology <KIN>
 F:617-625/Region: protein kinase ATP-binding motif
 Query Match 86.0%; Score 4533.5; DB 2; Length 1000;
 Best Local Similarity 85.6%; Pred. No. 4.1e-213;
 Matches 851; Conservative 56; Mismatches 84; Indels 3; Gaps 2;
 QY 1 MPALA-RDAGTVPLLVVFSAMIFGTTNQDLPIKVLINHNKNDSSGVKSSYPNVSES 59
 DB 1 MRALAQRSDRLALLVLSVMILEVTNQDLPIKVLINSHENNNGSAGKPSYRMVRGS 60
 QY 60 PEDLGALRPQSSGTVYEAAYVEVDVSASITLQVLVDAPGNISCLWVFKHSLNCQHPFD 119

DB 61 PEDLQCTPRRQSEGVYEAATVEAESGSIITLQVLATPGDLSCLWVFKHSLGQCPHFD 120
 QY 120 LQNRGVSMVILKMTETQAGYLLFIQSEATNYTTLFTVSRNTLLYTLRRPYEKKMENO 179
 DB 121 LQNRGIVSMATLNTETQAGYLLFIQSEAAANYTVLFTVNRVDTQLYVLRPFYFRMENO 180
 QY 180 DALVCISSEVPPIVWVLCDSQGESCKEESPAVVKKEKVLHFGTDIRCCARNELR 239
 DB 181 DALLCISGVPEPTVWVLCSSHRESCKEESPAVVKKEKVLHFGTDIRCCARNELR 240
 QY 240 ECTRLFTIDLNQTPOTLPQLFLKVGEPILWIRCKAVHVNHGGLTWELNKALEBGNYPE 299
 DB 241 ESTKLFTIDLNAQPOSTLPQLFLKVGEPILWIRCKAVHVNHGGLTWELNKALEBGNYPE 300
 QY 300 MSTYSTNRTMIRILPAFVSSVARNDTGYTTCSSSKHPSQSALVTIVGKFINATNSSEY 359
 DB 301 MSTYSTNRTMIRILPAFVSSVGRNDTYTTCSSSKHPSQSALVTILEKFINATSSQEEY 360
 QY 360 EIDQYEEFCFSVRKAYPOIRCTWTSRKSFPCEQKGLDNGYSISKFNHKKHQPGEYIFH 419
 DB 361 EIDPYEKFCSVRKAYPRIRCTWTFPSQASFPCEQKGLDNGYSISKFNHKKHQPGEYIFH 420
 QY 420 AENDDAQFTKMTFLNIRRKPOVLAEASASQASCFSDGYPLPSWTWKCSKSPNCTEIT 479
 DB 421 AENDDAQFTKMTFLNIRRKPOVLAEASASQASCFSDGYPLPSWTWKCSKSPNCTEIT 480
 QY 480 EGVWNRKANRVKFGQWSSSTLNMSEAIGFLVKCCAYNSLGTSCETILLNSPGPPFIQ 539
 DB 481 EGVWNRKANRVKFGQWSSSTLNMSEAIGFLVKCCAYNSLGTSCETILLNSPGPPFIQ 540
 QY 540 DNISVATIGVCLLFIIVLTLIHKYKQFVYESQLOQVQVTSDDNEFYFVDFREY 599
 DB 541 DNISVATIGVCLLFIIVLTLIHKYKQFVYESQLOQVQVTSDDNEFYFVDFREY 600
 QY 600 DLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLKEKADSSEREALM 659
 DB 601 DLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLKEKADSSEREALM 660
 QY 660 SELKMTQLGSHENIVNLLGACTLSGPIYLIPEYCCYGLLNLVLRSKRKFHRTWTETIFK 719
 DB 661 SELKMTQLGSHENIVNLLGACTLSGPIYLIPEYCCYGLLNLVLRSKRKFHRTWTETIFK 720
 QY 720 EHNFSFYPTFQSHPNSSMPGSRVQIHDPDSDOI SGLHGNFSHSEDEIEYENOKRLEEBED 777
 DB 721 EHNFSFYPTFQSHPNSSMPGSRVQIHDPDLQSLGNGNSHSEDEIEYENOKRLEEBED 780
 QY 778 EDLNVLTFFEDLLCFAYQVAKMEFLFKSCVHRDLAARNVLVTHGKVKIKCDFGLARDIM 837
 DB 781 EDLNVLTFFEDLLCFAYQVAKMEFLFKSCVHRDLAARNVLVTHGKVKIKCDFGLARDIL 840
 QY 838 SDSNYVVRGNARLPVKWMAPELFEIYIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 897
 DB 841 SDSNYVVRGNARLPVKWMAPELFEIYIKSDVMSYGILLWEIFSLGVNYPGIPVDAN 900
 QY 898 FYKLQNGFKMDQPPYATEEIIYIMOSCAWFDNRKRPFNLTSLFLGCOLADAEAMYNQ 957
 DB 901 FYKLQNGFKMDQPPYATEEIIYIMOSCAWFDNRKRPFNLTSLFLGCOLADAEAMYNQ 960
 QY 958 VDGVRSECPHYQNRPPFSREMDLGLLSPOAQVE 991
 DB 961 MGNVPEHPSIYQNRPPFSREMDLGLLSPOAQVK 994
 RESULT 3
 A39931
 protein-tyrosine kinase (BC 2.7.1.112) flk-2, hematopoietic - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 04-Feb-2000
 C:Accession: A39931
 R:Matthews, W.; Jordan, C.T.; Wiegand, G.W.; Pardoll, D.; Lemischka, I.R.
 Cell 65, 1143-1152, 1991
 A:Title: A receptor tyrosine kinase specific to hematopoietic stem and progenitor cel

A;Reference number: A39931; MUID:91292518; PMID:1648448

A;Accession: A39931

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-992 <MAT>

A;Cross-references: GB:M64689; NID:g193327; PIDN:AAA37634.1; PID:g193328

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki

F;609-953/Domain: protein kinase homology <KIN>

F;617-625/Region: protein kinase ATP-binding motif

Query Match 84.0%; Score 4429.5; DB 2; Length 992;
Best Local Similarity 84.1%; Pred. No. 4.6e-208;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

Qy 1 MPALA-RDAGTVPLLVFSGAMIFGITNODLPVVKVLINHNKNDSSVGKSSSPYMWVS 59

Db 1 MRALLQRDRRLLLVLLVSLVETVNTNODLPVVKVLISHENNGSSACKPSRYMVG 60

Qy 60 PEDLGCALRPQSSGTYEAAAVEVDVSAITLQVLVDAPGNISCLMVFKHSLNCPHF 119

Db 61 PEDLOCTPRQSEGTVEAATVEAESGSTITLQVLATPGDLSCLVFKHSLGCGPH 120

Qy 120 LQNRGVSVMLKMTQTQAGEVLLFIQSEATNYTLFTVSIENLTLYTLRRPYFRK 179

Db 121 LQNRGIVSMALNVTETQAGEVLLFIQSERANYTLFTVNRDTQLVLRPYFRK 180

Qy 180 DALVCISVPPIVEVWLCDGSGCKEESPAVVKKEKVLHELPGTDIRCCARNELGR 239

Db 181 DALLCISEGVPEPTVEVWLCSHRSCKEEGPAVVKKEKVLHELPGTDIRCCARN 240

Qy 240 ECTRLFTDLNQTPTTLPLQLKVGPELWIRCKAVHVNHGFLTWELNKALEEGN 299

Db 241 ECTKLTLDLQAQPOSTLPQLFKVGPELWIRCKAIHVNHGFLTWELNKALEEG 300

Qy 300 MSTYSTNTRMIRILPAFVSGVARNDGYTSCSSKHPQSALVTIVGKGFINATNS 359

Db 301 MSTYSTNTRMIRILAFVSGVRNDGYTSCSSKHPQSALVTILEKGFINATNS 360

Qy 360 EIDQVEECFVSVRKAYPOIRCTWTFSRKSFPCEQKGLDNGYSIKFCNKHQPG 419

Db 361 EIDPYKECFVSVRKAYPIRCTWTFSPCEQKGLDNGYSIKFCNKHQPGYIIF 420

Qy 420 AENDDAQFTKMTLNIRRPQVLAEASQASCFSDGYPLPMTWKKCKDKSPNCTEE 479

Db 421 AENDDAQFTKMTLNIRKPQVLANASQASCSGSDGYPLPMTWKKCKDKSPNCT 480

Qy 480 EGVNWKANRKYFGQWVSSSTLNMSAIGFLVKCCAYNSLGTSCETILLNSGPP 539

Db 481 EGVNWKANRKYFGQWVSSSTLNMSAIGLLVKCCAYNSMGTSCTIFLNSGPP 540

Qy 540 DNISFYATIGVCLLFTVLTLLIHKYKOPRYESOLQWQVQTGSSDNEYFYVD 599

Db 541 DNISFYATIGLCLPFTVLTLLIHKYKOPRYESOLQWQVGTPLDNEYFYVD 600

Qy 600 DLKWFPPRENLEFGVLGSAFGKVNATAYGISKTGVSIOAVKMLKEKADSSRE 659

Db 601 DLKWFPPRENLEFGVLGSGAFGRVNNATAYGISKTGVSIOAVKMLKEKADS 660

Qy 660 SELKQMTQLGSHENIVNLGACTLGGPIYLIPEYCCYGDLLNLYRSKREKFR 719

Db 661 SELKQMTLGHHDNI VNLGACTLGGPVYLIPEYCCYGDLLNLYRSKREKFR 720

Qy 720 EHNFSYPTFQSHPNSSMPGSRREVQHPDSDQISGLHGNFSHSEDIENQKRL 777

Db 721 EHNFSYPTFOAHNSNSMPGSRREVQLHPDQDLSGFNGNSIHSEDIENQKRL 780

Qy 778 EDNLNLTREDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHKVKIKD 837

Db 781 EDNLNLTREDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHKVKIKD 840

Qy 838 SDSNTYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGN 897

Db 839 SDSNTYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGN 900

Db 841 SDSYVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGN 900

Qy 898 FYKLIQNGFKMDQPFYATEEIIIMQSWAFDSRKRSPFNLTSLFLGCOLADA 957

Db 901 FYKLIQSGFKMQPFYATEEIIIMQSWAFDSRKRSPFNLTSLFLGCOLABE 957

Qy 958 VGRVSECHTQVNRPPFRSREMDLGLLSPOAQVE 991

Db 958 ----IRTSIHLPKQAAPQORG-GLRAQSPQOVK 986

RESULT 4

I45877

protein-tyrosine kinase (BC 2.7.1.112), receptor type kit precursor - aurochs

C;Species: Bos primigenius (aurochs)

C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 20-Apr-2000

C;Accession: I45877

R;Kubota, T.; Hikono, H.; Sasaki, E.; Sakurai, M.

Gene 141, 305-306, 1994

A;Title: Sequence of a bovine c-kit proto-oncogene cDNA.

A;Reference number: I45877; MUID:94215924; PMID:7512939

A;Accession: I45877

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-977 <KUB>

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homol

C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F;329-395/Domain: immunoglobulin homology <IMM>

F;588-932/Domain: protein kinase homology <KIN>

Query Match 24.4%; Score 1286; DB 2; Length 977;

Best Local Similarity 33.2%; Pred. No. 2.7e-55;

Matches 332; Conservative 172; Mismatches 344; Indels 152; Gaps 36;

Qy 47 VKKSSYPWVSSPEDLGC-ALRPQSSGTYEAAAVEVDVSAITLQVLVDAPGNISCLW 105

Db 20 VQTGSSQPSV--SPGELSPLSIHPAKS-----ELIVSGDEIRLLCTDPGVK--W 66

Qy 106 VFHSHSLNCPHFQDLQNRGVSVMLKMTQTQAGEVLLFIQSEAT---NVTILFTVSIRN 162

Db 67 TFE-----ILQOLSEKTNPEWIT-EKAEATNTGNTCTNKGGLSS 105

Qy 163 TL-----LYTLRRPYFRKMENODALVCISESPPEVPEVWLCDGSGCKEESPAV 213

Db 106 SIYVFRDPEKFLDLPYKKEEN-DTLVRCPLTDP-EVTNYSLTGCEGKPLPKDLTFV 163

Qy 214 -----VKKEEKVLHELFGTDIRC--CARNELGRE-CTRLFTID----LNQTPQTLTP 258

Db 164 ADPKAGITIRNVKREYHRL-----CLHCSANQGRKSMLSKFTLVKRAAIKAVPVVSVS 217

Qy 259 Q--LFLKVGPELWIRCKAVHVNHGFLTWELNKALEEGNYFEMSTYSTNTRMIRILFAF 316

Db 218 KTSYLLREGEFAVTCILIKDVSSVSDSMWIKENSQQTAKQATKKNSWHQGFDFSLQERLT 277

Qy 317 VGSVARNDGYTSCSSKHPQSALVT---IVGKGFINA-----TNSSDYEIDQY 364

Db 278 ISSARVNDGCVFNCYANNTFGSANVTITLEVVDKGFINIFPMANVTTFVNDGENVDL--- 334

Qy 365 EEFCSFVRKAYPQ-IRCTWTFSRKS-----FPCEQKGLDNGYSIKFCNKHK----- 411

Db 335 -----VVEYAEYKPVHRQWIYNNRTSTDKWDDYPKSE-----NESNIRYVNLHLTRLK 384

Qy 412 --QPGYIIFHAENDDAQFTKMTLNIRRPQVLAEASA--SQASCSGSDGYPLPSWTWK 467

Db 385 GTEGGYITFHVNSDVSNTVFNVVNTKPEILTHDRLVNGLQCVAAGPEPTIDWYFC 444

Qy 468 SDKSPNCTEIEI-TEGVNKRKANRKYFGQWVSSSTLNMSAIGFLVKCCAYNSLGTSCET 526

Db 445 PGTEQRCSPVGVDPVQIQNSSVSPFGKLVVYSTIDDDSTFKHNGTVECRAYNDVGKSSAS 504

Qy 527 ILLNSPGPPP-----FIQDNIISFVATIGVCLLFIWLTLLIHKYKOPRYESOLQM 578

```
Db 505 FNAFKGSKKEQIHAHTLFTPLLVIAAGLWCFVWMLT----YKYLQKPMYEQWVKV 560
Qy 579 V-QVTGSSDNEYFYVDREYEDLKWEPRENLECKVLGSGAFGKVMNATAYGSKTCGV 637
Db 561 VEEING---NNVYIDPTQLPYDHKWEPFRNLSFGKTLGAGAFGKGVATAYGLKSDA 617
Qy 638 SIQAVKMLKEKADSSEREALMSLKMTQGLSHENIVNLLGACTLSGPIYLIFFEYCCYG 697
Db 618 AMTAVKMLKPSAHLTEREALMSLKVLKSYLGNHNVNLLGACTIGGPTLVITEYCCYG 677
Qy 698 DLLNLYRSKREKFKHTWTE-----IFKEHNEFYVFTFOSHNSM---PGSREVOIHPD 748
Db 678 DLLNLFRRKRDSFICKQBDHAEVALYKNLLSKSESSNDSTNEYMDMKPGVSYV-VPTK 736
Qy 749 SDQISGLHNSPHSEDETEYENQKELEBEDLNVLTFEDLLCFAYQVAKGMEFLFKSCV 808
Db 737 ADKRRSARIGSY-----IERDVTPTAIMEDEL-ALDELLDSFYQVAKGMAFLASKNCI 790
Qy 809 HRDLAARNVLVTHGKVKICDFGLARDMSDNYVVRGNARLPVKWMAPESEFEGITYTIK 868
Db 791 HRDLAARNILLTHGRTIKICDFGLARDIKDSDNYVVRGNARLPVKWMAPESEFNCVYTFE 850
Qy 869 SDVWSYGILLMEIFSLGVNYPGIPVDANFYKLIQNGFKMDOPFYATEIYIIMQSCWAF 928
Db 851 SDVWSYGIFLWELFSLGSSPYGMPVDSEKFKYKMKIEGFRMLSPHAPAEWYDIMKTCNDA 910
Qy 929 DSRKPSPNLTSFLGCLADAEABMYQNVGVRSEC-PH 967
Db 911 DPLKEPTFKQIVOLIEKQISESTNNHIYSN-----LANCSPH 946

RESULT 5
TVMSKT
Protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - mouse
N:Alternate names: tyrosine kinase receptor c-kit
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1991 #sequence revision 31-Mar-1991 #text_change 31-Mar-2000
A:Accession: S00474; B44876; I49596
R:Qiu, F.; Ray, P.; Brown, K.; Barker, P.E.; Jhanwar, S.; Ruddle, F.H.; Beemer, P.
EMBO J. 7, 1003-1011, 1988
A:Title: Primary structure of c-kit: relationship with the CSF-1/PDGF receptor kinase fa
A:Reference number: S00474; MUID:88296403; PMID:2456920
A:Accession: S00474
A:Molecule type: mRNA
A:Residues: 1-975 <QIU>
A:Cross-references: GB:Y00864; MID:g50423; PIDN:CAA68772.1; PID:g50424
R:Rossi, P.; Marzali, G.; Albanesi, C.; Charlesworth, A.; Geremia, R.; Sorrentino, V.
Dev. Biol. 152, 203-207, 1992
A:Title: A novel c-kit transcript, potentially encoding a truncated receptor, originates
A:Reference number: A44876; MUID:92331813; PMID:1378413
A:Accession: B44876
A:Molecule type: DNA
A:Residues: 771-814 <ROS>
A:Note: sequence extracted from NCBI backbone (NCBIN:108837, NCBI:108840)
R:Yasuda, H.; Galli, S.J.; Geissler, E.N.
Biochem. Biophys. Res. Commun. 191, 893-901, 1993
A:Title: Cloning and functional analysis of the mouse c-kit promoter.
A:Reference number: I49596; MUID:93221533; PMID:7682073
A:Accession: I49596
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <RES>
A:Cross-references: GB:L11358; MID:g293325; PIDN:AAA37420.1; PID:g293326
C:Genetics:
A:Gene: kit; c-kit
A:Map position: 5
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-975/Product: protein-tyrosine kinase kit #status predicted <KTC>
F:23-519/Domain: extracellular #status predicted <EXT>
F:51-100/Domain: immunoglobulin homology <IMM1>
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F:130-189/Domain: immunoglobulin homology <IMM2>
F:227-295/Domain: immunoglobulin homology <IMM3>
F:331-397/Domain: immunoglobulin homology <IMM4>
F:426-496/Domain: immunoglobulin homology <IMM5>
F:520-542/Domain: transmembrane #status predicted <IMM>
F:543-975/Domain: intracellular #status predicted <INT>
F:586-929/Domain: protein kinase homology <KIN>
F:58-98.137-187, 223-293, 431-494/Disulfide bonds: #status predicted
F:146, 296, 303, 323, 355, 370, 466, 489/Binding site: carbohydrate (Asn) (covalent) #status
F:622, 639, 790/Active site: Lys, Glu, Asp #status predicted
F:795, 808/Binding site: magnesium (Asn, Asp) #status predicted
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Query Match 24.0%; Score 1266; DB 1; Length 975;

Best Local Similarity 33.2%; Pred. No. 2.5e-54;
Matches 336; Conservative 173; Mismatches 330; Indels 172; Gaps 41;

Qy 35 CVLIHNKNDSSVKGSSSPMVSESPEDLGICALRPOSSGTVYEAADVVDVSATLQVL 94

Db 12 CVLLVLLRGQTATSPASPGSPSP-----SIHPAQ-----ELIVEAGDTL--- 54

Qy 95 VDAPGNISCL-----WPKHSSLNCPHFDLQNRGVVSMVLKMTTQAGEYLLFIQSE 148

Db 55 -----SLTCIDPDFVRWTFK-----TYFN-----EMVENKKNWIIQ-EKAE 89

Qy 149 ATNYTILFTVSRNTL-----LYTLRRPYFRKMNODALVCISESVPEPIVE 195

Db 90 ATR-TGTYTCSNSNGLTSSIIYVVRDPAPKFLVGLPLFGK-EDSDALVRCPLTDPO-VSN 146

Qy 196 WVLCDQSGESCKEESPAV-----VKKEKVLHLEFGDIRCCARNELGRETLL--- 244

Db 147 YSLIEDCGKSLPTDLTFVDPNPKAGITIKVKKRAYHRLC---VRCAAQ-----RDGTWLHSD 199

Qy 245 -PTIDLNQ-----PQTLLPQL--FLKVGELPLWIRCKAVHVNHGFLTW-----E 286

Db 200 KFTLVKREAIIKAPVVSVPETSHLLKKGDTFTVVTCTIKDSTSVNSWLKKNPOPOHIAQ 259

Qy 287 LENKALEGNYPEMSTYSTNRTMIRILFAFVSSVARNDGYTCSSSKHPSQSALVT--- 343

Db 260 VKHNSWHRGDF-----NYERQETLT-----ISSARVDDSGVFCYANNTFGSANVTTLK 309

Qy 344 IVKGKFINATN-SSEDIYDQYEEFCFSVRKAYPO-IRCTWTFSRKSPFCEQKGLD--- 398

Db 310 VVEKGFNISPVKNTTVFTDGENVDLVVEYAYPKPEHQQIYMNRT--SANKGKDYVK 367

Qy 399 -NGYSISKECNKH-----OPGEYIFHAENDDAQFTKFTLIRKPKQVLA--EASAS 448

Db 368 SDNKNIRYVNLRLTLRKGTGGTYTFLVNSDASASVTFNVTYVNTKPEILTYDRLING 427

Qy 449 QASCFSDGYPLPSWTWKCKSDKSPNCTEITE-GVNNRKNRKNRVFGQWVSSSTLNMSAI 507

Db 428 MLQCVAGEPFETIDWYFCTGAEQRCTTPVSPVDVQVQVSVSPFGKLVQSSIDSVFR 487

Qy 508 KGLVKCCAYNSLGTSCETILLNSPGFPFF---IQDN-----ISFYATIGVCLLFIV 557

Db 488 HNGTVECKASNDVGKS--SAFEN---FAFKEIQIAHTLFTPLLVIAAGAGIIVM 541

Qy 558 LTLCHTKYKPRFBSQLQMV-QVTGSSDNEYFYVDREYEDLKWEPRENLEFGKVL 616

Db 542 LT-----YKYLQKPMYEQWVKVEEING---NNVYIDPTQLPYDHKWEPFRNLSFGKTL 594

Qy 617 GSGAFGKVMNATAYGISKGTGVSIVQAVKMLKEKADSSEREALMSLKMTQGLSHENIVN 676

Db 595 GAGAFKGVATAYGLTKSDAAMTAVKMLKPSAHLTEREALMSLKVLKSYLGNHNVN 654

Qy 677 LLGACTLSGPIYLIFFEYCCYGLNLYRSKREK-----HRTWTIEIFKEHNSFYPTFQ 730

Db 655 LLGACTVGGPTLVITEYCCYGLNLYRSKREKDSFISKQEEAEALYKNLLHSTBESCD 714

Qy 731 SHPNISM---PGSREVOIHPDSDQISGLHNSPHSEDETEYENQKELEBEDLNVLTFED 787

Db 715 S-SNEYMDMKPGVSYV-VPTKTDKRRSARIDS-----IERDVTPTAIMEDEL-ALDLD 766

Qy 788 LFCAYQVAKMEFLFKSCVHRDLAARNLVTHGKVKICDFGLARDIMSDNSVTVRGN 847
Db 767 LLSFSYQVAKMAFLKSKNHRDLAARNLLTHGRITKICDFGLARDIRNDSNVVWKN 826
Qy 848 ARLPVKWPAPSLFSGIYTIKSDVMSYGILLWEISLGNVPYGGIPVDANFYKLLIQGFK 907
Db 827 ARLPVKWPAPSLFSGIYTIKSDVMSYGILLWEISLGNVPYGGIPVDANFYKLLIQGFK 907
Qy 908 MDQPFYATETIYIIMOSWAFDSRRKPFNNLTSLGQCLADAEAMQNV 958
Db 887 MVSPEHAENYVNMKTCWDADPLKPTFKQVQVLEIKQISDSTKHYSNL 937
RESULT 6
A49814
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: A49814; S49088
R:Tsujimura, T.; Hirota, S.; Nomura, S.; Nomura, M.; Yamazaki, M.; Tono, T.; Morii, E.; Kitajima, T.; Tono, T.; Yamazaki, M.; Nomura, S.; Kitamura, Y.
Blood 78, 1942-1946, 1991
A:Title: Characterization of a mutant allele of rats: a 12-base deletion in tyrosine kinase gene
A:Reference number: A49814; MUID:92003944; PMID:1912577
A:Accession: A49814
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-978 <TSU>
A:Cross-references: GB:D12524; NID:g220707; PIDN:BAA02094.1; PID:g220708
R:Tsujimura, T.; Tono, T.; Yamazaki, M.; Nomura, S.; Kitamura, Y.
submitted to the EMBL Data Library, October 1991
A:Description: Two isoforms of rat c-kit receptor tyrosine kinase.
A:Reference number: S49088
A:Accession: S49088
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-511,516-978 <TS2>
A:Cross-references: EMBL:X62491; NID:g509135; PIDN:CAA44354.1; PID:g509136
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolog
C:Keywords: ATP; autophosphorylation; phosphotransferase; tyrosine-specific protein kinase
F:129-188/domain: immunoglobulin homolog <IM>
F:589-932/domain: protein kinase homology <KIN>
F:597-605/region: protein kinase ATP-binding motif

Query Match 24.0%; Score 1263.5; DB 1; Length 978;
Best Local Similarity 33.8%; Pred. No. 3.4e-54;
Matches 334; Conservative 171; Mismatches 361; Indels 121; Gaps 37;

Qy 35 CVLINHKNDSVSGKSSYPMVSPEDLGCALRQSGTGVYAAAEVDVVSATLQVL 94
Db 12 CVLLVLRGQTGTSQSPASGPSPSP-----SIQPAQS-----ELIVEAGDTIRLT 57
Qy 95 VDAPGNISCLWVFKHSLNCPHFLQNRGVVSMVLKYTE-TQAGEYLLPQSEATNYT 153
Db 58 CTDPAFVK-WTFE-----ILDVRIENKQSEWIREKAEATHGKTCVSGSLRSGI 107
Qy 154 ILFTVSIRN-TLLYLRPRFRKMNQDALVCISBVPPIVEWVLCDSQGSCKEESPA 212
Db 108 YVF---VVDPAVLPLVGLPLFKG-EDNALVRCPLTDQ-VSNYSLECDGKSLPTDLKF 162
Qy 213 V-----VKKBEKVLHFLFTDIRCCARNELGRECTRLFTID----LNQPTPTLPOL 260
Db 163 VPKPKAGITIKNVKAYHRLC---IRCAQREGKWMRSCKFTLKVRAAIKAIPVVSVPET 219
Qy 261 --FLKVGELMIRCAVHVHNGFGLTW-----ELENKALEEGNYFEMS--TSTWRTMIR 311
Db 220 SHLLKEGTFTVICTIKDVSVDMSVMTKLNPPQSKAQKNSWHQGDYFVERQETLT- 278
Qy 312 ILFAPVSVARNDTGYTSCSSKHPQSALVT---IVGKGFIN---ATNSSDEYIDQVE 365
Db 279 -----ISSARVNDSGVFMCIYANNTFGSANVTTLTKVKEGFNIPFVKMTT--VFVTGGE 331
Qy 366 EFCFSVRFKAYPQ-IRCTWTFSRKFPCEQKGLD-----NGYISIKFCNKHK-----QP 413

Db 332 NVDLVVEFEAYPKPEHQWYNNRT--PTNRGDEVYKSNQSNIRYVNELRRLTRLKGTEG 389
Qy 414 GSYIFHAENDDAQFTKFTLNIRRKQVLA--EASASQASCFSDGYPSPSWTWKCKSDKS 471
Db 390 GYTFVLSNDSVASVTFDYYVNTKPEILTYDLRMNGRLQCVAAAGPEPTIDWYFCTGAE 449
Qy 472 PNCETBEITE-GVMNRKANRKFQGVSSSTLNNMBAIKGFLVCKCAYNSLGTSCETILLN 530
Db 450 QRCTVPVPVQVQIQNASVSPGKLVQSSIDSSVFRHNGTVECKASNAVGKS--SAFVN 507
Qy 531 SFGPPFP-----IQDN-----ISFYATIGVCLLFIWLTLLCHKVKQKFRYESQL 576
Db 508 ----FAFKGNSKEQIQPHTLFTPLLIGFVVYTAG--LMGIIVMVL--AYKYLQKPMYEVQW 559
Qy 577 QMV-OVTSSDNEYFVDFREYEDLKWEFFRENLEFGKVLGSGAFKGVNATAYGISKT 635
Db 560 KVEEING---NNYVYIDPTQLPYDKWEFFPNRLSFGKTLGAGAFKGVVATAYGLIKS 616
Qy 636 GYSIQVAVKMLKEKADSSEREALMSLKMVQLGSHENIVNLLGACTLSGPIYLIFEYCC 695
Db 617 DAAMTVAVKMLKPSAHLTEREALMSLKVLSYLGNNHNVNLLGACTVGGPTLVITEYCC 676
Qy 696 YGDLNLYLRSKREKFRHTWTEIFKEHNSFYTFQSHPNSSMPGSR-VQIHDPDSQISG 754
Db 677 YGDLNLYLRSKREKFRHTWTEIFKEHNSFYTFQSHPNSSMPGSR-VQIHDPDSQISG 754
Qy 755 LHGNSFHS---EDEIYENQKLEBEEDLNVLTFEDLLCFAYQVAKMEFLFKSCVHRD 811
Db 735 TYTKRRSARIDSYIEROVTPTAIMEDEL-ALDLELLSFSYQVAKMAFLASKNCIHRD 793
Qy 812 LAARNVLVTHGKVKICDFGLARDIMSDNSVTVRGNARLPVKWMAPESLFEGITYTKSDV 871
Db 794 LAARNVLVTHGKVKICDFGLARDIRNDSNVVYKGNARLPVKWMAPESLFEGITYTKSDV 853
Qy 872 WSYGILLWEISLGNVPYGGIPVDANFYKLLQNGFQMDQPFYATEBIYIMQSCWAFDSR 931
Db 854 WSYGILLWEISLGNVPYGGIPVDANFYKLLQNGFQMDQPFYATEBIYIMQSCWAFDSR 931
Qy 932 KPSPNLTSFLGQCLADAEAMQNV 958
Db 914 KRPTFKVQVLEIKQISDSTKHYSNL 940
RESULT 7
TVHUKT
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - human
N:Alternate names: mast/stem cell growth factor receptor; tyrosine kinase receptor c-
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 21-Jul-2000
C:Accession: S01426; PC1015; A41815; B41815; C41815; I37948; I56954; I54336
R:Yarden, Y.; Kuang, W.J.; Yang-Feng, T.; Coussens, L.; Munemitsu, S.; Dull, T.J.; Ch-
EMBO J. 6, 3341-3351, 1987
A:Title: Human proto-oncogene c-kit: a new cell surface receptor tyrosine kinase for
A:Reference number: S01426; MUID:88111521; PMID:2448137
A:Accession: S01426
A:Molecule type: mRNA
A:Residues: 1-976 <YAS>
A:Cross-references: GB:X06182; NID:g34084; PIDN:CAA29548.1; PID:g34085
R:Hu, W.X.; Cornu, F.; Andre, C.; Galibert, F.
Chinese Biochem. J. 7, 618-629, 1991
A:Title: Nucleotide sequence of two neighbouring fragments of human c-kit proto-oncoge-
A:Reference number: PC1015
A:Accession: PC1015
A:Molecule type: DNA
A:Residues: 412-713 <HUV>
A>Note: article in Chinese with English abstract
R:Spritz, R.A.; Giebel, L.B.; Holmes, S.A.
Am. J. Hum. Genet. 50, 261-269, 1992
A:Title: Dominant negative and loss of function mutations of the c-kit (mast/stem cel-
A:Reference number: A41815; MUID:92133600; PMID:1370874
A:Accession: A41815
A:Molecule type: DNA
A:Residues: 579-583, 'L', 585-589 <SPR>


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RESULT 8
151703
c-kit-related kinase 1 (Xkrkl) - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C:Accession: I51703
R:Baker, C.V.; Sharpe, C.R.; Torpey, N.P.; Heasman, J.; Wylie, C.C.
Mech. Dev. 50, 217-228, 1995
A:Title: A Xenopus c-kit-related receptor tyrosine kinase expressed in migrating stem ce
A:Reference number: I51703; MUID:95344996; PMID:7619732
A:Accession: I51703
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-954 <BA>
A:Cross-references: EMBL:Z48770; NID:G763033; PIDN:CAA8688.1; PID:G763034
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C:Keywords: ATP
F:575-915/Domain: protein kinase homology <KIN>
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Best Local Similarity 33.1%; Pred. No. 2.2e-52;
Matches 305; Conservative 162; Mismatches 322; Indels 132; Gaps 30;
QY 107 FKHSLLNCPHFDLQNRGVVS-----WILKMTQAGEYLLFIQSEATNYTLITVSI 160
DB 52 FQKSLGKKPK-DLKSRLNNSETDQFFVIRKADLRHIGRYICTNTQENTSV--SLFV 108
QY 161 RNTLLYTLRRPVFRKMNEDALVCISSEVPEIVVWLCDSQESCKE-----ESPA 212
DB 109 KDPAPFLDIPIDVTEGADTGMCFPTDPMDDIAIEKCD--GSPLENFTFTDIEAGI 166
QY 213 VVKKEKVLHFLGTDIRCCARNEIGR-BCTRLFTIDLNQTTQLTLPQLF-----KV 264
DB 167 TIKTQLAFDSY-----VCSGKSGTWKKSSTFSHVKVPK-KVPTVFLSKSRQLVKT 220
QY 265 GEPLMIRKAVHNVHGFGLTW-ELENKALEEGNPEMSTYSTRNTRMIRILFAFVSSVARN 323
DB 221 GEFFETCAVLDFVSTKAQMLDVEGVTQKQANFRSSNVFSNLTLS-----DGVPS 274
QY 324 DTGYTCSSSKHPQ---SALVTIVGKGINAT-NSSEYEDIQVEEFCFSVRKAYPO- 378
DB 275 ESRTTQAEANAIGQVNAITFLDVIDVGYNLTVLENTTISWAGNVLVKYVIDAYHPH 334
QY 379 IRCTWTFRSKPFCEQKGLDNGYSISK-----FCNHKH-----QPGYEYFHAENDDA 425
DB 335 DGVWYTFNEUL---LNTSDHYVATKDEGNRYVSELHLRLKTEKGVYTFYTNSTD 390
QY 426 QFTKMTNIRKPKQVLAASASQAS--CFSDGYPLPSWTWKCKSDKSPNCTEETIEGVW 483
DB 391 DASVSFNIQVTRPEILIAERTSEGTLCQVATGFPVPAIQWYFCPGSEQRCTDYPLSPV 450
QY 484 NRK--ANRKFQWYSSSTLWNSAIKGLVKKCCAYNSLGTSCETILLNSPGFFPP-IDQ 540
DB 451 NEKFTQENSSLRIVVESTIDVNDLKKNGTVQCASNEVESAYSV-----FSFAIKE 502
QY 541 N-----ISFYATIGVCLLFIIVLTLICHYKKQFRYESQLOMV-QVTGSSDNE 588
DB 503 KLRTHTLTPPLIGIAAGLACIAVAVL---MYKLOKPKYEYQWKVVEING--NN 555
QY 599 YFYVDFRYEYDLKWEFPRENLEFGKVLGSAFGAKVMATAYGISKTGVSIOQAVKMLKE 648
DB 556 YVYIDPTQLPYDNKWEFRDRCLFCGKILGAGAFGKVEATAYGLLKEDSRLTVAVKMLKP 615
QY 649 KADSSERAAKMSLQWQTLGSHENIVNLGACTLSGPYILFIFFCCYGDLLNLYRSKRE 708
DB 616 SAHSTERAAKMSLVSLYGLGHKNIIVNLGACTVGGPTLVITEYCCYGDLLNLYRRKD 675
QY 709 KFHRTWTEIFKEHNFSEYPTFOHSPNS---SMPGSRVQIHPDSQDI----- 752
DB 676 SF-----ICPKEDNEAALYKMLNTRDMGCEGMSEYIDMKPAVSVVPT 721
QY 753 --SGLHGNFSHSEDEIYEYENQKRLBEEDLNVLTFEDLLCFAYQVAKGMFELEFKSCVHR 810
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Db 722 KTDKRRSGSFGDQDV-----SVSIPBEDDL-ALDTEDLINFSYQVACGMFLASKNCIHR 775
QY 811 DLARNVLTGHVKVVICDFGLARDMSDNYVVRGNARLPVKWMAPESLFEGYITIKSD 870
Db 776 DLARNVLTGHVTRITKICDFGLARDMSDNYVVRGNARLPVKWMAPESLFCHVYTFESD 835
QY 871 VMSYGILLWEIFSLGVPYFGIPVDANFYKLIQNGFKMDQPFVATEBIYIMQSCWAFDS 930
Db 836 VMSYGILLWEIFSLGSPYPRIPVDSKFYKWKIDGYRMMSPECAPLEMYEIMRSCWNSDP 895
QY 931 RKRPSPNLTSFLGCCOADAE 951
Db 896 LKPEPTFKQIVQMVVEQQLSDSK 916
RESULT 9
TVCTMD
macrophage colony-stimulating factor 1 receptor precursor - cat
N:Contains: protein-tyrosine kinase (EC 2.7.1.112) csflr/fms
C:Species: Felis silvestris catus (domestic cat)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 13-Jun-1997
C:Accession: A31636
R:Woolford, J.; McAuliffe, A.; Rohrschneider, L.R.
Cell 55, 965-977, 1988
A:Title: Activation of the feline c-fms proto-oncogene: multiple alterations are req
A:Reference number: A31636; MUID:89077553; PMID:2849512
A:Accession: A31636
A:Molecule type: mRNA
A:Residues: 1-980 <WOO>
A:Cross-references: EMBL:X03663
C:Genetics:
A:Gene: fms
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolo
C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming prote
fic protein kinase
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F:24-980/Product: macrophage colony-stimulating factor 1 receptor #status predicted <EXT>
F:24-509/Domain: extracellular #status predicted <EXT>
F:35-86/Domain: immunoglobulin homology <IMM1>
F:120-179/Domain: immunoglobulin homology <IMM2>
F:217-280/Domain: immunoglobulin homology <IMM3>
F:316-381/Domain: immunoglobulin homology <IMM4>
F:410-484/Domain: immunoglobulin homology <IMM5>
F:510-534/Domain: transmembrane #status predicted <TM>
F:535-980/Domain: intracellular #status predicted <INT>
F:577-915/Domain: intracellular #status predicted <INT>
F:585-593/Region: protein kinase ATP-binding motif
F:42-84,127-177,224-278,417-482/Disulfide bonds: #status predicted
F:45,73,94,153,275,302,335,410,477,490/Binding site: carbohydrate (Asn) (covalent) #s
F:613,630,776/Active site: Lys, Glu, Asp #status predicted
F:781,794/Binding site: magnesium (Asn, Asp) #status predicted
Query Match 23.2%; Score 1225.5; DB 1; Length 980;
Best Local Similarity 33.5%; Pred. No. 2.4e-52;
Matches 321; Conservative 168; Mismatches 321; Indels 149; Gaps 34;
QY 83 VDVSASITQLVLDAPGNISCLW---VFKHSSLNCP-----HFDLQNRGVSMVIL 131
Db 32 VEPGTTVTLRCV---GNGSVWDGPIPSHWNLDLPPSSILTTNNATQNTGYHCT-- 85
QY 132 KMTETOAGEYL--LFTQSEATNYTL---FTVSIRNTLYTLRRPYFRKMNQDALV-CI 195
Db 86 EFGNFGGNATHLVYKDPARPKVLAQEVTV-----LEGDALLPCL 128
QY 186 SESVPEPIVE--WVLCDSQESCKEE-----SP---AVVKEEKVLHFLGTDIRCCARN 235
Db 129 ---LTDPALEAGVSLVRVRGRPVLRQTNYSFSPWHGFTTHKAKFIENHYV-----QCSARV 181
QY 236 ELGRCTRL-----FTIDLNQTPQTL-PQLFLKV-GEPLMIRKAVHNVHGFGLTWELE 288
Db 182 D-GRTVTSMGVILKVKQKDISGATLTLEPAELVRIQGEAAQVCSASNIDVNFV----- 235
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Qy 289 NKALEEGN-----YFEMSTYSTNRNTRMIRILFAFVSSVARNDTGYTCSSSK---HPSQSAL 341
Db 236 --SLRHGDTKLTISQSDFDHNRQY-KVLTNLNDHVSFQDAGNYSCTATNAWGNHSAWV 292
Qy 342 VTIVGKGFINATN-SSEYEDIDQVEEPCFVRKAYPOIRC-TWTFSRKSPCEQKGLD- 398
Db 293 FRVVEAYNLNLSQSLQEVTVGKVDLQVKVEAYPGLESFNWY-LGPFSDYQDKLDF 351
Qy 399 ----NGYSISKFCN-----HKHOPGGYIEFHAENDDAQFTKMTLNRKRPQVLAESAQA 450
Db 352 VTIKDTYRTYTSLSPLRKREAGRYSLARNAGQNALTELTILRYPEVRVMTWLLING 411
Qy 451 S-----CFSDGYPPLSPWTKKCDSPNCTEE-----ITEGVNKRKANRKYFGQWVSSTLNM 503
Db 412 SDTLLCEASGYPOPSVTWVQCRSHTRDCEAGLVLEDHSEVLQVSPFHEVIVHSLAI 471
Qy 504 SEATKGLVKCAVNSLTSETILLNSPGPPFPFDNIISFYATIGVC---LLFIVLTL 560
Db 472 GTLEHNRTECRAFNSVNSQTFWPISIGAHTQLPDELLFTPVLLTCSIMALLLLLL 531
Qy 561 LICHYKKOPRYESOLOMVQVGTSSDNFYFVDPREYEDLKWEPPRENLEFGKVLGSGA 620
Db 532 LLLYKYPKQKQVWKIIE--SYEGNSYTFIDPTQLPYNEKWEPPRNLOFGKTLGAGA 589
Qy 621 FGKVNATAYGISKTVGSIQVAVKMLKEKADSSEREALMSLQMTOLGSHENIVNLLGA 680
Db 590 FGKVVETAFLGLGEDAVLKVAVKMLKSTAHADKEALMSLQMTOLGSHENIVNLLGA 649
Qy 681 CTLSPGPIVLFEYCCYGDLLNLYRSKRE-----KFRHTWTEIFEKE 720
Db 650 CTHGGPVLIVTEYCCYGDLLNLYRSKRE-----KFRHTWTEIFEKE 709
Qy 721 HNFSPYPTFQHPNNSMPGSRVQVHPDSQISGLHGNFSHSEDEIEYENOKRLEEBDL 780
Db 710 SDFS-----SQGVDTYVEMRPVSTSSNDSPSEEDLKGDRPLE----- 749
Qy 781 NVLTPEDLFCAYQVAKMEFEKSCVHRDLAARNVLTHTGKVKVVICDFGLARDIMSDS 840
Db 750 ----LRDLHFFSSQVAGMAFLASKNCIHRDVAARNVLLTSGRAKIGDFGLARDIMSDS 805
Qy 841 NYVVRGNARLPVKMAPSLFEGYITIKSDVWSYGILLWEIFSLGWNYPGIPVDANFYK 900
Db 806 NYIVKGNARLPVKMAPSIFDCVTVQSDVWSYGILLWEIFSLGWNYPGIPVLNYSKYK 865
Qy 901 LIQNGFKMDQPPYATEEIIYIMOSCAWFDSCRKRPFPNLTSLGCOL-ADAEEMQVNV 958
Db 866 LVKGTQMAQPAFAFNKIYSIMOACWALEPRTTRPFOQICSLLOKQAOEDRRVPNYTNL 924

RESULT 10
TMVMD
protein-tyrosine kinase (EC 2.7.1.112) fms precursor - feline sarcoma virus (strain McDC
C:Species: feline sarcoma virus
A:Note: host Felis sp. (cat)
C:Date: 27-Nov-1985 #sequence_revision 31-Dec-1991 #text_change 13-Jun-1997
C:Accession: A00654
R:Hampe, A.; Gobet, M.; Sherr, C.J.; Galibert, F.
Proc. Natl. Acad. Sci. U.S.A. 81, 85-89, 1984
A:Title: Nucleotide sequence of the feline retroviral oncogene v-fms shows unexpected ho
A:Reference number: A00654; MUID:84119469; PMID:6582485
A:Accession: A00654
A:Molecule type: DNA
A:Residues: 1-941 <HAM>
C:Comment: This protein is synthesized as a gag-fms polyprotein.
C:Genetics:
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
rotein kinase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-941/product: protein-tyrosine kinase fms #status predicted <MAT>
F:24-509/Domain: extracellular #status predicted <EXT>
F:35-86/Domain: immunoglobulin homology <IMM1>

```

```

F:120-179/Domain: immunoglobulin homology <IMM2>
F:217-280/Domain: immunoglobulin homology <IMM3>
F:316-381/Domain: immunoglobulin homology <IMM4>
F:410-484/Domain: immunoglobulin homology <IMM5>
F:510-534/Domain: transmembrane #status predicted <TMM>
F:535-941/Domain: intracellular #status predicted <INT>
F:577-915/Domain: protein kinase homology <KIN>
F:585-593/Region: protein kinase ATP-binding motif
F:42-84,127-177,224-278,417-482/Disulfide bonds: #status predicted
F:45,73,94,153,275,286,302,335,410,477,490/Binding site: carbohydrate (Asn) (covalent
F:613,630,776/Active site: Lys, Glu, Asp #status predicted
F:781,794/Binding site: magnesium (Asn, Asp) #status predicted

```

Query Match 23.1%; Score 1218; DB 1; Length 941;

Best Local Similarity 33.2%; Pred. No. 5.3e-52;

Matches 327; Conservative 170; Mismatches 316; Indels 172; Gaps 37;

Qy 83 VDVASITLQVLVADPAGNISCLW---VFKHSSLNCP-----HFDLQNGVSMVL 131

Db 32 VEPGTTVTLRCV---GNGSVWDGPISPHWNLDLDPSPSSILTTNNATFQNTGYHC--- 84

Qy 132 KMTETQAGE-----YLLFIQSEATNYTIL---FTVISIRNTLLYTLRPPYRKMNODA 181

Db 85 ----TEPNRPGGNATHLYVKDPAKPKVLAQEVTV-----LEGQDA 123

Qy 182 LV-CISESVPPPIVE--WVLCDSQGESCKEE-----SP---AVVKEEKVLHFGTDIR 230

Db 124 LLPCL---LTPALEAGVSLVRVRGPRVLRQTNYSFSPWHGFTIHKAKFIENHYV---Q 176

Qy 231 CCARNELGRECTRL-----FTIDLNOTPTTL-POLFUKV-CEPLWIRKCAVHVNHGSL 283

Db 177 CSARVD-GRVTSMGILWLVKQKDISPATLTLEPAELVRIQGEAAQIVCSASNIIDVNFV 235

Qy 284 TWELNKALEGN-----YFEMSTYSTNRNTRMIRILFAFVSSVARNDTGYTCSSSK---HP 336

Db 236 ----SLRHGDTKLTISQSDFDHNRQY-KVLTNLNDHVSFQDAGNYSCTATNAWGNH 287

Qy 337 SOSALVTIVGKGFINATN-SSEYEDIDQVEEPCFVRKAYPOIRC-TWTFSRKSPCEQ 394

Db 288 SASMVFRVVEASAYSNLTSEQSLLOEVTVGKVDLQVKVEAYPGLESFNWY-LGPFSDYQ 346

Qy 395 KGLD-----NGYSISKFCN-----HKHOPGGYIEFHAENDDAQFTKMTLNRKRPQVLA 445

Db 347 DKLDPTVTKTYRTSTLSPLRKREAGRYSLARNAGQNALTELTILRYPEVRVMT 406

Qy 446 SASQAS---CFSDGYPLSPWTKKCDSPNCTEE---ITEGVNKRKANRKYFGQWVS 498

Db 407 TLINGSDTLLCEASGYPOPSVTWVQCRSHTRDCEAGLVLEDHSEVLQVSPFHEVIVH 466

Qy 499 STLNNSEAIKGLVKCCAYNSLGTSETILLNSPGPPFPFIQDNIISFYATIGVC---LLFI 555

Db 467 SLLAIGTLEHNRTECRAFNSVNSQTFWPISIGAHTPLPDELLFTPVLLTCSIMALL 526

Qy 556 VVLTLLICHYKKOPRYESOLOMVQVGTSSDNFYFVDPREYEDLKWEPPRENLEFGKV 615

Db 527 LLLLLLLLYKKQKPKYQVRWKIIE--SYEGNSYTFIDPTQLPYNEKWEPPRNLOFGKT 584

Qy 616 LGSAGFGKVNATAYGISKTVGSIQVAVKMLKEKADSSEREALMSLQMTOLGSHENIV 675

Db 585 LGTGAFGKVEATAFGLGEDAVLKVAVKMLKSTAHADKEALMSLQMTOLGSHENIV 644

Qy 676 NLGAGTLLSGPIVLFEYCCYGDLLNLYRSKRE-----KFRHTWT 715

Db 645 NLLGACTHGGPVLIVTEYCCYGDLLNLYRSKRE-----KFRHTWT 704

Qy 716 EIFKEHNFSTYPTFQHPNNSMPGSRVQVHPDSQISGLHGNFSHSEDEIEYENOKRLE 775

Db 705 YVRDSDGS-----SQGVDTYVEMRPVSTSSNDSPSEEDLKGDRPLE 749

Qy 776 BEEDLNVLTFEDLLCFAYQVAKMEFEKSCVHRDLAARNVLTHTGKVKVVICDFGLARD 835

Db 750 ----LRDLHFFSSQVAGMAFLASKNCIHRDVAARNVLLTSGRAKIGDFGLARD 800

QY 836 IMSDSNVVRGNARLPVKWMAPELFEGLYTIKSDVMSGILLWEIFSLGVPYGPICPVD 895
 Db 801 IMNDSNIVKGNARLPVKWMAPELFDVYTVQSDVMSYGILLWEIFSLGVPYGPICLVN 860
 QY 896 ANFYKLIQNGFKMDPPFYATEBIYIMOSWAFDSRKPSPFNLTSLFGLCCQLADAEEMY 955
 Db 861 SKFYKLVKDGVCMAQAPAPKPNYISIMACWALEPFRPTFQQICSLQKQ---AQE--- 914
 QY 956 QNVGRV---SECPTYQNR---RPF 975
 Db 915 ---DRVPVNTNLPSSSSRLRPW 936

RESULT 11
 TVHMD
 macrophage colony-stimulating factor 1 receptor precursor - human
 N;Contains: protein-tyrosine kinase (SC 2.7.1.112) csf1r/fms
 C;Species: Homo sapiens (man)
 C;Date: 28-Dec-1987 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
 C;Accession: S08123; A24533; I56672; I57648; I59083; I52772
 R;Hampe, A.; Shamoon, B.M.; Gobet, M.; Sherr, C.J.; Galibert, F.
 Oncogene Res. 4, 9-17, 1989
 A;Title: Nucleotide sequence and structural organization of the human FMS proto-oncogene
 A;Reference number: S08123; MUID:892339490; PMID:2524025
 A;Accession: S08123
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-972 <HAM>
 A;Cross-references: GB:U63963; EMBL:X14720; NID:G1915975; PIDN:AA851696.1; PID:G1915976
 A;Note: this sequence was submitted to the EMBL Data Library, March 1989
 R;Cousens, L.; Van Beversen, C.; Smith, D.; Chen, E.; Mitchell, R.L.; Isacke, C.M.; Vert
 Nature 320, 277-280, 1986
 A;Title: Structural alteration of viral homologue of receptor proto-oncogene fms at carb
 A;Reference number: A24533; MUID:86175013; PMID:2421165
 A;Accession: A24533
 A;Molecule type: mRNA
 A;Residues: 1-53, 'A', 55-972 <COU>
 A;Cross-references: GB:J03149
 A;Note: the authors translated the codon GCA for residue 54 as Pro
 R;Wheeler, E.F.; Roussel, M.F.; Hampe, A.; Walker, M.H.; Fried, V.A.; Look, A.T.; Retter
 J. Virol. 59, 224-233, 1986
 A;Title: The amino-terminal domain of the v-fms oncogene product includes a functional s
 sequences.
 A;Reference number: I56672; MUID:86281820; PMID:3525854
 A;Accession: I56672
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-16 <RES>
 A;Cross-references: GB:M14002; NID:G182676; PIDN:AAA35849.1; PID:G553292
 R;Visvader, J.; Verma, I.M.
 Mol. Cell. Biol. 9, 1336-1341, 1989
 A;Title: Differential transcription of exon 1 of the human c-fms gene in placental troph
 A;Reference number: I57648; MUID:89261741; PMID:2524648
 A;Accession: I57648
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-16 <RE2>
 A;Cross-references: GB:M25786; NID:G349454; PIDN:AAA58421.1; PID:G553224
 R;Browning, P.J.; Bunn, H.F.; Cline, A.; Shuman, M.; Nienhuis, A.W.
 Proc. Natl. Acad. Sci. U.S.A. 83, 7800-7804, 1986
 A;Title: Replacement of COOH-terminal truncation of v-fms with c-fms sequences markedly
 A;Reference number: I59083; MUID:87017034; PMID:3532121
 A;Accession: I59083
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 874-972 <RE3>
 A;Cross-references: GB:M14193; NID:G182521; PIDN:AAA35834.1; PID:G182522
 R;Nienhuis, A.W.; Bunn, H.F.; Turner, P.H.; Gopal, T.V.; Nash, W.G.; O'Brien, S.
 Cell 42, 421-428, 1985
 A;Title: Expression of the human c-fms proto-oncogene in hematopoietic cells and its del
 A;Reference number: I52772; MUID:85282599; PMID:4028159
 A;Accession: I52772
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
 A;Residues: 244-295 <RE4>
 A;Cross-references: GB:M11067; NID:G182674; PIDN:AAA35848.1; PID:G442423
 C;Genetics:
 A;Gene: GDB:CSF1R; FMS
 A;Cross-references: GDB:120600; OMIM:164770
 A;Map position: Sq33.2-5q33.3
 A;Introns: 17/1; 103/1; 198/1; 243/3; 297/1; 361/2; 400/1; 440/2; 504/1; 542/3; 585/1
 C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homol
 C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming prote
 fic protein kinase
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-972/Product: macrophage colony-stimulating factor 1 receptor #status predicted <
 F;24-512/Domain: extracellular #status predicted <EXT>
 F;35-86/Domain: immunoglobulin homology <IMM1>
 F;120-179/Domain: immunoglobulin homology <IMM2>
 F;217-280/Domain: immunoglobulin homology <IMM3>
 F;316-383/Domain: immunoglobulin homology <IMM4>
 F;412-487/Domain: immunoglobulin homology <IMM5>
 F;513-537/Domain: transmembrane #status predicted <TMM>
 F;538-972/Domain: intracellular #status predicted <INT>
 F;580-917/Domain: protein kinase homology <KIN>
 F;588-596/Region: protein kinase ATP-binding motif
 F;42-84, 127-177, 224-278, 419-485/Disulfide bonds: #status predicted
 F;45, 73, 153, 240, 275, 302, 335, 412, 428, 480/Binding site: carbohydrate (Asn) (covalen
 F;616, 633, 778/Active site: Lys, Glu, Asp #status predicted
 F;783, 796/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 23.1%; Score 1216.5; DB 1; Length 972;
 Best Local Similarity 32.8%; Pred. No. 6.4e-52;
 Matches 325; Conservative 156; Mismatches 316; Indels 195; Gaps 33;

QY 75 VYEAADV--SASITLQVLVDAPGNSICLWFKHSLNCQPHFDLQNRGVVSMVLK 132
 Db 22 VIEPSVPELVKPGATVLRV---GNGSVNDGPPS-----PHTLVSDGSSSLSTN 72
 QY 133 MTE-----TQAGEYL-----LFIQSEATNTILFTVSIIRNTLLYLRPPYFRKM 176
 Db 73 NATFQNTGYRCTEPDPLGGSAATHLVKDPAPMNVL---AQEVVVF----- 118
 QY 177 ENODALV-CISESVEPIVEVWLCDSQESCKEESPAVVKKEK-----VLHE--- 223
 Db 119 EDQDALPCL---LTDVPLE-----AGSLVRVRGRPLMRHTNYSFSPWHGFTIHRKF 169
 QY 224 LFGTDIRCCARNELCRECTRLFTIDLNOTPOTLP-----OLFLKVGELPWIRCK 273
 Db 170 IQSDYQCSALMG-GR---KWSISIRLKVKVQKVPGLPALTLPVPAELVIRGEAAQVCS 225
 QY 274 AVVNHGFLTWELNKALEGNYPFEMSTYTNRTMIRILFAFVSSVARNDTGYYTCSSS 333
 Db 256 ASSVDVDFVFLQHNNTKLA---IPQSDFNHNRVQ-KVLTNLNQDQDFQHAGNYSQVAS 281
 QY 334 ---KHPQSQALVTIVGKGFNATNSSD---YETDQVEEFCSVRFKAYPOIR-CTWTF 385
 Db 282 NVQGHK-STSMFFRVYESAYLNL--SSEQNLTQEVTVGEGNLKVMVEAYPGLGQFNWY 338
 QY 386 SRKSPFCQKGLDNGYSISKCNHKKQP-----GEYIF 418
 Db 339 -----LGPFSDFHPEPKLANATKOTYRHTFTLSLPLRKPEAGRYSF 381
 QY 419 HAENDDAQFTKMTLINIRKQVLAESAASQAS-----CFSDGYPLPSWTWKCSKSPNC 474
 Db 382 LARNPGGWRALTFTLTAYPEVSVIWTFFINGSGTLTCAASGYPOPNTWLQCSGHTDRC 441
 QY 475 TEEITEGVN---RKANRKFVGQWSSSTLNMSBAIKGFLVKCCAYNSLGTSCTLLN 530
 Db 442 DEAQVLQWDDPYPELVSQEPFHKTQVQSLLTETLEHNTQVTECRAHNSVSGSNAFPI 501
 QY 531 SPGPPFPFDQNISFATYIGVC---LLFIVLTLLCHYKQKQFYESQLQWQVGTSSDN 587
 Db 502 SAGATHPPDDEFLTPVVVACMSINALLLLLLLLYKQKPKYQVRWKITE--SYEGN 559
 QY 588 EYFYVDREYEDLKWEPFRENLEFGKVLGSGAFGKVNATAYGISKTGVSITQAVKMLK 647


```
Db 560 SYTFIDPTQPLPYNEKWEFPRNNLQFGKTLGAGAFKGVVEATAFGLGKEDAVLKUAVRMLK 619
Qy 648 EKADSSREALMSLKMTOLGSHENLVNLLGACTLSPVILIEYCCYGDLLANLRSKR 707
Db 620 STAHADKEALMSLKIMSHLGSHENLVNLLGACTHGGPVLVITTEYCCYGDLLNPLRKA 679
Qy 708 E-----KFHRTWTEIFKHNHFFSYPTFQSHPNSSMPGSRVQIHP 747
Db 680 EAMLPSPSQDEPGGVYKNIHLEKKYVRDGSF-----SQGVDTYV 724
Qy 748 DSDQISGLHGNSFHSDEIEYENOKRLBEEDNLVLFEDLLCPAYQVAKMEFLFKSC 807
Db 725 EMRPVSTSSNDSF-SEODLKDGEDRPLE-----LRDLLHFSQVQAQMAFLASKNC 774
Qy 808 VHRDLAARNVLVTHGVKVKICDGLARDIMSDSNVVRGNARLPVKMAPESLPEGYTI 867
Db 775 IHRDVAARNVLLTNGHVAKIGDGLARDIMDSNIYVGNARLPVKMAPESIFDCVTIV 834
Qy 868 KSDVMSYGILLWEITFSLGVNYPGIPVDANFYKLIQNGFKMDQPFYATEIYIIMQSCWA 927
Db 835 QSDVMSYGILLWEITFSLGVNYPGILVNSKRYKLVKDGYNQAQAPAPAKNIYSIMQACWA 894
Qy 928 FDSKRPSPFNLTSLFGLCOL-ADAEAEAMQNV 958
Db 895 LEPTHRPTFQICSLFQEQAOEDRRERYTNL 926

RESULT 12
JN0677
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - chicken
N;Alternate names: tyrosine kinase receptor kit
A;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JN0677
R;Sasaki, E.; Okamura, H.; Chikamune, T.; Kanai, Y.; Watanabe, M.; Naito, M.; Sakurai, M
Gene 128, 257-261, 1993
A;Title: Cloning and expression of the chicken c-kit proto-oncogene.
A;Reference number: JN0677; MUID:93292995; PMID:7685729
A;Accession: JN0677
A;Molecule type: mRNA
A;Residues: 1-960 <SAS>
A;Cross-references: DDBJ:D13225; NID:g303532; PIDN:BAA02506.1; PID:g303533
A;Experimental source: brain
A;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase related transforming protein;
protein kinase
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-960/Product: tyrosine kinase receptor #status predicted <MAT>
F;314-380/Domain: immunoglobulin homology <IMM>
F;573-916/Domain: protein kinase homology <KIN>
F;581-589/Region: protein kinase ATP-binding motif
F;76,135,149,269,286,306,318,338,356,453,469/Binding site: carbohydrate (Asn) (covalent)
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Query Match 23.0%; Score 1215; DB 1; Length 960;
Best Local Similarity 32.3%; Pred. No. 7.5e-52;
Matches 314; Conservative 165; Mismatches 370; Indels 124; Gaps 34;
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Qy 66 ALRQSGSTVVEAAAEVDVDSASTLQVLVDAPGNISCLVWPKSS-----LNCQPHFD 119
Db 18 SLIPAGSGVPHESSLVNKGELRLKCNBERP-----VTWNFQNSDPSAKTRISNEKEWH 73
Qy 120 LONRGV--VSMVLKMTQAGEVLLFTQSEATNYTLFTVTSIRNTLYTLRRPYFRKWE 177
Db 74 TKNATIRDIGECKSGSIVNSFVFKDP-----NVLFV---DSLIY-----GKED 119
Qy 178 NQDALVCISESVPPE-IVEWVLCDQSQGESCKEESPAVVVKKEE-----KVLHLEFGTDIRCC 232
Db 120 $DILLVC---ELTPDDVLNFTLRKCDGRLPKNMTTFINPQKGIILKNVQSRFKCYOCL 176
Qy 233 AR-NELGRECTRLFTIDLNQPT-OTTLPOL-----FLKVGEPWLWIRCKAVVNHGRL 283
Db 177 AKHNGVEKISEHIF---LNVRFVHKALPVITLSKSYELLKEGEPEVTCIITDVS SVKA 233
```

```
Qy 284 TWLEENKALBEGNYFEMSTYSTNRTMIRILPAFVSSVARNDTYGTYCSSKHP--SQSAL 341
Db 234 SWISYKSAIVTSKRNLDGYERK-----LTNIRS VGNDSGEFTC-QAENPFKTKNAT 288
Qy 342 VTI--VKGGIN---ATNSSDEYIDQVEFCFVRKAYQAIR-CTWTFRKSPPCQK 395
Db 289 VTKALAKGFVRLFPATMTTIDINAGQNG--LTVEYAYPKPEEVMVMYNETL---QN 343
Qy 396 GLDNGYSISKFCNHK-----OPGEYIFHAENDDAQFTKMTFLIRRKPOVLA 443
Db 344 SSDIYVKFTVGNNSYISELHLFLKGTGGIYTFVNSDASSSVTFNVVVKTEPILT 403
Qy 444 EASASQ--ASCFSQGYPLPSMTWKCKSDKSPNCTBEITEGVNMRKANRKKVFGQWSSSTL 501
Db 404 LDMGLNDILOCVATGFPAPTIYWFYFCPTGEORCLDSPISPMVKVS-----YTNSSVP 457
Qy 502 NMSEAIKGLVKCCAYNSLGTSCETILLNSGPPFF-----IQDNISFYA-----TIGV 550
Db 458 SFERILVESTVNASMFKSTGTICCEASSNGDKSVFFNFAIKEQIRHTLFTPLLIAFGV 517
Qy 551 CLLFIIVLTLLICHYKKOPRYESOLQWV-OVTGSSDNEYFVDPREYEDLKWFFPREN 609
Db 518 AAGLMCIIVMLVYIYLOKPKYEVQWVVEING---NNYVIIDTQLPYDHKWFFPRNR 574
Qy 610 LEFGKVLGSGAFGKVMNATAYGISKTGVSIQVAVKMLKEKADSSEREALMSLKMTOLG 669
Db 575 LSGKTLGAGAFGVVEATAYGLFKSDAAMTVAVKMLKPSAHLTEREALMSLKVLSYL 634
Qy 670 SHENIVNLLGACTLSPVILIEYCCYGDLLNLYRSKKEP-----HRTWTEIFKHNHNSF 725
Db 635 NHINIVNLLGACTTGGTPLVITEYCCYGDLLNFLRRKRDSCFCPKHEEHAEEAVYENL-- 692
Qy 726 YPTFQSHNS-----SMPGSRVQIHPDSDQISGLHGNSFHSDEIEYENOKLEEE 778
Db 693 --LHQAEPTADAVNEYMDKPGVSYAVPPKADKKRPVKSSTDDQ----VTLSMLEDE 746
Qy 779 DLNVLITFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGVKVKICDPLGLARDIMS 838
Db 747 --LALDVEDLLSFSYQVAKGMSFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIRN 804
Qy 839 DSNVVRGNARLPVKMAPESLPEGYIYTKSDVMSYGLLWEITFSLGVNYPGIPVDANF 898
Db 805 DSNVVRGNARLPVKMAPESIFNCVYTFESDVMVSYGLLWEITFSLGSSPYGMPVDSKF 864
Qy 899 YKLQNGFKMDQPFYATEIYIIMQSCWAFDSRKRPSFNLTSLFGLCOLADAEAEAMQNV 958
Db 865 YKMIKEGYRMPSPCSPPEMYDMKSCWDADPLQRPFTKQIVQLIEQQQLSDNAPRVAN- 923
Qy 959 DGRVSECPHTYQN 971
Db 924 ---FSTPSTQGN 933
```

RESULT 13

```
T30816
macrophage colony-stimulating factor receptor - Japanese pufferfish
C;Species: Fugu rubripes (Japanese pufferfish)
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Jun-2000
C;Accession: T30816
R;How, G.F.; Venkatesh, B.; Brenner, S.
Genome Res. 6, 1185-1191, 1996
A;Title: Conserved linkage between the pufferfish (Fugu rubripes) and human genes for I
A;Reference number: 220882; MUID:97129405; PMID:8973913
A;Accession: T30816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-975 <HOW>
A;Cross-references: EMBL:U63926; NID:g1752706; PID:g1752708; PIDN:AAC60063.1
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology
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Query Match 23.0%; Score 1213; DB 2; Length 975;
Best Local Similarity 31.7%; Pred. No. 9.6e-52;
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Search completed: May 24, 2003, 17:00:37
Job time : 39.5174 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:38:45 ; Search time 18.0091 Seconds
(without alignments)
2286.959 Million cell updates/sec

Title: US-09-919-408-4

Perfect score: 5274

Sequence: 1 MPALARDAGTVLLWFSAM.....PFSREMDIGLLSPQAQVEDS 993

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	5274	100.0	993	1 FLT3_HUMAN	P36888 homo sapien
2	4429.5	84.0	992	1 FLT3_MOUSE	Q00342 mus musculus
3	1295.5	24.6	978	1 KIT_CAPHI	Q28317 capra hircu
4	1286	24.4	977	1 KIT_BOVIN	P43481 bos taurus
5	1266	24.0	975	1 KIT_MOUSE	P05532 mus musculus
6	1251	23.7	976	1 KIT_HUMAN	P10721 homo sapien
7	1247.5	23.7	975	1 KIT_CANFA	O97799 canis fami
8	1225.5	23.2	980	1 KFSM_FELCA	P13369 felis silve
9	1224.5	23.2	978	1 KIT_FELCA	Q28889 felis silve
10	1224	23.2	978	1 KFSM_FSVMD	P00545 feline sarc
11	1216.5	23.1	972	1 KFSM_HUMAN	P07333 homo sapien
12	1215	23.0	960	1 KIT_CHICK	Q08156 gallus gall
13	1204	22.8	977	1 KFSM_MOUSE	P09581 mus musculus
14	1194	22.6	978	1 KFSM_RAT	Q00495 rattus norv
15	1176	22.3	1088	1 PGDS_RAT	P20786 rattus norv
16	1169	22.2	1089	1 PGDS_MOUSE	P26618 mus musculus
17	1166	22.1	1089	1 PGDS_HUMAN	P16234 homo sapien
18	1128	21.4	1087	1 PGDS_XENLA	P26619 xenopus lae
19	1105.5	21.0	1098	1 PGDR_MOUSE	P05622 mus musculus
20	1086.5	20.6	1106	1 PGDR_HUMAN	P09619 homo sapien
21	990	18.8	1338	1 VGR1_HUMAN	P17948 h vascular
22	989.5	18.2	370	1 KIT_FSVHZ	P04048 feline sarc
23	959.5	18.2	1333	1 VGR1_MOUSE	P35969 mus musculus
24	956	18.1	1336	1 VGR1_RAT	P53767 rattus norv
25	951.5	18.0	1356	1 VGR2_HUMAN	P35968 homo sapien
26	935	17.7	1348	1 VGR2_COTJA	P52583 coturnix co
27	923	17.5	1367	1 VGR2_MOUSE	P35918 mus musculus
28	917.5	17.4	1343	1 VGR2_RAT	Q08775 rattus norv
29	907.5	17.2	1363	1 VGR3_MOUSE	P35917 mus musculus
30	904.5	17.2	1298	1 VGR3_HUMAN	P35916 homo sapien
31	874.5	16.6	823	1 CEK3_CHICK	P18461 gallus gall
32	849	16.1	821	1 FGR2_HUMAN	P21802 homo sapien
33	845	16.0	813	1 FGR2_XENLA	Q03364 xenopus lae

RESULT 1

ID	FLT3_HUMAN	STANDARD;	PRT;	993 AA.
AC	P36888; Q13414;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DE	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	FL cytokine receptor precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor FLT3) (Stem cell tyrosine kinase 1) (STK-1) (CD135 antigen).			
GN	FLT3 OR STK1			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94119906; PubMed=7507245;			
RA	Small D., Levenstein M., Kim E., Carow C., Amin S., Rockwell P., Witte L., Burrow C., Ratajczak M.Z., Gewirtz A.M., Civin C.I.;			
RT	"STK-1, the human homolog of Flk-2/Flt-3, is selectively expressed in CD34+ human bone marrow cells and is involved in the proliferation of early progenitor/stem cells."			
RT	Proc. Natl. Acad. Sci. U.S.A. 91:459-463(1994).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93357464; PubMed=8394751;			
RA	Rosnet O., Schiff C., Pebusque M.J., Marchetto S., Tonnelle C., Toiron Y., Big F., Birnbaum D.;			
RT	"Human FLT3/Flk2 gene: cDNA cloning and expression in hematopoietic cells."			
RT	Blood 82:1110-1119(1993).			
RL	[3]			
RP	SEQUENCE OF 783-942 FROM N.A.			
RX	MEDLINE=91169547; PubMed=2004790;			
RA	Rosnet O., Mattei M.-G., Marchetto S., Birnbaum D.;			
RT	"Isolation and chromosomal localization of a novel FMS-like tyrosine kinase gene."			
RL	Genomics 9:380-385(1991).			
CC	!- FUNCTION: RECEPTOR FOR THE FL CYTOKINE. HAS A TYROSINE-PROTEIN KINASE ACTIVITY.			
CC	!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.			
CC	!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	!- TISSUE SPECIFICITY: BONE MARROW CELLS.			
CC	!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.			
CC	!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
CC	!- DATABASE: NAME=PROW; NOTE=CD guide CD135 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd135.htm"			
CC	!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.; WWW="http://www.infobiogen.fr/services/Chromancer/Genes/FLT3ID144.html"			
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ALIGNMENTS

34	827	15.7	821	1	FGR2_MOUSE	P21803 mus musculus
35	807	15.3	806	1	CEK2_CHICK	P18460 gallus gall
36	803.5	15.2	819	1	FGR1_CHICK	P21804 gallus gall
37	790.5	15.0	654	1	BFR2_HUMAN	Q01742 homo sapien
38	784	14.9	812	1	FGR1_XENLA	P22182 xenopus lae
39	779.5	14.8	822	1	FGR1_HUMAN	P11362 homo sapien
40	779	14.8	822	1	FGR1_MOUSE	P16092 mus musculus
41	766.5	14.5	806	1	FGR3_HUMAN	P22607 homo sapien
42	765	14.5	822	1	FGR1_RAT	Q04589 rattus norv
43	754	14.3	801	1	FGR3_MOUSE	Q61851 mus musculus
44	728.5	13.8	1052	1	FGR2_DROME	Q09147 drosophila
45	716	13.6	1115	1	RET_MOUSE	P35546 mus musculus

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CC EMBL; U02687; AAA18947.1; -
CC EMBL; Z26652; CAA81393.1; -
CC EMBL; L36162; CAA35487.1; -
CC HSSP; P11362; IFCK.
CC Genew; HGNC:3765; FLT3.
DR MIN; 136351; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR001824; RYKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR Signal; Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain.
FT SIGNAL 1 26
FT CHAIN 27 993 FL CYTOKINE RECEPTOR.
FT DOMAIN 27 543 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 544 563 POTENTIAL.
FT DOMAIN 564 993 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 610 943 PROTEIN KINASE.
FT NP_BIND 616 624 ATP (BY SIMILARITY).
FT BINDING 644 644 ATP (BY SIMILARITY).
FT ACT_SITE 811 811 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 323 323 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 473 473 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 502 502 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 541 541 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 8 8 A -> G (IN REF. 2).
FT CONFLICT 10 11 TV -> QL (IN REF. 2).
FT CONFLICT 78 78 A -> R (IN REF. 2).
FT CONFLICT 227 227 T -> M (IN REF. 2).
FT CONFLICT 346 346 G -> E (IN REF. 2).
FT CONFLICT 940 940 T -> H (IN REF. 3).
SQ SEQUENCE 993 AA; 112804 MW; 16790124B02F6BBF CRC64;

Query Match 100.0%; Score 5274; DB 1; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVLLVVFSAIMFGTITNQDLPVTKVLINHKNDSSVGKSSYPMVVSESP 60
Db 1 MPALARDAGTVLLVVFSAIMFGTITNQDLPVTKVLINHKNDSSVGKSSYPMVVSESP 60

Qy 61 EDLGCALPQSSGTYYEAAAVDVDSASITLQVLVDAPGNISCLVFKHSSLNCOPHFDL 120
Db 61 EDLGCALPQSSGTYYEAAAVDVDSASITLQVLVDAPGNISCLVFKHSSLNCOPHFDL 120

Qy 121 QNRGVSVWLKMTQAGEYLLFTQSEATNTYLTFTVSRINTLYTLRRPYFRKMNQD 180
Db 121 QNRGVSVWLKMTQAGEYLLFTQSEATNTYLTFTVSRINTLYTLRRPYFRKMNQD 180

Qy 181 ALVCISSEVPEIVWLCDSSGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISSEVPEIVWLCDSSGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240

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Qy 241 CTRLFTIDLNTQPTTLPOLFLKVGEPWIRCKAVVNHGFLGTWELNKALEEGNYFEM 300
Db 241 CTRLFTIDLNTQPTTLPOLFLKVGEPWIRCKAVVNHGFLGTWELNKALEEGNYFEM 300

Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTCSKSPQSALVTIVGKGFINTATNSSEDEY 360
Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTCSKSPQSALVTIVGKGFINTATNSSEDEY 360

Qy 361 IDQYEEFCFSVRFKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFNHGHQPGVEIFHA 420
Db 361 IDQYEEFCFSVRFKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFNHGHQPGVEIFHA 420

Qy 421 ENDDAFTQKMTLNIRRRKPOVLAESAASQSCFSDGYPPLPSWTWKCKSDKSPNCTEITE 480
Db 421 ENDDAFTQKMTLNIRRRKPOVLAESAASQSCFSDGYPPLPSWTWKCKSDKSPNCTEITE 480

Qy 481 GVMNRKANRKVFQWVSSSTLNSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Db 481 GVMNRKANRKVFQWVSSSTLNSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540

Qy 541 NISFYATIGVCLLFIWLTLLIHKYKKQFRYESQLOMVOVTGSSDNEYFYVDREYEYD 600
Db 541 NISFYATIGVCLLFIWLTLLIHKYKKQFRYESQLOMVOVTGSSDNEYFYVDREYEYD 600

Qy 601 LKWEFPRENLEFGKVLGSAFGKVMNATAYGSKTGVSIQAVKMLKEKADSSERALMS 660
Db 601 LKWEFPRENLEFGKVLGSAFGKVMNATAYGSKTGVSIQAVKMLKEKADSSERALMS 660

Qy 661 ELKMTQLGSHENIVNLLGACTLSGPYILIFYCVCYDGLLNLRSKREKPHRTWTIFKE 720
Db 661 ELKMTQLGSHENIVNLLGACTLSGPYILIFYCVCYDGLLNLRSKREKPHRTWTIFKE 720

Qy 721 HNFSPYPTFQSHPSNMPGSRVQIHPDSQISGLHNSFHSEDEIEYENQKLEEEEDL 780
Db 721 HNFSPYPTFQSHPSNMPGSRVQIHPDSQISGLHNSFHSEDEIEYENQKLEEEEDL 780

Qy 781 NVLTTFEDLLCFAYQVAKGMFELEKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDS 840
Db 781 NVLTTFEDLLCFAYQVAKGMFELEKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDS 840

Qy 841 NYVVRGNARLPVKWAPESLFGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWAPESLFGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK 900

Qy 901 LIQNGFKMDQPPYATEEYIIMQSCWAFDSRKRPSPPNLTSLGCOLADAEAEYQNVGD 960
Db 901 LIQNGFKMDQPPYATEEYIIMQSCWAFDSRKRPSPPNLTSLGCOLADAEAEYQNVGD 960

Qy 961 RVSECPHTYQNRPRPFSREMDLGLLSPQAQVEDS 993
Db 961 RVSECPHTYQNRPRPFSREMDLGLLSPQAQVEDS 993

RESULT 2
FLT3 MOUSE
ID FLT3 MOUSE STANDARD; PRT; 992 AA.
AC Q00342;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FL cytokine receptor precursor (EC 2.7.1.112) (Tyrosine-protein kinase
GN FL3 OR FLT-3 OR FLK-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91292518; PubMed=1648448;
RA Matthews W., Jordan C.T., Wiegand G.W., Pardoll D., Lemischka I.R.;

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RT "A receptor tyrosine kinase specific to hematopoietic stem and
 RT progenitor cell-enriched populations.";
 RL Cell 65:1143-1152(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92019834; PubMed=1656368;
 RA Rosnet O., Marchetto S., Delapeyriere O., Birnbaum D.;
 RT "Murine Flt3, a gene encoding a novel tyrosine kinase receptor of the
 RT PDGFR/CSF1R family.";
 RL Oncogene 6:1641-1650(1991).
 RN [3]
 RP CHARACTERIZATION
 RX MEDLINE=93205405; PubMed=8384358;
 RA Maron N., Rotapel R., Rosnet O., Marchetto S., Lavezzi C.,
 RA Mannoni P., Birnbaum D., Dubreuil P.;
 RT "Biochemical characterization and analysis of the transforming
 RT potential of the Flt3/Flk2 receptor tyrosine kinase.";
 RL Oncogene 8:909-918(1993).
 CC -1- FUNCTION: RECEPTOR FOR THE FL CYTOKINE. HAS A TYROSINE-PROTEIN
 CC KINASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: HEMATOPOIETIC STEM AND PROGENITOR CELL-
 CC ENRICHED POPULATIONS. FOUND IN BRAIN, PLACENTA AND TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGFR RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M64689; AAA37634.1; -;
 DR EMBL; X59398; CAA42041.1; -;
 DR PIR; A39931; A39931.
 DR HSSP; P11362; 1FGK.
 DR MGD; MGI:95559; Flt3.
 DR InterPro; IPR000719; Ruk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; IG_Like; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR Signal; Transferrase; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 992 FL CYTOKINE RECEPTOR.
 FT DOMAIN 28 544 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 545 564 POTENTIAL.
 FT DOMAIN 565 992 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 611 946 PROTEIN KINASE.
 FT NP_BIND 617 625 ATP (BY SIMILARITY).
 FT BINDING 645 645 ATP (BY SIMILARITY).
 FT ACT_SITE 814 814 BY SIMILARITY.
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	445	445	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	474	474	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	503	503	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	542	542	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	150	150	R -> A (IN REF. 2).
FT	CONFLICT	242	242	C -> S (IN REF. 2).
FT	CONFLICT	726	726	S -> F (IN REF. 2).
FT	CONFLICT	957	979	CIRTSIHLPKQAPOQGGGLRAQ -> MYQNMGNVPEHPS
FT	CONFLICT	983	983	IYQNRPLRSRAGSEPP (IN REF. 2).
FT	CONFLICT	983	983	R -> A (IN REF. 2).
SQ	SEQUENCE	992	RA; 112639	MM; 407A087853372100
				CHC64;

Query Match 84.0%; Score 4429.5; DB 1; Length 992;
 Best Local Similarity 84.1%; Pred. No. 3.7e-289;
 Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

QY	1	MPALA-RDAGTVPLAVFSA	MI	FGIT	IQD	LPV	KV	IK	NH	KND	SS	V	G	K	S	S	P	M	V	S	E	59	
DB	1	MPALAQRDRRL	LL	LV	LS	VM	LE	TV	TD	LP	V	K	CV	LS	H	EN	G	S	S	A	K	P	60
QY	60	PEDLGCALR	PO	SG	TV	Y	E	A	A	V	E	D	V	S	A	I	T	L	Q	V	L	V	119
DB	61	PEDLOCTPR	Q	SE	GI	V	E	A	T	V	E	A	E	S	G	I	T	L	Q	V	L	V	120
QY	120	LQNRGVSM	VL	K	M	T	E	T	Q	A	E	Y	L	L	F	I	Q	S	E	A	T	N	179
DB	121	LQNRGIVS	M	A	I	N	V	T	E	T	Q	A	E	Y	L	L	I	Q	S	E	A	T	180
QY	180	DALVCIS	V	P	E	P	I	V	E	W	L	C	D	S	O	G	E	S	C	K	E	S	239
DB	181	DALLCIS	E	G	V	P	E	T	V	E	W	L	C	S	H	R	E	S	C	K	E	G	240
QY	240	ECTRLFT	D	L	N	O	P	T	T	L	P	Q	L	K	V	G	E	P	L	I	R	C	299
DB	241	ECKUFT	D	L	N	O	A	P	O	S	T	L	P	Q	L	K	V	G	E	P	L	I	300
QY	300	MSTYSTNR	T	M	I	R	L	F	A	V	S	S	V	A	R	N	D	T	G	Y	T	C	359
DB	301	MSTYSTNR	T	M	I	R	L	F	A	V	S	S	V	A	R	N	D	T	G	Y	T	C	360
QY	360	EIDQYEE	R	C	F	S	V	R	F	K	A	P	O	I	R	C	T	W	T	F	S	R	419
DB	361	EIDPYEK	F	C	S	V	R	F	K	A	P	O	I	R	C	T	W	T	F	S	R	K	420
QY	420	ARNDDAQ	T	T	O	M	F	T	L	N	I	R	R	K	P	O	V	L	A	S	A	S	479
DB	421	ARNDDAQ	T	T	O	M	F	T	L	N	I	R	R	K	P	O	V	L	A	S	A	S	480
QY	480	EGVMNR	K	A	N	R	K	V	G	W	S	S	T	L	N	M	S	E	A	I	K	G	539
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QY	600	DLKWEF	P	R	E	N	E	F	G	V	L	G	S	G	A	F	G	K	V	N	A	T	659
DB	601	DLKWEF	P	R	E	N	E	F	G	V	L	G	S	G	A	F	G	K	V	N	A	T	660
QY	660	SELKMT	O	L	G	S	H	E	N	I	V	N	L	L	G	A	C	T	L	S	G	P	719
DB	661	SELKMT	O	L	G	S	H	E	N	I	V	N	L	L	G	A	C	T	L	S	G	P	720
QY	720	EHNF	S	F	Y	T	P	S	H	P	N	S	M	P	G	S	R	E	V	O	I	H	777
DB	721	EHNF	S	S	Y	T	P	S	H	P	N	S	M	P	G	S	R	E	V	O	I	H	780
QY	778	EDLN	V	T	E	D	L	L	C	F	A	Y	O	V	A	K	M	E	F	L	E	P	837
DB	781	EDLN	V	T	E	D	L	L	C	F	A	Y	O	V	A	K	M	E	F	L	E	P	840
QY	838	SDSN	V	V	R	G	N	A	R	L	P	V	K	M	A	P	E	S	L	F	E	G	897

Db 841 SDSSVVRGNARLPVKWAPSLFEGIVTIKSDVMSYGILLWEIFSLGWNYPGIPVDAN 900
QY 898 FYKLIQNGKMDQPFYATEEYIIMQSCWAFDSKRSPFNLTSLFGLCOLADAEAMYQN 957
Db 901 FYKLIQSGFKMEQPFYATEGYIFYMOSCWAFDSKRSPFNLTSLFGLCOLAEAEAC--- 957
QY 958 VDRGVSECPHYQNRPRFSDREMDLGLLSPOAQVE 991
Db 958 ----IRTSIHLPKQAAPOORG-GLRAQSPQK 986
RESULT 3
KIT_CAPHI
ID_KIT_CAPHI STANDARD; PRT; 978 AA.
AC Q28317;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN KIT.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Shiba; TISSUE=Cerebellum;
RX MEDLINE=97342548; PubMed=9199245;
RA Tanaka S., Yanagisawa N., Tojo H., Kim Y.-J., Tsujimura T.,
RA Kitamura Y., Sawasaki T., Tachi C.;
RT "Molecular cloning of cDNA encoding the c-kit receptor of Shiba goats
RT and a novel alanine insertion specific to goats and sheep in the
RT kinase insert region";
RL Biochim. Biophys. Acta 1352:151-155(1997).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
CC 3-KINASE (PI3K).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC
CC EMBL; D45168; BAA08116.1; -;
DR HSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00410; IG-like; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain.
FT SIGNAL 1 22
FT CHAIN 23 978
FT DOMAIN 23 521
FT TRANSMEM 522 544
FT DOMAIN 545 978
FT DOMAIN 590 939
FT NP_BIND 596 604
FT BINDING 624 624
FT ACT_SITE 794 794
FT MOD_RES 825 825
FT CARBOHYD 94 94
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FT CARBOHYD 145 145
FT CARBOHYD 284 284
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FT CARBOHYD 487 487
SQ SEQUENCE 978 AA; 109722 MW; CA4D663F98205CA9 CRC64;
Query Match 24.6%; Score 1295.5; DB 1; Length 978;
Best Local Similarity 33.3%; Pred. No. 3.9e-79;
Matches 335; Conservative 169; Mismatches 339; Indels 163; Gaps 35;
QY 47 VKSSSPVMSESPEDLGC-ALRPOSSGTYYEAAVEVDVSASITLQVLVDAPAGNISLW 105
Db 20 VQTGSSQPSV--SPCELSLPSIHPAKS-----ELIVSVGDEIRLLCTDPPGFVK--W 66
QY 106 VFHSSLLNCQPHFDLQNRGVVSMVLKMTETQAGELLYLFIOSEAT---NYTILFTVSIEN 162
Db 67 TFE-----ILQLSEKTNPEWIT-EKAEATNGTNYTCTNKGUSS 105
QY 163 TL-----LYTLRRPYFRKMENQDALVCISVPPIVVEWVLCDSQGESCKEESPAV 213
Db 106 SIYVVRDPEKFLIDLPLYKEEN-DTLVRCLPTDPE-VTNYSLTGCEGKPLKDLTV 163
QY 214 -----VKEEKVLHELFGTDIRC--CARNELGRE-CTRLFTID---LNQTPQTILP 258
Db 164 ADPRAGITIRNVKREYHRL-----CLHCSANQKSKMLSKKFTLVKRAAIKAVPVSVS 217
QY 259 Q--LFLKVGELPLWIRCKAVHVNHGFLTWELNKALEBGNFEMSTYSTNRIMAILPAF 316
Db 218 KTSYLLREGEEFAVTCILIKDVSSSDVMWIKENSOOSKAQTKKNSWHQGDFFSYLQERLT 277
QY 317 VSSVARNDTGYTTCSSSKHPQSALVT---IVGKGFINA-----TNSSEYDEIDQY 364
Db 278 ISSARVNDSGVFMCYANNTPGSANVTTLLEVVDKGFINIFPMNTTVFVNDGENDL--- 334
QY 365 EBFCSVRFRKAYQO-----IRCTWTFSRKSPFCEQKGLDNGYSISKFCNHKH----- 411
Db 335 -----VVEYEAYPKPEHRQWYMNRTSTDKWDDYPKSE-----NESNIRYVNNELHLTRLK 384
QY 412 --QPGEYIFHAENDDAQFTKMTNLNIRKPKQVLAESA--SOASCFSDGYPPLPSWTWKC 467
Db 385 GTEGGTYTFHVSNDSVNSSVTFNVNVTNPKPILTHDLVNGMLQCVAAAGFPPTIDWYFC 444
QY 468 SDKSPNCTEEI-TEGVNMRKANRVFGOWSSSTLNMSEAIGFLVKVCAYNSLGTSCBT 526
Db 445 PGTQRCSVPVGVVDVQIQNSVSPFFGKLVVYSLIDDTTFKHNGTVCEBRAYNDVKGSSAS 504
QY 527 ILLNSPGFPFPFIQDN-----ISFYATIGVCLLFIIVVLTLLICHYKKQFQY 572
Db 505 F-----NFAFGKNKEQIHAHTLFTPLTLLIGFVIAAGLWICFVMTLT---YKYLQKPMY 554


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QY 573 ESQLOMV-QVTGSSDNEYFVDPREYEDLKWEPFRENLEFGKVLGSGAFGKUNNATAYG 631
Db 555 EWQKVEEING---NNYVTDTPQPYDHKEFPFNRRLUSFGKTLGAGAPVVEATAYG 611
QY 632 ISKTGVSIOAVKMLKEKADSSEREALMSKMTOLGSHENIVNLLGACTLSGPIYLIF 691
Db 612 LIKSDAAMTVAVKMLKPSAHLTEREALMSKLVSLVGNHMINVLLGACTIGGPLVIT 671
QY 692 EYCCYGDLLNLYRSKREKHFRTWTE-----IPKEHNFSPYFPFQSHPNSSM---PGRRE 742
Db 672 EYCCYGDLLNLYRSKREKHFRTWTE-----IPKEHNFSPYFPFQSHPNSSM---PGRRE 742
QY 743 VOIHPDSOISGLHNGSHSEDEIEVENOKRLEEEEDLVNLFEDLLCAYQVAKGMEFL 802
Db 732 VVPTKAADKRRSARISGYS-----IERDVTTPAIMEDEL-ALOEDLLSFSYQVAKGMFL 785
QY 803 EFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDSNVVRGNARLPVKWMAPESLFE.862
Db 786 ASKNCIHRDLAARNVLLTHGRITKICDFGLARDIKNDSNVVKGARLPVKWMAPESEFN 845
QY 863 GIYTIKSDVMSYGILLWEIFSGVNPYPGIPVDANFYKLIQNGFKMDQPPYATEEYIIM 922
Db 846 CVYTESDVMYSYGIFLWELFSLGSPYPCMPVDSPKFKMIKEGFRMLSPHAPAEYDIM 905
QY 923 QSCWAFDSKRPSPNLTSLFCQLADAEAEYQVNDGRVSEC-PH 967
Db 906 KTCWDADPLKRPTRQIVQLEIKQISESTNHIYSN----LANCSPH 947

RESULT 4
KIT_BOVIN
ID KIT_BOVIN STANDARD; PRT; 977 AA.
AC P43481;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCPR)
DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN KIT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94215924; PubMed=7512939;
RA Kubota T., Hikono H., Sasaki E., Sakurai M.;
RT "Sequence of a bovine c-kit proto-oncogene cDNA.";
RL Gene 141:305-306(1994).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
CC 3-KINASE (PI3K).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; D16680; BAA04084.1; -.
CC HSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.

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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tys_kinase.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00410; IG like; 2.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain.
SIGNAL 1 22
FT CHAIN 23 977
FT DOMAIN 23 521
FT TRANSMEM 522 544
FT DOMAIN 545 977
FT DOMAIN 590 938
FT NP_BIND 596 604
FT BINDING 624 624
FT ACT_SITE 793 793
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FT CARBOHYD 130 130
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SQ SEQUENCE 977 AA; 109685 MW; 4B2719050893B7EF CRC64;

Query Match 24.4%; Score 1286; DB 1; Length 977;
Best Local Similarity 33.2%; Pred. No. 1.7e-78;
Matches 332; Conservative 172; Mismatches 344; Indels 152; Gaps 36;

QY 47 VKSSSYPMWSESPDLGC-ALRPOSSGTVYRAAAVEDVVSASITLQVLVADPAGNISCLW 105
Db 20 VQTGSSQPSV--SPGELSIPSIHPAKS-----ELIVSVGDEIRLLCTDPGFVK--W 66
QY 106 VFHSSSLNCPHFDLQNRGVSMVLKMTETQAGEVLLFLIOSEAT---NYTILFTVSI RN 162
Db 67 TPE-----ILGQSEKTNPEVIT-EKAEATNTGNYCTNKGGLSS 105
QY 163 TL-----LYTLRRPYFRKMNQDALVCISESVPEPIVEWLVCDGSCCKESPAPV 213
Db 106 SIYVVRDPEKFLIDLPLYGKEEN-DTLVRCPLTDPE-VTNYSLTGCGEGKPKDLTFV 163
QY 214 -----VKKEEKVLHFLFGTDIRC--CARNELGRE-CTRLFTID-----LNQTPOTPLP 258
Db 164 ADPKAGITIRNVKREYHRL-----CLHCSANQRGKSMLSKFTLKVRAAIKAVPVVSVS 217
QY 259 Q--LELKVEGLPIWIRCKAVHNVHGLTWELNKALEEGNYEMSTYSTNRTMIRILFAP 316
Db 218 KTSYLLRGEPEFAVTCVCLINDSSVSDSMWKENSQQTAKQTKKNSWHQDGFSLYRQERLT 277
QY 317 VSSVNRNDTGYTCSSSKHPSQSALVT---IVGKGFINA-----TNSSEDYEDIDQY 364
Db 278 ISSARVNSGVFMCYANNVTFGSANVTTLLEVVDKGFINIFPMNMTVTVFNDGENVDL--- 334
QY 365 BEFCFSVRFKAYPO-IRCTWTFSRKS-----PFCEQKGLDNGYSISKFCNKH----- 411
Db 335 -----VVEYEAYPEVHRQWIYMNRTSTDWKDDYPKSE-----NESNIYVNLHLTRUK 394

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 QY 468 SDKSPNCTEEI--TEGVNMRKANRKFQGVSSSTLNSEAIGFLVKCCAYNSIGTSCET 526
 Db 445 PGTQRCSVPVGPVDVQIQNSVSPFGKLVVYSDIDSTFKHNGTVCECRAYNDVKGSSAS 504
 QY 527 ILLNSPGPFP-----FIODNISFATIGVCLLFIIVLTLCHIKYKQFRIESQLQM 578
 Db 505 FNFAPKGNSEKQIHAHTLFTPLLIGFVIAAGLMCFWMLT-----YKYLQKPMYEVQWKV 560
 QY 579 V-QVYSSDNEYFYVDREYEDYDLKFFPRENLEFGVLGSGAFGKVMNATAYGISKTGV 637
 Db 561 VEEING---NNVYIDPTQLPYDHKWFFPRNRLSFGKTLGAGAFGKVVATAYGLIKSDA 617
 QY 638 SIQAVKMLKEKADSSEREAALMSKLMQTLGSHENIVNLGACTLSGPIYLIFEYCCYG 697
 Db 618 AMTAVKMLKPSAHLTEREALMSKLVLSYLGHNHNVNLGACTIGGPTLVITEYCCYG 677
 QY 698 DLLNVLRSKRKFHRTWTE-----IPKEHNFSPYPTFQSHPNSSM----PGSREVQIHPD 748
 Db 678 DLLNFLRRKRDSFICSKQEDHAELVYKNLLHSKSSCNDSTNEMDMKPGVSYV-VPTK 736
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 Db 737 ADKRSARIGSY-----IERDVTFAIMEDDEL-ALDLELLSFSYQVAKGMFLASKNCI 790
 QY 809 HRDLAARNVLVTHGKVKVICDFGLARDIMSDSNVYVRGNARLPVKWAPESLFGIYTIK 868
 Db 791 HRDLAARNILLTHGRITKICDFGLARDIKNDSNVYVKNARLPVKWAPESIFNCVITYE 850
 QY 869 SDVWSYGILLWEIFSLGVNYPGPVDANFYKLIQNGFKMDQPPVATEIIVIMQSWAF 928
 Db 851 SDVWSYGIFLWELFSLGSPYCPGMPVDSFKYMKIEGFRMLSPHAPAEYMDIMKTWDA 910
 QY 929 DSRKRSPFNLTSLFGCOLADAEAEAMYNQVDRVSEC-PH 967
 Db 911 DPLKRPTFKQVQLIEKQISESTNHIYSN-----LANCSFH 946

RESULT 5
 KIT_MOUSE
 ID_KIT_MOUSE STANDARD; PRT; 975 AA.
 AC P0532; Q61415; Q61416; Q61417;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mast/stem cell growth factor receptor precursor (BC 2.7.1.112) (SCFR)
 DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
 GN KIT OR SL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC STRAIN=BALE/c;
 RC STRAIN=BALE/c;
 RC MEDLINE=89296403; PubMed=2456920;
 RA Qiu F., Ray P., Brown K., Barker P.E., Jhanwar S., Ruddle F.H.,
 RA Besmer P.;
 RT "Primary structure of c-kit: relationship with the CSF-1/PDGF
 RT receptor kinase family -- oncogenic activation of v-kit involves
 RT deletion of extracellular domain and C terminus."
 RL EMBO J. 7:1003-1011(1988).
 RN [2]
 RP SEQUENCE FROM N.A. (TRUNCATED FORM).
 RC STRAIN=ICR;
 RX MEDLINE=92331813; PubMed=1378413;
 RA Rossi P., Marziali G., Albanesi C., Charlesworth A., Geremia R.,
 RA Sorrentino V.;
 RT "A novel c-kit transcript, potentially encoding a truncated receptor,

RT originates within a kit gene intron in mouse spermatids.";
 RL Dev. Biol. 152:203-207(1992).
 RN [3]
 RP LIGAND.
 RX MEDLINE=91006023; PubMed=1698611;
 RA Tan J.C., Buck J., Levi E., Besmer P.;
 RT "Candidate ligand for the c-kit transmembrane kinase receptor: KL, a
 RT fibroblast derived growth factor stimulates mast cells and erythroid
 RT progenitors.";
 RL EMBO J. 9:3287-3294(1990).
 RN [4]
 RP VARIANT W42 ASN-790.
 RX MEDLINE=90100577; PubMed=1688471;
 RA Tan J.C., Nocka K., Ray P., Traktman P., Besmer P.;
 RT "The dominant W42 spotting phenotype results from a missense mutation
 RT in the c-kit receptor kinase.";
 RL Science 247:209-212(1990).
 RN [5]
 RP VARIANT W37 LYS-582; WV MET-660 AND W41 MET-831.
 RX MEDLINE=90269214; PubMed=1693331;
 RA Nocka K., Tan J.C., Chiu E., Chu T.Y., Ray P., Traktman P.,
 RA Besmer P.;
 RT "Molecular bases of dominant negative and loss of function mutations
 RT at the murine c-kit/white spotting locus: W37, W41 and W.";
 RL EMBO J. 9:1805-1813(1990).
 CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
 CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DISEASE: WHITE-SPOTTING VARIANTS INDUCES SEVERE EFFECTS ON
 CC PIGMENTATION, GAMETOGENESIS AND HEMATOPOIESIS. MICE HOMOZYGOUS
 CC FOR W42 DIE PERINATALLY OF MACROCYTIC ANEMIA.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC
 CC EMBL; Y00864; CAA68772.1; -;
 CC EMBL; X65997; CAA46798.1; -;
 CC EMBL; X65998; CAA46799.1; ALT_SEQ.
 CC EMBL; X65998; CAA46800.1; -;
 CC PIR; S00474; TVMSKT.
 CC HSSP; P11362; 1FGK.
 CC MGD; MGI:96677; Kit.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR003006; Ig_MEC.
 CC InterPro; IPR003598; Ig_c2.
 CC InterPro; IPR003600; Ig_like.
 CC InterPro; IPR001824; RTKinaseIII.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00047; Ig; 1.
 CC Pfam; PF00069; Pkinase; 1.
 CC ProDom; PD000001; Euk_pkinase; 2.
 CC SMART; SM00410; IG_like; 3.
 CC SMART; SM00408; IGC2; 1.
 CC SMART; SM00219; TyrKc; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 CC Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;

Immunoglobulin domain; Disease mutation.

1 22
FT SIGNAL 1 22
FT CHAIN 23 975
FT DOMAIN 23 519
FT TRANSMEM 520 542
FT DOMAIN 543 975
FT DOMAIN 588 935
FT NP BIND 594 602
FT BINDING 622 622
FT ACT SITE 790 790
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FT VARIANT 582 582
FT VARIANT 660 660
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FT VARIANT 831 831
SQ SEQUENCE 975 AA; 109001 MW; BAB5CA4D9AF9CD2A CRC64;

Query Match 24.08; Score 1266; DB 1; Length 975;
Best Local Similarity 33.24; Pred. No. 3.7e-77;
Matches 336; Conservative 173; Mismatches 330; Indels 172; Gaps 41;

QY 35 CVLHKNNDSSVSGKSSPMVSPEDLGCALPQSGTGYVEAAAEVDVDSASITLQVL 94
Db 12 CVLVLRLGQTATSPQASGPSP-----SIHPAQS-----ELIVEAGDTL--- 54
QY 95 VDAFGNISCL-----NVFKHSSLNCPHFDLQNRGVSMVLKMTQAGEYLLFTQSE 148
Db 55 -----SLTCIDPDVPRWTFK-----TYFN-----EMVENKKEWIIQ-EKAE 89
QY 149 ATNYTLFTVSIKNTL-----LYTLRPPVFRKMNQDALVCISEVPEPIVE 195
Db 90 ATR-TGYTTCNSNGLTSSIIYFVRDPKFLVLGLPLFGK-EDSDALVRCPLTDPQ-VSN 146
QY 196 WVLCDQGESCKERSPAV-----VKKEKVLHFLGTDIRCCARNELGRECTRL--- 244
Db 147 YSLIEDCKSLPTDLTFVNPAGITIKVNRVHRLC-----VRCAAQ-----RDGTWLHSD 199
QY 245 -FTIDLNQ-----PQTLPLQ-----FLKVGPELWIRCKAVHNVHGFGLTW-----E 286
Db 200 KFTLKVREAIKAI PVSVPEPSTSHLKKGDTFTVCTIKDVSTSVSMWLMKMPQPHIAQ 259
QY 287 LENKALBEGNVFEMSTVSTNRMTIRILPAFVSSVARNDTGYTCTSSKHPQSQALVT--- 343
Db 260 VKHNSMRHGD-----NYERQETL-----ISSARVDDSGVFMFCYANNFTGSANVTTLK 309
QY 344 IVKGGFNATN-SSIEDYELDQYEEFCFSVREKAYPQ-IRCTWTFSRKSFPCEQKGLD--- 398
Db 310 VVEKGFNISPVRNTTVFTVDGENVDLVVEYEAIPKPEHQOQWIIYNNRT--SANKGRDYVK 367
QY 399 -NGYSISKFCNKHK-----QPGEYIFHAENDDAQFTKMTLNRKRPQVLA--EASAS 448
Db 368 SDNKSNIYVYNQLRLTKLGTGGTYTFLVNSDSASASVTENVYVNTKPELTYDRLING 427
QY 449 QASCFSDGYLPSTWTKCKSDKSNCTEITE-GVMNRKANRKYFGQWSSSTLNMSBAI 507
Db 428 MLQCVAREGFPEPTIDWYFCTGAEQRCCTTPVSPVDVQVQNVSVSPFGKLVQSSIDSSVFR 487
QY 508 KGFVAVKCAVNSLGTSCETILLNSFGPPFP---TODN-----ISFYATTGCVLLFIW 557
Db 488 HNGTVECKASNDVGKS--SAFFN-----FAPKEQIQAHTLFTPLLIGFVVAAGAMGIIVW 541
QY 558 LTLILCHYKKOPRYESQLQMV-QVTGSSDNEYFVVDREYEDLKWEEFFRENLEFGKVL 616

Db 542 LT-----YKLOKPMYEQMKVVEEING---NNYVIDTQLPYDHKWEFFPRNLSFGKTL 594
QY 617 GSGAFGKVMNATAGISKTGYSIOVAVKMLKEKADSSREALMSLKMTOLGSHENIVN 676
Db 595 GAGAFGKVEATAGLIKSDAAMTVAVKMLKPSAHLTEREALMSLKVLSYLGNNHNIIVN 654
QY 677 LLGACTLSGPIYLIFCYCYGDLNLYLSKREKF-----HRTWTEIFKEHNFSFYPTQ 730
Db 655 LLGACTVGGPLTVITEYCYCYGDLNLYLSKREKDSFIFSKQEQAALYKNLLHSTEPSCD 714
QY 731 SHPNSSM---PGSREVQIHPDSDOISLHGNSFHSEDIENYQKRLEBEEDNLVLTPE 787
Db 715 S-SNEYMDMKFGSVV-VPTKTDKRRSARIDSY-----IERDVTPAIMEDDEL-ALDLD 766
QY 788 LLCPAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKIKDFGLARDTMSDNYVVRGN 847
Db 767 LLSFSYQVAKAMAFSLAKNCHRDLAARNILTHGRITKICDFGLARDIRDSNVVVRGN 826
QY 848 ARLPVKMAPELSEFEGYITIKSDVMSYIGILLWEIFSLGVNVPYGPVPDANFYKLIQNGFK 907
Db 827 ARLPVKMAPESEIFSVYTFESDVMSYIGIFLWELFSLGSSYPGMPVDSKFKYMKIKEGR 886
QY 908 MDQPFYATEEIIYIMQSCWAFDSRKRSPFNLTSLFGCLADAEAMYQNV 958
Db 887 MVSPEHAPAEYMDVWTKCWDADPLKPTFKQVQVQLIEKQISDSTKHYSNL 937

RESULT 6
KIT HUMAN
ID - KIT HUMAN STANDARD; PRT; 976 AA.
AC P10721;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mast/stem cell growth factor receptor precursor (BC 2.7.1.112) (SCFR).
DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit) (CD117 antigen).
GN KIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Term placenta, and Fetal brain;
RX MEDLINE=88111521; PubMed=2448137;
RA Yarden Y., Kuang W.-J., Yang-Feng T., Coussens L., Munemitsu S.,
RA Dull T.J., Chen E., Schlessinger J., Francke U., Ullrich A.;
RT "Human proto-oncogene c-kit: a new cell surface receptor tyrosine
RL kinase for an unidentified ligand.";
RL EMBO J. 6:3341-3351(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93064697; PubMed=1279499;
RX Giebel L.B., Strunk K.M., Holmes S.A., Spritz R.A.;
RA "Organization and nucleotide sequence of the human KIT (mast/stem
RT cell growth factor receptor) proto-oncogene.";
RL Oncogene 7:2207-2217(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97179223; PubMed=9027509;
RA Andre C., Hampe A., Lachaux P., Martin E., Wang X.P., Manus V.,
RA Hu W.X., Gaubert F.;
RT "Sequence analysis of two genomic regions containing the KIT and the
RL FMS receptor tyrosine kinase genes.";
RL Genomics 39:216-226(1997).
RN [4]
RP VARIANT LYS-583.
RX MEDLINE=92291284; PubMed=1376329;
RA Fleischman R.A.;
RT "Human piebald trait resulting from a dominant negative mutant allele
RT of the c-kit membrane receptor gene.";
RL J. Clin. Invest. 89:1713-1717(1992).

RN [5] VARIANTS LEU-584.
 RP MEDLINE=92133600; PubMed=1370874;
 RA Spritz R.A., Giebel L.B., Holmes S.A.;
 RT "Dominant negative and loss of function mutations of the c-kit
 RT (mast/stem cell growth factor receptor) proto-oncogene in human
 RT piebaldism.";
 RL Am. J. Hum. Genet. 50:261-269(1992).
 RN [6] VARIANTS ARG-664.
 RP MEDLINE=92020918; PubMed=1717985;
 RA Giebel L.B., Spritz R.A.;
 RT "Mutation of the KIT (mast/stem cell growth factor receptor)
 RT proto-oncogene in human piebaldism.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8696-8699(1991).
 RN [7] VARIANTS VAL-816.
 RP MEDLINE=94013473; PubMed=7691885;
 RA Furitsu T., Tsujimura T., Tono T., Ikeda H., Kitayama H.,
 RA Koshimizu U., Sugahara H., Butterfield J.H., Ashman L.K.,
 RA Kanayama Y., Matsuzawa Y., Kitamura Y., Kanakura Y.;
 RT "Identification of mutations in the coding sequence of the proto-
 RT oncogene c-kit in a human mast cell leukemia cell line causing
 RT ligand-independent activation of c-kit product.";
 RL J. Clin. Invest. 92:1736-1744(1993).
 RN [8] VARIANTS PIEBALDISM GLY-791 AND VAL-812.
 RP MEDLINE=93322624; PubMed=7687267;
 RA Spritz R.A., Holmes S.A., Itin P., Kuester W.;
 RT "Novel mutations of the KIT (mast/stem cell growth factor receptor)
 RT proto-oncogene in human piebaldism.";
 RL J. Invest. Dermatol. 101:22-25(1993).
 RN [9] VARIANTS PIEBALDISM 893-GLU--PRO-896 DEL.
 RP MEDLINE=96287384; PubMed=8680409;
 RA Riva P., Milani N., Gandolfi P., Larizza L.;
 RA "A 12-bp deletion (7818del112) in the c-kit protooncogene in a large
 RT Italian kindred with piebaldism.";
 RL Hum. Mutat. 6:343-345(1995).
 RN [10] VARIANTS GIST VAL-559 DEL.
 RP MEDLINE=98361155; PubMed=9697690;
 RA Nishida T., Hirota S., Taniguchi M., Hashimoto K., Isozaki K.,
 RA Nakamura H., Kanakura Y., Tanaka T., Takabayashi A., Matsuda H.,
 RA Kitamura Y.;
 RT "Familial gastrointestinal stromal tumours with germline mutation of
 RT the KIT gene.";
 RL Nat. Genet. 19:323-324(1998).
 CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
 CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DISEASE: DEFECTS IN KIT ARE THE CAUSE OF A DEVELOPMENTAL
 CC ABNORMALITY KNOWN AS PIEBALDISM. AN AUTOSOMAL DOMINANT GENETIC
 CC DISORDER OF PIGMENTATION CHARACTERIZED BY CONGENITAL PATCHES OF
 CC WHITE SKIN AND HAIR THAT LACK MELANOCYTES.
 CC -1- DISEASE: DEFECTS IN KIT ARE THE CAUSE OF A GASTROINTESTINAL
 CC STROMAL TUMOR (GIST).
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD117 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd117.htm".
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiochem.fr/services/chromancer/Genes/KITD127.html".
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X66182; CAA29548.1; -
 DR EMBL; X69301; CAA49159.1; JOINED.
 DR EMBL; X69302; CAA49159.1; JOINED.
 DR EMBL; X69303; CAA49159.1; JOINED.
 DR EMBL; X69304; CAA49159.1; JOINED.
 DR EMBL; X69305; CAA49159.1; JOINED.
 DR EMBL; X69306; CAA49159.1; JOINED.
 DR EMBL; X69307; CAA49159.1; JOINED.
 DR EMBL; X69308; CAA49159.1; JOINED.
 DR EMBL; X69309; CAA49159.1; JOINED.
 DR EMBL; X69310; CAA49159.1; JOINED.
 DR EMBL; X69311; CAA49159.1; JOINED.
 DR EMBL; X69312; CAA49159.1; JOINED.
 DR EMBL; X69313; CAA49159.1; JOINED.
 DR EMBL; X69314; CAA49159.1; JOINED.
 DR EMBL; X69315; CAA49159.1; JOINED.
 DR EMBL; X69316; CAA49159.1; JOINED.
 DR EMBL; U63834; AAC50968.1; -
 DR PIR; S01426; TVHUKT.
 DR HSSP; P11362; IFGK.
 DR Genew; HGNC:6342; KIT.
 DR MIM; 164920; -
 DR MIM; 172800; -
 DR MIM; 606764; -
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00240; RECEPTOR TYR_KIN_III; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain; Disease mutation.
 FT SIGNAL 1 22
 FT CHAIN 23 976 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
 FT DOMAIN 23 520 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 521 543 POTENTIAL.
 FT DOMAIN 544 976 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 589 937 PROTEIN KINASE.
 FT NP BIND 595 603 ATP (BY SIMILARITY).
 FT BINDING 623 623 ATP (BY SIMILARITY).
 FT ACT SITE 792 792 BY SIMILARITY.
 FT MOD_RES 823 823 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 130 130 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 320 320 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 367 367 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 486 486 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 559 559 MISSING (IN GIST).
 FT VARIANT 583 583 /FTId=VAR_007965.
 FT VARIANT 584 584 E -> K (IN PIEBALDISM).
 FT VARIANT 584 584 F -> L (IN PIEBALDISM).
 FT VARIANT 664 664 /FTId=VAR_004105.
 FT VARIANT 664 664 G -> R (IN PIEBALDISM).

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FT VARIANT 791 791 /FTID=VAR_004106.
FT R -> G (IN PIEBALDISM).
FT /FTID=VAR_004107.
FT VARIANT 812 812 G -> V (IN PIEBALDISM).
FT /FTID=VAR_004108.
FT VARIANT 816 816 D -> V (IN MAST CELL LEUKEMIA;
FT CONSTITUTIVELY ACTIVATED).
FT /FTID=VAR_004109.
FT VARIANT 893 896 MISSING (IN SEVERE PIEBALDISM).
FT /FTID=VAR_004110.
SQ SEQUENCE 976 AA; 109864 MW; 81BCD76817F3454 CRC64;

Query Match 23.7%; Score 1251; DB 1; Length 976;
Best Local Similarity 32.7%; Pred. No. 3.8e-76;
Matches 324; Conservative 166; Mismatches 352; Indels 148; Gaps 34;

QY 47 VGRSSVPMVSESPEDLCALRPOSSGVYEAADVEVDVSASITLQVLVDAPGNISCLWV 106
Db 20 VQTGSSQPSVSPG-EPSPPSIHPOKSLI-----VRVGDIRLLCTDPGFVK--WT 67
QY 107 FKHSLLNCQPHFDLQNRGVSMVILKMTQAGBYLLFIQSEATN---YTLFTVTSIRNT 163
Db 68 FE-----ILDETNEKNQEWIT-EKAEATNTGKYCTCNKHGLSNS 106
QY 164 L-----LYTLRRPYFRKMNQDALVCISESVPEPIVEWVLCDQSGESCKEE----- 209
Db 107 IYFVRDPKFLFLVDRSLYK-EDNDTLVRCLPTDPE-VTNYSLKGCGQKPLPKDLRFP 164
QY 210 ---SPAVVKEEVLHFGDTRICCARNELGRETRFLTIDL-----NOTPTTLQ--L 260
Db 165 DPRAGIMIKSVKRAYRLC---LHCSVDQEGSVLSSEKFLUKPAPKAVPVSVSKASY 221
QY 261 FLKVGELWIRKAVHVNHGFLTWELN---KALEBGNYPENSTYSTRNTRIMRILFAFV 317
Db 222 LLRGEBEFTVCTIKOVSSSVYSTKRENSQTKLOEKYNSMHGDFNVERQAT---LTI 277
QY 318 SSVARNDTGYTCCSSKHPQSOSALVT---IVGKGFINA-----TNSSEYDEIDQYE 365
Db 278 SSARVNDSGVFCVNAVNTFGSANVTTLLEVVDKGFINFIPMINTTVFVNDGENVDL---- 333
QY 366 EFCFSVFKAQPO-IRCTWTFSRKSF--PCQKGLDNGYSISKFCNKH-----QPGE 415
Db 334 ----IVYEAFPKPEHQOMIYMNRTFTDKWEDYPKSNESNIRYVSELHLTRLKGTEGGT 389
QY 416 YIFHAENDDAQTKWFTLINIRKQVLA--EASASQASCSFGDGYPLPSWTWKCSDRSPN 473
Db 390 YTFVLSNDSYNAAFNAYVYNTKPEILTYDELVNGMLQCVAAGFPBTDIWDYFCPTQR 449
QY 474 CTBEITE-GVWNRKANRKFQGWVSSSTLNMSEAIGFLKCCAYNSLGTSCETILLNSP 532
Db 450 CSASVLPVDVQTLNSSGPPFKLVQSSIDSSAFKHNGTVECKAYNDVGKT--SAYFN-- 505
QY 533 GPPEFIODN-----ISFYATIGVCLLFIVLTLLICHKYKQFVRESQLOM 578
Db 506 --FAFGNNKEQIHPHTLFTPLLLTGFVIVAGMCCIIVMLT----YKLOKPMYEVQMKV 559
QY 579 V-QVTGSSDNEYFYVDREYEDLKWFFPRENLEFGVLGSGAFGKVMNATAYGISKTGV 637
Db 560 VEEING---NNYVYIDTQLPYDHWKFFPRNRLSFGKTLGAGAGKVVEATAYGLIKSDA 616
QY 638 SIQAVVRLKEKADSREALMSKLKMTQGLSHENIVNLGACTLGGPIYLIFEYCCYG 697
Db 617 AMTVAVRMLKPSAHLTREALMSKLKLVGNHNMIVNLGACTIGGTLVITEYCCYG 676
QY 698 DLLNLYLSKKEKPHRTWTE-----IKFHNFSYPTFQSHPNSM---PGSREVOIHPD 748
Db 677 DLLNFLRRKRDSFICSQEDQAEAAALYNLLHLSKESCDSTNENYMDMKPGVSYV-VPTK 735
QY 749 SDQISGLHSGHFSHSEDEIEYENQKRLBEEDNLVLTREDLLCPAYQVAKGMFELEFSCV 808
Db 736 ADKRSVRIGSY-----IERDVTVAIMWDEL-ALDLEDDLSFSIQVAKGNFALASKNCI 789
QY 809 HRDLAARNVLVTHGKVKIKCDFGLARDIMSDSNYVVRGNARLPVKWMAPESLFGIYTIK 868
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Db 790 HRDLAARNILLTHGRITKICDFGLARDIKNDNSYVVRGNARLPVKWMAPESLFCVITYPE 849
QY 869 SDVMSYIGILLWEIFSLGVNYPGIPVDANFYKLIQNGFKMDQPFYATBEIYIIMOSCWAF 928
Db 850 SDVMSYIGFLWELFSLGSSPYGMPVDSKFKYMKIEGFRMLSPERHAPAEYMDIMKTWDA 909
QY 929 DSRKRPPFNLTSLFLGQLADAEAMYNQV 958
Db 910 DPLKRPTFKQIVQLIEKQISESTNHYSNL 939

RESULT 7
KIT_CANPA
ID - KIT CANFA STANDARD; PRT; 975 AA.
AC O97799;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mast/stem cell growth factor receptor precursor (BC 2.7.1.112) (SCPR)
DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN KIT.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99142897; PubMed=989791;
RA Ma Y., Longley B.J., Wang X., Blount J.L., Langley K., Caughey G.H.;
RT "Clustering of activating mutations in c-KIT's juxtamembrane coding
RT region in canine mast cell neoplasms.";
RL J. Invest. Dermatol. 112:165-170(1999).
CC -I- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
CC 3-KINASE (PI3K).
CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -I- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
CC EMBL; AF042449; AAD02327.1; -.
CC HSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00219; TYKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
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Immunoglobulin domain.
 KW SIGNAL 1 24
 FT CHAIN 25 975
 FT DOMAIN 25 519
 FT TRANSMEM 520 542
 FT DOMAIN 543 975
 FT DOMAIN 588 936
 FT NP BIND 594 602
 FT BINDING 622 622
 FT ACT SITE 791 791
 FT MOD_RES 822 822
 FT CARBOHYD 96 96
 FT CARBOHYD 132 132
 FT CARBOHYD 147 147
 FT CARBOHYD 286 286
 FT CARBOHYD 296 296
 FT CARBOHYD 303 303
 FT CARBOHYD 355 355
 FT CARBOHYD 370 370
 FT CARBOHYD 403 403
 FT CARBOHYD 466 466
 FT CARBOHYD 489 489
 SQ SEQUENCE 975 AA; 109335 MW; 8F570BDB9F05B1CB CRC64;

Query Match 23.7%; Score 1247.5; DB 1; Length 975;
 Best Local Similarity 33.7%; Pred. No. 6.5e-76;
 Matches 333; Conservative 161; Mismatches 346; Indels 149; Gaps 39;

QY 47 VGKSSSPMSESPEDIGCALRPOSSGTVEAAAEVDVDSASITLQVLVDAPGNISCLWV 106
 DB 22 VRTGSSQFSVSPGSPSLP-SIHPAKS-----ELIVSGDELRLSLCTDPPGVK--WT 69
 QY 107 FKH--SSLNQCQHPDLQNGVSMVLKMTQACEYLLFIQSEATNYTL-----FT 157
 DB 70 FETGQUNENTH-----NEWITE-----KAEAG-----HTGNYTCWRDGLRSIY 110
 QY 158 VSIRN-TLLYLRLRPYFRKMNQDALVCISSEVPPIVWVLCDSQGSCKEESPAV--- 213
 DB 111 VFVDPKALFLVDLPYLYCK-EGNDTLVRCPLTDPE-VTNYSLRGCEGKPLPKDLTFVADP 168
 QY 214 -----VKKEKVLHLEFDTIRC--CARNELGRE-CTRLFTID-----INQPTQTLPLQ- 260
 DB 169 KAGITIRNVKREYHRL-----CLHCSADQKGRVLSKKFTLKRAATRAVPPVMSVSKTS 222
 QY 261 -FLAVGPEPLMTRCKAVHVNCHGFLGTWELN---KALEEGNVFEMSTYSTVTRTIRILFA 315
 DB 223 SLLKEGEAFSVMCFIKDVSSVFDMSWIKENSQQNTAQTSNWHHGFNFERQEKLI--- 279
 QY 316 FVSSVARNDTGYTCCSSSKHPQSALVT---IVGKGFINA-----TNSSEDEYIDQ 363
 DB 280 -ISSARVNDSGVFCVYANNTFGSANVTTLLEVVDKGFNIPFMSTTIFVNDGQNVDL-- 336
 QY 364 YEFCFVSFRVAYPQ-IRCTWTFGRKSPPCQKGL---DNGYSISKFCNHKH-----Q 412
 DB 337 -----IVEYEAYPEKPEHQOQIYNNRTFTDKEWDPKSDNESNI-RYVSELHLTLKNGE 389
 QY 413 PGEYIHAENDDAQFTKMTFLNIRRKPOVLAEASQA--SCFSDGYPLPSWTWKCKSDK 470
 DB 390 GGTFTFQVNSDNDVSSVTNFTVYVNTKPBILTHESLUNGMLQCVVAGPPVAVGVTFPCGA 449
 QY 471 SPNCTEEI-TEGVNVRKANRVFGQVSSSTLNMSIAIKGLVKCAYNLSLGTSCETILL 529
 DB 450 EQRCSVPFGPMDVQMSLSPSGKLVQSSIDYSAFKHNGTVCERAYNNVGRS--SAFF 507
 QY 530 NSPGFFPPIQD-----NISFYATIGVCLFPIVVLTLLCHIKYKQPRYESQLQMV 579
 DB 508 N-----FAPKEQIHPTLFTPLLIGFVIAAGNMCIIVMLT-----YKYLQKQMYEVQWKV 559
 QY 580 -QVTGSSDNEFYVDFFREYEDLKWEPFRENLEKGLVSGAGFQVMNATAYGISKTGV 638
 DB 560 BEING---NNVYIDPTQLPDYDHKWEFFPRNRLSPFKTLGAGFGKGVAVETAYGLIKSDAA 616
 QY 639 IQVAYKMLKEKADSSEREAALMSLQKMTQLGSHENIVNLLGACTLSGPIYLIFEYCCYGD 698

Db 617 MTVAVKMLKPSAHLTEREALMSLKVLSYLGHNHNVNLLGACTVGGPTLVITEYCCYGD 676
 QY 699 LLNAYLRSKREKEHRTWTE-----IFKEHNFYFPTQSHENSSM---PGSREVQIHDS 749
 Db 677 LLNFLRRKRDSFICSKQEDHGEVALYKNLHLSKSSCSDSTNEYMDMKPGVSYV-VPTKA 735
 QY 750 DOISSLGHGNSFHSDETEYENQKLEBEEDLNVLTFEDLLCFAYQVAKGMFLEPKSCVH 809
 Db 736 DKRSARIGSY-----IERDVTIPAIMEDEL-ALDLELLSFSYQVAKGMFLASKNCIH 789
 QY 810 RDLAARNVLVTHGKWKICDFGLARDIMSDNSYVVRGNARLPVKNMADPESLFEGIYTIKS 869
 Db 790 RDLAARNILLTHGRITKICDFGLARDIKDINSYVVKGNARLPVKNMADPESIFNCVYTFES 849
 QY 870 DVMSYGLLLEIFSLGVNPGIPVDANFYKLIQNGFKMDQOPFYATEEIIYIMQSCWAFD 929
 Db 850 DVMSYGLFELFSLGSPYPGMPVDSKFKYWKIEGFRMLSPERHAPAEWYDINKTCWAD 909
 QY 930 SRKRSPSPNLTSFLGCOLADAEAEAMYNQV 958
 Db 910 PLKEPTFKQIVQLLEKQISDSTNHIYSNL 938

RESULT 8
 ID_KFMS_FELCA STANDARD; PRT; 980 AA.
 AC P13369;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Macrophage colony stimulating factor I receptor precursor (CSF-1-R)
 DE (EC 2.7.1.112) (Fms proto-oncogene) (c-fms).
 GN CSF1R OR FMS.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8907753; PubMed=2849512;
 RA Woolford J., McAuliffe A., Rohrschneider L.R.;
 RT "Activation of the feline c-fms proto-oncogene: multiple alterations
 are required to generate a fully transformed phenotype";
 RL Cell 55:965-977(1998)
 CC -!- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
 TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: J03149; AAA30811.1; --
 DR PIR: A31636; TVCTMD.
 DR HSPSP; P13362; IFGK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; ig; 3.
 DR Pfam; PF00069; pkinase; 1.

DR ProDom: PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; IG-like; 4.
 DR SMART; SM00408; IGG2; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 980 MACROPHAGE COLONY STIMULATING FACTOR I
 FT RECEPTOR.
 FT DOMAIN 20 509 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 510 535 POTENTIAL.
 FT DOMAIN 536 980 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 24 104 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 107 197 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 204 298 IG-LIKE C2-TYPE DOMAIN 3.
 FT DOMAIN 299 397 IG-LIKE C2-TYPE DOMAIN 4.
 FT DOMAIN 398 502 IG-LIKE C2-TYPE DOMAIN 5.
 FT DOMAIN 579 908 PROTEIN KINASE.
 FT NP_BIND 585 593 ATP (BY SIMILARITY).
 FT BINDING 613 613 ATP (BY SIMILARITY).
 FT ACT_SITE 776 776 BY SIMILARITY.
 FT DISULFID 42 84 POTENTIAL.
 FT DISULFID 127 177 POTENTIAL.
 FT DISULFID 224 278 POTENTIAL.
 FT DISULFID 417 482 POTENTIAL.
 FT MOD_RES 807 807 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 275 275 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 410 410 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 490 490 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 980 AA; 108506 MW; 4ESCF661E97CF6FF CRC64;
 Query Match 23.2%; Score 1225.5; DB 1; Length 980;
 Best Local Similarity 33.5%; Pred No. 1.9e-74;
 Matches 32; Conservative 168; Mismatches 32; Indels 149; Gaps 34;
 QY 83 VDVSASITLQVLVDAPGNISCLW---VFKHSSLNCP-----HFDLQNRGVVSMVIL 131
 DB 32 VEPGTTVTLRCV-----GNGSVWDGPISPHNWLDLDPSSILTTNNATFQNTGYHCT-- 85
 QY 132 KWETQAGEYL--LFIQSEATNYTL---FTVSTINTLLYTLRPYFRKMENQDALV-CI 185
 DB 86 EPGNPGQGNATIHLYVKDPAKPKVLAQEVTV-----LEGQDALLPCL 128
 QY 186 SESYPEPIVE--WVLCDSDQESCKEE-----SP---AVVKEEKVHLPGTDIRCCARN 235
 DB 129 ---LTDPALEAGVSLVRVRGPVLRTQNTSPSPWHGFTIHKAKFIENHYV---QCSARV 181
 QY 236 ELGRECTRL-----FTIDLNOTPTLL-PQLFLKV-GEPLMIRCKAVHNVHFGLTWELE 288
 DB 182 D-GRVTSMGIWLKVQKDISPATLTLEPAELVRIQEAQIVCSASNDVNFV----- 235
 QY 289 NKALEEN-----YFEMSTYSNTRMIRILFAPVSSVARNDTGYVTSCKK---HPSQAL 341
 DB 236 --SLRHGDTKLITISQSDFDHNRQY-KVLTLNLDHVSFDQAGNYSCTATNAGWNHSAVMV 292
 QY 342 VTIVGKGFINATN--SSEYDEIDQVEECFVSFRKAYQIIRC-TWTFSRKSPFCQKGLD- 398
 DB 293 FRVVEAYLNTSQSLQLQEVTVGKVDLQVKVEAYFCLESFNWTV-LGPPSDYQDKLDF 351
 QY 399 ----NGYSISKFCN----HKHQPGEYIFHAENDDAQFTKMTLIRKPKVLAESAQA 450

DB 352 VTIKDTYRTSTSLPRLKRSEAGYSFLARNAGGNALTFELTLRYPEVRVTMTLNG 411
 QY 451 S-----CFSDGYPLPSWTWKCKSDKSPNCTEE---ITEGVNKRANKRKVFGOWSSSTLANM 503
 DB 412 SNTLLCEASGYPPQSVTVWQCRSHTRDRCDSEAGLVLEDSHSVLSQVPPHEVIVHSLAI 471
 QY 504 SEAIKGLVKCAVNSLGTSCETILLNSPGPPFFIQDNISFYATIGVC---LLFIVVLT 560
 DB 472 GTLEHNRVTECFRAFNSGVNSSTQTFWPISIGAHTQLPDELFTPVLLTCSIMALLLLLL 531
 QY 561 LICHYKQKQFRIESQLQMVQVTCSSDNEYFYVDPRYEYDLKWEPPRENLEFKVKGSGA 620
 DB 532 LLLYKQKPKYQVWKIIE--SYEGNSYTFIDPTQLPYNEKWEPPRNQLQFGKTLGAGA 589
 QY 621 FGKVNATAYGISTGTGVSIOVAVKMLKEKADSSREALMSLKMMTOLGSHENIVNLGA 680
 DB 590 FGKVEATAFGLGKEDAVLKAVKMLKSTAHADKEALMSLKIMSHLGOHENIVNLGA 649
 QY 681 CTLSPGYLIPEYCCYGDLLNLYRSKRE-----KPHRTWTETIFE 720
 DB 650 CTHGGPVLVITEYCCYGDLLNLYRSKRE-----KPHRTWTETIFE 709
 QY 721 HNFSPYPTFQSHPNSSMPGSRVQIHPSDDQISGLHGNSFHSSEDEIEYENQKRELEEEDL 780
 DB 710 SDFS-----SQGVDTYVEMRPVSTSSNDSFSEEDLKGEDGRPLE---- 749
 QY 781 NVLPEDILLCFAYQVAKGWEFLFKSCVHRDLAARNVLVTHGKVKVICDFGLARDIMSDS 840
 DB 750 ----LRDLLHFSQVQAQMAFLASKNCHRDVAARNVLLTSGRVAKIGDGLARDIMNDS 805
 QY 841 NVVVRGNARLPVKWMAPELPGIYTIKSDVMSYGILLWEIFSLGVNVPYGPVDPANFYK 900
 DB 806 NYIVKGNARLPVKWMAPELPGIYTIKSDVMSYGILLWEIFSLGVNVPYGPVDPANFYK 865
 QY 901 LIQNGKMDQPPYATEEYIIMQSCWAFDSRKRPFNPLTSLGCOL-ADAEEMAYQNV 958
 DB 866 LVKDGQYMAQPAFAFKNIYSIMQACWALEPTEPFTFQICSLQLQKQAOEDRRVPNTNL 924
 RESULT 9
 KIT_FELCA
 ID - KIT_FELCA STANDARD; PRT; 978 AA.
 AC Q28889;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mast/stem cell growth factor receptor precursor (BC 2.7.1.112) (SCFR)
 DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
 GN KIT.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=95140426; PubMed=7530827;
 RA Herbst R., Munemitsu S., Ullrich A.;
 RT "Oncogenic activation of v-kit involves deletion of a putative
 tyrosine-substrate interaction site.";
 RL Oncogene 10:369-379(1995).
 CC -/- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
 GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 3-KINASE (PI3K).
 CC -/- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 CC -/- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -/- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 PROTEIN KINASES.
 CC -/- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S76596; AB33207.1; --
DR HSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003606; Ig_MHC.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR001824; rKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
KW Proto-oncogene; tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 978 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
FT DOMAIN 23 521 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 522 544 POTENTIAL.
FT DOMAIN 545 978 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 590 938 PROTEIN KINASE.
FT NP_BIND 596 604 ATP (BY SIMILARITY).
FT BINDING 624 624 ATP (BY SIMILARITY).
FT ACT_SITE 793 793 BY SIMILARITY.
FT MOD_RES 824 824 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 94 94 N-LINKED (GLCNAC.) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC.) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC.) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC.) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC.) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC.) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC.) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC.) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC.) (POTENTIAL).
FT CARBOHYD 464 464 N-LINKED (GLCNAC.) (POTENTIAL).
FT CARBOHYD 487 487 N-LINKED (GLCNAC.) (POTENTIAL).
SQ SEQUENCE 978 AA; 109449 MW; 6D43472E0744056B CRC64;

Query Match 23.2%; Score 1224.5; DB 1; Length 978;
Best Local Similarity 32.9%; Pred. No. 2.3e-74;
Matches 325; Conservative 167; Mismatches 352; Indels 145; Gaps 35;

Qy 47 VKGSSYPWVSEPDLCG-ALRPOSSGVVYEAAYVVDVDSASITLQVLVDPAGNISCLW 105
Db 20 VQTGSSQP--SASPGWSLPSHPATS-----ELIVSAGDEIRLLCTDPGFVK--W 66

Qy 106 VFKHSLLNCQPHFDLQNGVSVMLKMTQTQAGYLLFIQSEAT--NYTIL----- 155
Db 67 TFE-----TIQSSSEITHNEWIT-EKAEANTGNYCTNCGGLSS 105

Qy 156 -FTVSIRN-TLLYTLRRPYFRKMNQDALVCISSEVPPEVWVLCDSQGSCKEESPAV 213
Db 106 SIYVVRDPKFLVDLPLYGK-EDHDTLVRCLPTDPE-VTNYSLRGCEGKPLKDLTFV 163

Qy 214 -----VKKEEVLHFLFGTDIRCCA-----RNELGRECTRLFTIDLNQPTTLPOL- 260
Db 164 TDPKAGITIRNVKREYHRLC---LHCSADRGKSVLSKKFTLKVRAAIRAVPVVSVSKAS 220

Qy 261 -FLKVGSEPLMIRKAVVHNGFGTLWELENKALEEGNYFEMSTYSTNRTMIRILPAFVSS 319
Db 221 HLLREGEEFSWCLIKDVSSSDSMWIKENSQPTNAQPSQNSWHQGFNFVQRERLTISS 280

Qy 320 VARNDTGYTCSSSKHFSQSALVT---IVGKGFNA-----TNSSEYEDIDYEZF 367
Db 281 ARVNDSGVFCWYANNFTGSANVTTLLEVAKGFNIPPMNTTTFVNDGENVDL----- 334

Qy 368 CFSVRPKAYPO-----IRCTWTFSRKSPCKQKGLDNGYSISKFCNKHK-----Q 412
Db 335 --IVEYAYPKPEHQRVVYVNRTLTDKWDYPKS-----DNESNI-RYVSELHLRLKNE 387

Qy 413 PGEYIFHAENDDAQFTKMTLNIIRKQVLAES--ASQSCFSDGYPLPMTWKCKSDK 470
Db 388 GGYTFQVNSDVSNSVTLNVVYVNTKPEILLTHESILVSGILQCLVAGRPPEPTVDWYFCGA 447

Qy 471 SPNTEETE-GVWNRKANRVKQWVSSTLNMSSEALKGLVKCCAYNSLGTSCETILL 529
Db 448 EQRCPVPVGPLDVQMSVSPSGKLVVQSSIDYSAFKHNGTVECRASNNVGT--SAFF 505

Qy 530 NSPGPFPIODN-----ISFYATIGVCLLFIVVLTLLICHKYKKOPRYESQ 575
Db 506 N----FAFKGNSKEOMHPHTFTPLLIGFVTAAGMCIIVMILT-----YKLDKPMYEVQ 557

Qy 576 LQMV-QVTSSDNEYFYVDREYEDLKWEPPRENLEFGKVLGSGAFKGMNATAYGISK 634
Db 558 WKVVEEING---NNYVIDPTQLPYDHKWEPPRNLSFGKTLGAGAFKGVVEATAYGLIK 614

Qy 635 TGVSIOAVKMLKESREALKMSLKMVTQLGSHENIVNLLGACTLSGPIYILFEYC 694
Db 615 SDAAMTAVAKMLKPSAHLTEREALMSLVLSYLGNNHNVNLLGACTVGGPTLVITEYC 674

Qy 695 CYGDLNVLRSKREKHTWTEIKHEHNFYPT-FQSHPNSSMPGSR-EVOIHDSDOI 752
Db 675 CYGDLNPLRRKRSDFICSKQEDHAE--VALYKNLLQSKESCDNSTNEYMDMKFGSVV 732

Qy 753 SGLHGNPSHSE--DEIEYENQKLEEBEDNLVTFELLCFAYQVAKGMEFLFKSCVH 809
Db 733 VPTKADKERSARIGSYIERDVTPTAIMEDEL-ALDLELLSFSYQVAKGMAFLASKNCIH 791

Qy 810 RDLAARNVLVTHGKVKVTCDFGLARDINSDSNVYVVRGNARLPVKWMAPESLPEGIYTKS 869
Db 792 RDLAARNILLTHGRITKICDFGLARDIKNDNSVYVVGKGNARLPVKWMAPESFNVCYTTES 851

Qy 870 DVWSYGLLWEIFSLGVNYPYGPVDANFYKLIQNGFMDOPFYATEIYIIMQSCWAFD 929
Db 852 DVWSYGLFWELFSLGSSPYGPMVDVSKFYKMKEGFRMLSPHAPAEAMYDIMKTCDAD 911

Qy 930 SRKRPSPFNLSFLGCLQADAEAEAMYQNV 958
Db 912 PLKRPFTKQIVQLIEKQISDSTNNHIYSNL 940

RESULT 10
KFMS FSVM
ID_KFMS FSVM STANDARD; PRT; 978 AA.
AC P00545; Q86597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase transforming protein fms (EC 2.7.1.112).
GN V-FMS.
OS Feline sarcoma virus (strain McDonough).
OC Viruses; Retroviridae; Retroviridae; Mammalian type C retroviruses.
ON NCBI_TaxID=11778;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=84119469; PubMed=6582485;
RA Hampe A.; Gobet M.; Sherr C.J.; Galibert F.;
RT "Nucleotide sequence of the feline retroviral oncogene v-fms shows
RT unexpected homology with oncogenes encoding tyrosine-specific protein
RT kinases."
RL Proc. Natl. Acad. Sci. U.S.A. 81:85-89(1984).

[2]
 RN REVISIONS, SEQUENCE FROM N.A.
 RP MEDLINE=92015516; PubMed=1833563;
 RA Smola U., Hennig D., Hadwiger-Fangmeier A., Schuetz B., Pfaff E.,
 RA Niemann H., Tamura T.;
 RT "Reassessment of the v-fms sequence: threonine phosphorylation of the
 COOH-terminal domain.";
 RL J. Virol. 65:6181-6187(1991).
 CC -!- FUNCTION: V-FMS IS DERIVED FROM THE RECEPTOR FOR COLONY
 CC STIMULATING FACTOR 1 (CSF-1).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-FMS
 CC POLYPEPTIDE.
 CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC
 CC EMBL; K01643; AAA43045.1; -;
 CC EMBL; S59588; AAB20028.1; -;
 CC PIR; A06544; TVMWD.
 CC HSP; P11362; IFGK.
 CC InterPro; IPR000719; Euk pkinase.
 CC InterPro; IPR003006; Ig MHC.
 CC InterPro; IPR003598; Ig C2.
 CC InterPro; IPR003600; Ig-like.
 CC InterPro; IPR001824; Rikinsell.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00047; Ig; 3.
 CC Pfam; PF00069; pkinase; 1.
 CC ProDom; PD000001; Euk pkinase; 2.
 CC SMART; SM00410; Ig-like; 4.
 CC SMART; SM00408; IGC2; 1.
 CC SMART; SM00219; Tyrc; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 CC PROSITE; PS00240; RECEPTOR TYR KIN III; 1.
 CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 CC PolyProtein; Tyrosine-protein kinase; Oncogene; Transferase; Receptor;
 KW Transmembrane; Glycoprotein; Phosphorylation; ATP-binding;
 KW Immunoglobulin domain; Repeat.
 FT DOMAIN 1 543
 FT TRANSMBM 544 568
 FT DOMAIN 569 978
 FT DOMAIN 58 138
 FT DOMAIN 141 231
 FT DOMAIN 238 332
 FT DOMAIN 333 431
 FT DOMAIN 432 536
 FT DOMAIN 613 942
 FT NP_BIND 619 627
 FT BINDING 647 647
 FT DISULFID 76 118
 FT DISULFID 161 211
 FT DISULFID 258 312
 FT DISULFID 451 516
 FT MOD_RES 841 841
 FT MOD_RES 973 973
 FT CARBOHYD 79 79
 FT CARBOHYD 107 107
 FT CARBOHYD 128 128
 FT CARBOHYD 187 187
 FT CARBOHYD 309 309
 FT CARBOHYD 320 320

FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 369 369 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 511 511 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 524 524 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 714 714 L -> P (IN REF. 1).
 FT CONFLICT 971 978 QRTPPVAR -> RGPPL (IN REF. 1).
 SQ SEQUENCE 978 AA; 108491 MW; 4C7CAC4835185EBF CRC64;
 Query Match 23.2%; Score 1224; DB 1; Length 978;
 Best Local Similarity 32.6%; Pred. No. 2.4e-74;
 Matches 334; Conservative 173; Mismatches 326; Indels 192; Gaps 39;
 QY 65 CALRPQSSG-----TYEAAAVE-----VDVSASITLQVLVDAPGNISCL 104
 DB 28 CCLPTEAMPRLALLVLLMATAHQAQVPIQSPGLVVEPGTIVTLRCV-----GNGSVE 83
 QY 105 W---VFKSSINCQP-----HFDLQNRGVVSMVILKMTETQAGE-----YLLFIQ 146
 DB 84 WDPGISPHWNLDDPPSSILTTNNATFQNTGYHC-----TEPGNPRGNATIHLYVK 136
 QY 147 SEATNYTIL---FTVSIRNTLYTLRRPYFRKMENQDALV-CISESVPEPIVE--WVLC 200
 DB 137 DPARPWKVLAQEVTV-----LEGODALLPCL---LTPDALEAGVSLVR 176
 QY 201 SOGESCKEE-----SP---AVVKEEKVLHELFGTDIRCCARNEIGRECTRL-----FTI 247
 DB 177 VGRPVLQRTNYSFSPWHGFTTHKAKFIENHYV-----QCSARVD-GRVTSMGIWLKVQK 231
 QY 248 DLNQTPQTTL-PQLFLKV-GEPLWIRCKAVHNVHGFLTWELNKALEBGN-----YFEMS 301
 DB 232 DISGPATLTLEPAELVRIQGEAAQVCSASNDVNPDV-----SLRHGDTKLITISQQS 284
 QY 302 TYSTNRTMIRILFAFVSSVARNDTGYITCSSK---HPSQALVTIVGKFINATN--SSE 357
 DB 285 DFHDNRYQ-KVLTINLDHVSFDAGNYSCTATNAGNHSASMVFRVESAYSNLTSEQSL 343
 QY 358 DYEIDQYEEFCFSVRFKAYPQIRCT-TWTFSRKSPCEQKGLD-----NGYSISKFCN--- 408
 DB 344 LQEVTVGKVDLQVKVEAYPGLESFNWTV-LGFFSDYQDKLDFVTIKTYRTYSTLSLR 402
 QY 409 -HKHQFGYIPIHAENDDAQFTKMTLINIRKQVLAESAASQAS-----CFSDGYPLPSWT 463
 DB 403 LKRSRGYSFLARNAGGQNALTFELTLRYPEVVRTMTLINGSDTLLCEASGPQPSVT 462
 QY 464 WKCKSDKSPNCTEE---ITEGVNRKANRKYFGQVWVSSSTLNMSEAIKGLVKCCAYNSL 520
 DB 463 WYQCRSHTRDCRDESAGLVLEDSHSEVLSQVPFYEIVHSLAIGTLHNRTYECRAFNSV 522
 QY 521 GTSCTILLNSPGPPFFIODNISFYATIGVC---LLFIVVLTLLICHYKKQPRYESQLQ 577
 DB 523 GNSSTFWPISIGAUHTPLPDELFTVLTCTMSIALLLLLLLLLLLYKKQKPKYQVRWK 582
 QY 578 MVQVTGSSDNEYFYVDPREYEDLKEWEPRENLEFGKVLGSGAFKVMNATAYGISKTGV 637
 DB 583 IIE--SYEGNSYTFIDPTQLPNEYKEWEPERNLQFGKTLGTGAFGKVVEATAGLCKEDA 640
 QY 638 SIQVAVKMLKEKADSSERBALMSLKMMTQLGSHENIVNLLGACTLSGPIYLIPEYCCY 697
 DB 641 VLKVAVKMLKSTAHADKEALMSLKMHLGQHENIVNLLGACTHGGPVLVITEYCCY 700
 QY 698 DLLNVLRSKRE-----KFHRTWTEIPKEHNPSFYPTQSHNSSM 737
 DB 701 DLLNFRQAEAMLGFSLSVGQDPAGAGYKNHLEKKYVRDRSGFS----- 747
 QY 738 PGSRVQIHPDSQDQISGLHSGNSFHSDETEYENQKRLBEEEDLNVLTFEDLLCFAYQVAK 797
 DB 748 --SQGVDTYVENRPFVSTSSNDSFSEEDLCKEDGGRPLE-----LRDLHFSQVAK 796
 QY 798 GMEFLPFCVHRDLAARNVLVTHGKVKICDPGLARDIMSDSNVYVRGNARLPVKWMAF 857
 DB 797 GMAFLASKNCIHRDVAARNVLLTSGRVAKIGDFGLARDIMDSNVIYKGNARLPVKWMAF 856

Db 835 QSDVMSYGILLWEIFSLGLNPFYFGLVNSKFYKLVKVDGYQMAQFAPAFKNIYSIMQACWA 894
 Qy 928 FDSRKRSFPNLTSLGCOL-ADAEAMYNQV 958
 Db 895 LEPTHRPTFOQICSLFQEQAEQRRDRDYTNL 926
 RESULT 12
 KIT_CHICK
 ID_KIT_CHICK STANDARD; PRT; 960 AA.
 AC Q08156;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
 DE (Proto-oncogene tyrosine-protein kinase kit) (C-kit).
 GN KIT.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=white leghorn; TISSUE=Brain;
 RX MEDLINE=93292995; PubMed=7685729;
 RA Sasaki E., Okamura H., Chikamune T., Kanai Y., Watanabe M.,
 RA Naoto M., Sakurai M.;
 RA "Cloning and expression of the chicken c-kit proto-oncogene."; J.
 RL Gene 128:257-261 (1993).
 CC -1- FUNCTION: THIS IS THE RECEPTOR FOR STEM CELL FACTOR (MAST CELL
 CC GROWTH FACTOR). IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC BINDING OF THE LIGANDS LEADS TO THE AUTOPHOSPHORYLATION KIT AND
 CC ITS ASSOCIATION WITH SUBSTRATES SUCH AS PHOSPHATIDYLINOSITOL
 CC 3-KINASE (PI3K).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: HIGH IN THE BRAIN AND TESTES AND ALSO
 CC PRESENT IN THE BURSA OF FABRICUS, HEART, KIDNEY, LUNG, SPLEEN
 CC THYMUS AND OVARY.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE
 CC PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC modified and this statement is not removed. Usage by and for comm
 CC entities requires a license agreement (See <http://www.isb-sib.ch/anno>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D13225, BAA02506.1, --
 CC PIR: JN0677; JN0677.
 CC HSP: P11362; IFGK.
 CC InterPro: IPR000719; Euk_pkinase.
 CC InterPro: IPR003598; Ig_c2.
 CC InterPro: IPR001824; RTKaseII.
 CC InterPro: IPR001245; Tyr_pkinase.
 CC Pfam: PF00047; ig; 3.
 CC Pfam: PF00069; pkinase; 1.
 CC ProDom: PD000001; Euk_pkinase; 2.
 CC SMART: SM00408; IGC2; 1.
 CC SMART: SM00219; TyrKC; 1.
 CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE: PS00109; PROTEIN KINASE_TYR; 1.
 CC PROSITE: PS00240; RECEPTOR_TYR_KIN_III; 1.
 CC PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 CC Proto-oncogene, Tyrosine-protein kinase; Receptor; Transmembrane;
 CC Kinase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 CC Immunoglobulin domain

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FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 960 MAST/STEM CELL GROWTH FACTOR RECEPTOR.
FT DOMAIN 25 505 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 506 530 POTENTIAL.
FT DOMAIN 531 960 CYTOPLASMIC (POTENTIAL).
FT NP BIND 575 913 PROTEIN KINASE.
FT BINDING 609 589 ATP (BY SIMILARITY).
FT ACT SITE 777 777 BY SIMILARITY.
FT MOD_RES 808 808 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 343 343 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 469 469 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 960 AA; 107311 MW; 0E93850527AB68F6 CRC64;

Query Match 23.0%; Score 1215; DB 1; Length 960;
Best Local Similarity 32.3%; Pred. No. 9.6e-74;
Matches 314; Conservative 165; Mismatches 370; Indels 124; Gaps 34;

Qy 66 ALRPOSGTVVEAARVDVDSASITLQVLDAPGNISCLWFKVQISS-----LNCQPHFD 119
Db 18 SLIPAGGSVPHEESSLVNKGELRLKCNBERP-----VTNPNQSDPSAKTRISNEKEWH 73
Qy 120 LONRGV--VSMVLKMTQAGEVLLFTQSEATNVTILFTVSIINTLTYLTLRRPYFRQWE 177
Db 74 TKNATIRDIGEYCKSKGSIWNSFVFKOP-----NVLFV-----DSLII-----GKED 119
Qy 178 NQDALVCISESVPEP-IVEWVLCDSSQGSCKEESPAVVKKEB-----KVLHFLFGTDIRCC 232
Db 120 SDILLVC---PLTDPDLNFTLRKCDGKPLPKNMTFIPNPKQGIILKNVQSFQCYOCL 176
Qy 233 AR-NELGRECTRLFTIDLQNP-OTTLPOL-----FLKVGPELWIRCKAVHVNHGRL 283
Db 177 AKHNGVEKISHF----LNVRPVHKAFLPVITLSKSYELLKEGEPEVETCIITDVS SVKA 233
Qy 284 TWELNKALEBEGNFEMSTYSTNRTMIRILFAFVSSVARNDTGYVTCSSSKHP--SQSAL 341
Db 234 SWISYKAIVTSKRNLDGYVERK-----LTNIRKSVGNDSGEFTC-QAENPFQKTNAT 288
Qy 342 VTI--VGKGFN---ATNSSDEYIDQYEEFCFSVRFRKAYPOIR-CTWTFGRKSPFCBQK 395
Db 289 VTLKALAKGFVRLPATMNTTIDINAGONG--LTVVEYAPKPKKEEVWYMNNTL--QN 343
Qy 396 GLDNGYSISKFCNHK-----OPEYIFHANNDAQFTKMTLIRKPKQVLA 443
Db 344 SSDHVVKFTVGNNSYTSSELHLTRLKGTGGTYTFVSNSSDASSSVTFNVVYVKTKPEILT 403
Qy 444 EASASQ--ASCFSGOYPLPSWTWKCKSDKSPNCTEITEGVNWRKANRKFQWVSSSTL 501
Db 404 LDMGLNDILQCVATGFPAPTIIYWFPCGTEORCLDSPTISPMVDKVS-----YTNSSVP 457
Qy 502 NWSBAIKGFLVKCCAYNSLGTSCETILNLSPGPPFF-----IQDNISFYA-----TIGV 550
Db 458 SFERILVESTVNASMFKGTGTICCEASSNGDKSVFFNFAIKEQIRTHLTPFLIAGV 517
Qy 551 CLLFIVLTLILCHYKQFYRESQIMV-QVTGSSDNEYFYVDPREYEDLKWFFPREN 609
Db 518 AAGLMCIIMVILYLOKPKYEQVMQVVEING--NNYVYIDPTQLPYDKHKEFPRNR 574
Qy 610 LEFGKVLGSGAFGKMNATAYCISKTGYSIQVAVKMLKEKADSSREALMSELKMTOLG 669
Db 575 LSFQKTLGAGAFGKVEATAYGLFKFSDAAMTVAVKMLKPSAHLTREALMSELKYSYLG 634
Qy 670 SHENIVNLLGACTLSGPIYLIFFEYCCYGDLLNLYLRSKREK-----HRTWTEIFKEHNFSF 725
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Db 635 NHINIVNLLGACTLGGPTLVITEYCCYGDLLNFLRRKEDSFICPKHSEHAAAYVENL-- 692
Qy 726 YPTQSPNS-----SMFGSREVQIHPDSDOISGLHGNSFHSEDETEYENQKLEBEE 778
Db 693 --LHQAEPTADAVNEYMDMKPGVSYAVPPKADKKRPVSGSYTTQDD-----VTLSMLEDE 746
Qy 779 DLNVLTFEDLLCFAYQVAKGMFELEFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMS 838
Db 747 --LALDVEDLLSFSYQVAKGMSFLASKNCHIRDLAARNILLTHGRITKICDFGLARDIRN 804
Qy 839 DSNVTVGNARLPVKWNAPELSPGEGITYTIKSDVMSYGLLLWEIFSLGVNPFPGIPVDANF 898
Db 805 DSNVTVGNARLPVKWNAPELSPGEGITYTIKSDVMSYGLLLWEIFSLGVNPFPGIPVDANF 864
Qy 899 YKLQNGFKMDQPFYATEEIIIMOSCAWPDNRKRPSPNLTSLFGCOLADAEEAEMYNQV 958
Db 865 YKMIKEGTRMPSPECPPEMYDIMKSCWDADPLORPTPKQIVOLIEQQQLSDNAPRYAN- 923
Qy 959 DGRVSECPHTYQN 971
Db 924 ---FSTPPSTQGN 933

RESULT 13
KFMS MOUSE
ID KFMS MOUSE STANDARD; PRT; 977 AA.
AC P09581; Q9DBH9;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Macrophage colony stimulating factor I receptor precursor (CSF-1-R)
DE (BC 2.7.1.112) (Fms proto-oncogene) (c-fms).
DE CSF1R OR CSFMR OR FMS.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=88217329; PubMed=2966922;
RA Rothwell V.M., Rohrschneider L.R.;
RT "Murine c-fms cDNA: cloning, sequence analysis and retroviral
expression."
RL Oncogene Res. 1:311-324 (1987).
RN [2]
RP REVISIONS.
RA Rothwell V.M.;
RL Submitted (SEP-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RX MEDLINE=93181280; PubMed=8441691;
RA de Parseval N., Bordenaux D., Gisselbrecht S., Sola B.;
RT "Reassessment of the murine c-fms proto-oncogene sequence."
RL Nucleic Acids Res. 21:750-750 (1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Harai A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
RA Schrim L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
```

RA Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [5]
 RP SEQUENCE OF 1-16 FROM N.A.
 RX MEDLINE=93268269; PubMed=8497248;
 RA Yue X., Favot P., Dunn T.L., Cassidy A.I., Hume D.A.;
 RT "Expression of mRNA encoding the macrophage colony-stimulating factor
 RT receptor (c-fms) is controlled by a constitutive promoter and tissue-
 RT specific transcription elongation";
 RL Mol. Cell. Biol. 13:3191-3201(1993).
 RN [6]
 RP AUTOPHOSPHORYLATION SITES.
 RX MEDLINE=90258890; PubMed=2160591;
 RA van der Geer P., Hunter T.;
 RT "Identification of tyrosine 706 in the kinase insert as the major
 RT colony-stimulating factor 1 (CSF-1)-stimulated autophosphorylation
 RT site in the CSF-1 receptor in a murine macrophage cell line";
 RL Mol. Cell. Biol. 10:2991-3002(1990).
 CC -!- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
 CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X06368; CAA29666.1; ALT_SEQ.
 DR EMBL; AK004947; BAB23691.1; -
 DR EMBL; S62219; -; NOT_ANNOTATED_CDS.
 DR PIR; S01880; TVMSMD.
 DR HSSP; P11362; IFGK.
 DR MGD; MGI:1339758; Csf1r.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR001824; RTKinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00410; Ig_Like; 3.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 19
 FT CHAIN 20 977
 FT
 FT DOMAIN 20 511
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 512 536
 FT POTENTIAL.
 FT DOMAIN 537 977
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 24 104
 FT IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 107 197
 FT IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 204 298
 FT IG-LIKE C2-TYPE DOMAIN 3.

FT DOMAIN 299 397
 FT DOMAIN 398 503
 FT DOMAIN 580 913
 FT NP_BIND 586 594
 FT BINDING 614 614
 FT ACT_SITE 776 776
 FT DISULFID 42 84
 FT DISULFID 127 177
 FT DISULFID 224 278
 FT DISULFID 417 483
 FT MOD_RES 697 697
 FT MOD_RES 706 706
 FT MOD_RES 807 807
 FT CARBOHYD 45 45
 FT CARBOHYD 73 73
 FT CARBOHYD 302 335
 FT CARBOHYD 335 335
 FT CARBOHYD 389 389
 FT CARBOHYD 410 410
 FT CARBOHYD 449 449
 FT CARBOHYD 478 478
 FT CARBOHYD 491 491
 FT CONFLICT 446 446
 FT CONFLICT 553 553
 FT CONFLICT 616 616
 FT CONFLICT 744 744
 FT CONFLICT 814 814
 SQ SEQUENCE 977 AA; 109178 MW; 7EDF8310CCF98906 CRC64;
 Query Match 22.8%; Score 1204; DB 1; Length 977;
 Best Local Similarity 33.2%; Pred. No. 5.3e-73;
 Matches 322; Conservative 155; Mismatches 330; Indels 164; Gaps 32;
 QY 83 VDVSAITLQVL---VDAPGNISCLVFKHSLNCQPHFDLQNGVV-----SWILKM 133
 DB 32 VPEGETVTLRCSNGSVNDGPISPYWTLDPS-----PGSTLTTRNATFKNTGYRTEL 87
 QY 134 TETQAGEYL--LFIQSEATNYTIL---FTVSIRNTLLTYLRPFYRKMENQDALVCISES 188
 DB 88 EDPMAGSTTHLYVKDPAHSMNLLAQEVTV-----VEQEA----- 124
 QY 189 VPEPIVWVLCDSQGESCKEESPAVKK-----EKKVLHELFGTDIRCCAR 234
 DB 125 LPCLITDPAKDSV--SLMREGGRQVLRKTVYFFSPWRGFIIRKAKVL-----DSNTYVCKT 179
 QY 235 NELGRECTRL-FTIDLN---QTPQTL-LPOLFLVK-GEPLMIRCKAVHVNHCGLTWEL 287
 DB 180 MVNGRESTSTGIWLKVNVRVHPEPQIKLEPSKLVIRGEAAQIVCSATNABVGFNVLKR 239
 QY 288 ENKALE-----EGNYFEMSTYSTNRTMIRILFAFVSSVARNDTGYTC-SSSKHPSQS 339
 DB 240 GDTKLEIPLNSDFQNYK-----KVRALSLNAVDFQDAGIYSCVANDVGTRT 288
 QY 340 ALVT--IVKKGFINATN--SSDYEDIDQVEEFCFVRFKAYQPIR-CTWTFSRKSPFCEQK 395
 DB 289 ATMNFQVVEASAYNLTSQSLQEVSGDSLITLVHADAYPSIQHYNTWYLVGFPE-DQR 347
 QY 396 GLD-----NGYSISKFCNH--KHQPGYEYIHAENDDAQFTMTFLNRRKQVLAEBAS 446
 DB 348 KLEFTIQRAIVRYTPKLFLNVRKASEAQYFLMAQNKAGMNNLTPELTILRYPEVSVTWM 407
 QY 447 ASQAS---CFSDGYPLPSWTWKCKSDKSPNCTEETEGVWN-----RKANRKYFGQWVSS 498
 DB 408 PVNGSDVLFCDSVGYQPQSVTWMECRGHTDRCDQAALQVWNDTHPEVLVSQKPFDKVIQ 467
 QY 499 STLNMSEAIGFLVCKCAYNSLGTSCETILLNSPGFPFPFIQDNISFYATIGVC---LLFI 555
 DB 468 SQLPIGLTKHNTYFCCKTHNSVGNSSQYFRAVSLGSKQLPDESFTTPVVVACMSVMSLL 527
 QY 556 VVLTLLICHKKQPRYESQLQMVQVTSSTSSNEYFYVDPREYEDLKWEFPRENLEFGKV 615
 DB 528 VLLLLLLLYKKQPKYQVRWKIIE--RYEGNSYTFIDPTQLPYNEKWEFPFRNLLQFGKT 585

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Qy 616 LGSAGFGKVMNATAYGIGTGVSIQAVKMLKEKADSSEREAELMSLKMOTQLGSHENIV 675
Db 586 LGAGAGFGKVVETATGLGKEDAVLKVAVKMLKSTAHADKEALMSLKMOTQLGSHENIV 645
Qy 676 NLLGACTLSGPIYLFYCCYCGDLNLYLRKRE-----KEHRTWT 715
Db 646 NLLGACTHGGPVLVITECCYCGDLNLYLRKRE-----KEHRTWT 715
Qy 716 EIFKEHNSFYPTFQSHPNSSMPGSRVQIHPDSDQISGLHGNSFHSDELEYENQKLE 775
Db 706 YVRDSGFS-----SQGVDTYVEMRPVPTSSSDSFKKQ-LDKSEASRELE 749
Qy 776 EEDLNVLTFEDLLCFAYQAKMEFLBFKSCVHRDLARNVLTGHVKVXICDFGLARD 835
Db 750 -----LWDLHFSSQVAGMAFLASKNCIHRDVAARNVLTGHVAKIGDFGLARD 800
Qy 836 IMSDSNVVRGNARLPVKWMAPESEFEGIIYTKSDVWSYGILLWEIFSLGVNYPGIPVD 895
Db 801 IMDSNVVVKGNARLPVKWMAPESEFDCVYTVQSDVWSYGILLWEIFSLGLNYPGILVN 860
Qy 896 ANFYKLIQNGKMDQPFVATERIYIIMOSWAFDGRKRPSPNLTSLGCOLADAEAMY 955
Db 861 NKFYKLVKDGYOAGQVFPAPKNYISIMOSWDLPTRRPTFOQICELL-----QEQARL 914
Qy 956 QNVDRVSECP 966
Db 915 EERDQYANLP 925

RESULT 14
KFMS RAT
ID_KFMS RAT STANDARD; PRT; 978 AA.
AC Q00495;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Macrophage colony stimulating factor I receptor precursor (CSP-1-R)
DE (EC 2.7.1.112) (Fms proto-oncogene) (c-Fms).
GN CSF1R OR CSFMR OR FMS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WiStar; TISSUE=Skeletal muscle;
RX MEDLINE=93001225; PubMed=1389227;
RA Borycki A.G., Guillier M., Leibovitch M.P., Leibovitch S.A.;
RT "Molecular cloning of CSF-1 receptor from rat myoblasts. Sequence
RT analysis and regulation during myogenesis.";
RL Growth Factors 6:209-218(1992)
CC -!- FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSP-1, IT IS A PROTEIN
CC TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X61479; CAA43706.1; -.
DR PIR; S16385; S16385.
DR HSSP; P11362; 1FGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003006; Ig_MHC.
```

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DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 4.
DR Pfam; PF00069; pkinase; 1.
DR PRODOM; PD000001; Euk_pkinase; 2.
DR SMART; SM00410; IG_Like; 3.
DR SMART; SM00408; IGS2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Proto-oncogene Tyrosine-protein kinase; Receptor; Transmembrane;
KW Transferase; Glycoprotein; Phosphorylation; ATP-binding; Signal;
KW Immunoglobulin domain; Repeat..
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 978 MACROPHAGE COLONY STIMULATING FACTOR I
FT RECEPTOR.
FT DOMAIN 20 511 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 512 536 POTENTIAL.
FT DOMAIN 537 978 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 24 104 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 107 197 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 204 298 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 299 397 IG-LIKE C2-TYPE DOMAIN 4.
FT DOMAIN 398 503 IG-LIKE C2-TYPE DOMAIN 5.
FT DOMAIN 580 914 PROTEIN KINASE.
FT NP_BIND 586 594 ATP (BY SIMILARITY).
FT BINDING 614 614 ATP (BY SIMILARITY).
FT ACT_SITE 776 776 POTENTIAL.
FT DISULFID 42 84 POTENTIAL.
FT DISULFID 127 177 POTENTIAL.
FT DISULFID 224 278 POTENTIAL.
FT DISULFID 417 483 POTENTIAL.
FT MOD_RES 697 697 PHOSPHORYLATION (AUTO-) (IN VITRO)
FT MOD_RES 706 706 PHOSPHORYLATION (AUTO-) (IN VIVO)
FT MOD_RES 807 807 PHOSPHORYLATION (AUTO-) (IN VITRO)
FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 410 410 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 449 449 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 478 478 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 491 491 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 978 AA; 109264 MW; 0A684568F56BC7E3 CRC64;
```

```
Query Match 22.6%; Score 1194; DB 1; Length 978;
Best Local Similarity 33.1%; Pred. No. 2.5e-72;
Matches 321; Conservative 154; Mismatches 332; Indels 164; Gaps 32;

Qy 83 VDVSASITLOVL-----VDAPGNISCLWFKHSLNCQPHFDLQNGV-----SWILKM 133
Db 32 VEPGETVTLRCVNSGVWDGPISPYVTLDPES-----PGSTLTTRNATPKNTGYRCTEL 87
Qy 134 TETQAGEYL--LFIOSEANTYIL---FTVSIRNTLLTYLRPRFKRMENQDALVCISES 188
Db 88 EDPMAGSTTHLYVKDPAISWILLAQEVTV-----VSGQEA----- 124
Qy 189 VPEPIVWVLCDSQGESCKEESPAVVK-----EKKYHLEHFGTDIRCCAR 234
Db 125 LFCLITDPALKDSV-SLMREGGRQVLRKTVYFFSAMRGFIIRKAKVL-----DSNTVVCVT 179
Qy 235 NELGRECTRL-FTIDLN-----QTPQTL-PQLFLKV-GEPLWIRCAVHVHNGFGLTWEL 287
Db 180 MVNGRESTGTGIWLKYNVRVHPEPPQKLBPSKLVRIRGEAAQIVCSATNAEUVGNILKR 239
```


Sat May 24 16:50:26 2003

```
Query Match      22.3%; Score 1176; DB 1; Length 1088;
Best Local Similarity 35.6%; Pred. No. 4.6e-71;
Matches 294; Conservative 128; Mismatches 288; Indels 115; Gaps 24;

Qy 246 TIDLNOTPTTLPLQFLKVBPLMIRCAVHNHGFGLTW-----ELENKA---LEEGNYF 298
Db 210 TSELNLEMDTR--QTVYKAGETIVVTC-AVFNEVVDLQWTYPGEVRNKGITMLEE-----262

Qy 299 EMSTYSTNRWIRILFAP-VSSVARNDGYTCS---SSKHPQSALATIV--GKGFIN- 351
Db 263 -----IKLPSIKLVYTLTVKATVKGSDGYECAARQAKVKEMKMTVTISVHEKGFVOI 316

Qy 352 --ATNSSDEYIDQVEEFCFSVRKAPQIRCTWTFRSKSF-----PCEQKGLDNGY 401
Db 317 RPTFGHLETVNLHQVRETV--VEVOAYFTPRISMLKNDLTLIENLTEITTDVQRSQETRY 374

Qy 402 -SISKFCNHHQ-POEYIFHAENDDAQFTKMTLNIIRKPOVL-----AEASASQASC 452
Db 375 QSKLIRAKEEDSGHYTIIQNDDDMKSYTFELSTLVPASILELVDDHGGSGGGQTVRC 434

Qy 453 FSDGYPPLSWTW-----KKCDK-----SPNCTEETEGVWNRKANRKYFGQWVSST 500
Db 435 TAEGTFLPNIEWMICKDKCNDTSWTVLASVNSNIITE--FHQRGSTVEGR-----486

Qy 501 LNMSEAIGFLVKCCAVNSLGTSCETILLNSPGPPFFIODNISFYATIGVCILLFIWVLT 560
Db 487 VSFAKVEETIAVRCLAKNDLGLGNRELKLVAPS-----LRSELTVAADVLLVIVISLI 542

Qy 561 LICHKYKQFRYESQLQVQVVTGSSDNEYFYVDREYEDLKWEFPRENLEFGKVLGSGA 620
Db 543 VLVVWIKQPRYEIRWRVIESIPDGHEIYVYDPMQLPYDSRWEFFRDGLVLRILGSGA 602

Qy 621 FGKVNATAYGLSKTGVSIQAVAKLKEKADSSERREALMSELKMTOLGSHENIUNLLGA 680
Db 603 FGKVVEGTAYGLSRQPMKVAKMLKPTARSSEKQALMSELKIMTHLGPLHNIUNLLGA 662

Qy 681 CTLGPIYLIPEYCCYGLLNLVLRSKREKF-----HRTWTEI 717
Db 663 CTGSGPIYIITEYCFYGLVNLVLRNDSFMSRHPKPKKLDLIFGLNPADESTRSYVIL 722

Qy 718 FKEHNFSPYPTFQSHPNSSMPGSRREVQIHPDSQISGLHN--SFHSEDEIEYENOKRLE 775
Db 723 SFENNGDYVDMKQADTTQVPMLEKREVSYSIDIQRSLYDRPASYSKKSMLDSE-AKNLL 781

Qy 776 EEDLNVLTFEDLLCPAYQVAKGMBEFLEKSCVHRDLAARNVLVTHGVVVKICDFGLARD 835
Db 782 SDDSEGLTLLDLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGGKIVKICDFGLARD 841

Qy 836 IMSDSNVYVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPNPQIPVD 895
Db 842 IMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGVLLWEIFSLGGTFYFGMWVD 901

Qy 896 ANFYKLIQNGFRMDQPFYATEEIIYIMOSCAFDKSRPSFPNLTSLFCQCLADAEEMY 955
Db 902 STFYNKIKSGYRMAKPDHATSEVYEIMVQCNSEPEKPSFYHLSSEIVENLLPQGVKSY 961

Qy 956 QNV--DGRVSECPH-----TYQNRPFPSREMDLGL 983
Db 962 EKIHLDFLSDHPAVARMRVDSNAYIGVTKNEEDKJKEWEGGL 1006
```

Search completed: May 24, 2003, 16:56:54
Job time : 23.0091 secs

GenCore version 5.1.4_p5 4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:51:00 ; Search time 71.0358 Seconds
(without alignments)
2880.307 Million cell updates/sec

Title: US-09-919-408-4

Perfect score: 5274

Sequence: 1 MPALARDAGTVPLLVVFSAM.....PFSREMDLGLLSPQAQVEDS 993

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_ivirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1271.5	24.1	976	13 Q9W755	Q9W755 brachydanio
2	1265.5	24.0	974	11 Q63702	Q63702 rattus ratt
3	1263.5	24.0	978	11 Q63116	Q63116 rattus norv
4	1262.5	23.9	964	6 Q97744	Q97744 sus scrofa
5	1261.5	23.9	964	6 Q97Q01	Q97Q01 sus scrofa
6	1261.5	23.9	964	6 Q97Q00	Q97Q00 sus scrofa
7	1250.5	23.7	979	6 Q8W23	Q8W23 canis famil
8	1247	23.6	972	4 Q99662	Q99662 homo sapien
9	1244	23.6	978	6 Q9X593	Q9X593 canis famil
10	1230.5	23.3	977	13 Q98S01	Q98S01 danio nigro
11	1229	23.3	945	6 Q77589	Q77589 equus cabal
12	1228	23.3	974	13 Q98SU3	Q98SU3 danio dangi
13	1226	23.2	954	13 Q91909	Q91909 xenopus lae
14	1223.5	23.2	977	13 Q918N6	Q918N6 brachydanio
15	1221	23.2	948	6 Q9TTD7	Q9TTD7 trichosurus
16	1219	23.1	724	6 Q9MYN0	Q9MYN0 bos taurus

ALIGNMENTS

RESULT 1

Q9W755 PRELIMINARY; PRT; 976 AA.
ID Q9W755;
AC Q9W755;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Kit receptor tyrosine kinase.
GN KIT.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99396707; PubMed=10393121;
RA Parichy D.M., Rawls J.F., Pratt S.J., Whitfield T.T., Johnson S.L.;
RT "Zebrafish sparse corresponds to an orthologue of c-kit and is
RT required for the morphogenesis of a subpopulation of melanocytes, but
RT is not essential for hematopoiesis or primordial germ cell
RT development."
RL Development 126:3425-3436 (1999).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AF153446; AAD41890.1; -.
DR HSSP; P11362; 1FGK.
DR ZFIN; ZDB-GENE-980526-464; kit.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 3.
DR ProDom; PD000069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00408; Igc2; 1.

Q98SU2 danio kerri
P79750 fugu rubrip
Q98SU4 danio albol
Q9DE49 brachydanio
Q9PUF6 gallus gall
Q8406 rattus norv
P79749 fugu rubrip
Q8UVR8 fugu rubrip
Q97745 sus scrofa
Q8UVR9 fugu rubrip
Q925F7 rattus norv
Q9PTL0 brachydanio
Q8UW9 brachydanio
Q8HL3 gallus gall
Q8VCD0 mus musculu
P79701 coturnix co
Q9EQ22 rattus norv
Q9IZT1 rattus norv
Q96KM0 homo sapien
Q96KM2 homo sapien
Q96KM1 homo sapien
Q90749 gallus gall
Q96KL9 homo sapien
Q9TTZ3 oryctolagus
Q91416 xenopus lae
Q91286 pleurodeles
Q14672 homo sapien
Q91287 pleurodeles

Db 930 GTYTLVNSDVSAVTFDVTYVNTKPEILTYDRLMNGRLQCVAAAGPEPTIDWYFCTGAE 449
 Qy 472 PNCTEEITE-GYNNRKANKRVFGQWSSSTLNMSEAIKGLFLVKCCAYNSLGTSCETILN 530
 Db 450 QRCCTVPPVVDVQIQNASVSPGKLVQSSIDSSVFRHNGTVECKASNAVGKS--SAFFN 507
 Qy 531 SPGPPPP-----IQDN-----ISFYATIGVCLLFIIVLTLCHIKYKQFRYESQLQWY- 579
 Db 508 ----FAFKGSKSEQIOPHTLFTPLLGIFVVVTAAG--LMGIIVMVL--AYKYLQKPMYEVQWVVE 559
 Qy 580 QVTSSDNEYFVDPREYEDLKWEFPRENLEFPGKLVGSGAFKVMNATAYGISKTVGSI 639
 Db 560 EING---NNYVIIDPTQPYDHWKWEFPNRNLSFGKTLGAGAFKGVVEATAYGLIKSDAAM 616
 Qy 640 QVAVKMLKEKADSSREALMSLKMTQLGSHENIVNLGACTLSGPIYLIFFEYCCYGD 699
 Db 617 TVAVKMLKPSAHLTEREALMSKLVSLYGLNHNINVLGACTVGGPTLVITEYCCYGD 676
 Qy 700 LNYLRKREKHFRTWTEIFKEHNFSPYPTFQSHPNSSMPGSR--VOIHPDSDQISGLHGN 758
 Db 677 LNFLLRRKEDSF--IPSKQEQADAAALYKNLLHKSKESSCDSSNEYMMDKPGVSYVPTKTD 734
 Qy 759 SFHS---EDETEYENQKLEBEEDLNVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAAR 815
 Db 735 KRSARIDSYIERDVTPTAIMEDEL-ALDLEDLLSFSYQVAKGMAPLASKNCIHRDLAAR 793
 Qy 816 NVLTHGVKVKICDGLARDIMSDSNVYVRGNARLPVKWMAPELFEGIYTIKSDVWSYG 875
 Db 794 NILLTHGRITKICDGLARDINDSNVYVKGARLPVKWMAPELFEINCYVTTESDVWSYG 853
 Qy 876 ILLWEIFSLGNYPGIPVDANFYKLIQNGKMDOPFYATEIYIIMQSCWAFDSEKRP 935
 Db 854 IFLWELFSLGSPYPCMPVDSKPYKMKIEGFRMLSPHAPAAAYEVMKTCWADPLKRP 913
 Qy 936 FPNLTSFLGCLADAEAEYQNV 958
 Db 914 FKQVQLIEKQISDSSKHYSNL 936
 RESULT 3
 Q63116 PRELIMINARY; PRT; 978 AA.
 AC Q63116;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE C-kit receptor tyrosine kinase.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA MEDLINE=92003944; PubMed=1912577;
 RA Tsujimura T., Hirota S., Nomura S., Niwa Y., Yamazaki M., Tono T.,
 RA Morii E., Kim H., Kondo K., Nishimune Y., Kitamura Y.
 RT "Characterization of Ws mutant allele of rats: A 12-base deletion in
 RT tyrosine kinase domain of c-kit gene."
 RL Blood 78:1942-1946(1991).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES
 DR EMBL; D12524; BAA02094.1; -;
 DR HSSP; P11362; IFGK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001824; RtkinaseIII.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Euk_pkinase; 2.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00410; IG-like; 3.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
 KW Phosphorylation; Receptor; Transferase; Transmembrane;
 KW Tyrosine-protein kinase.
 SQ SEQUENCE 978 AA; 109341 MW; 0958C33F19899051 CRC64;
 Query Match 24.0%; Score 1263.5; DB 11; Length 978;
 Best Local Similarity 33.8%; Pred. No. 1.6e-95;
 Matches 334; Conservative 171; Mismatches 361; Indels 121; Gaps 37;
 Qy 35 CYLIHNKNDSSVGVKSSYPMTVSESPEDLGCALRPOSSGTVTVEAAAVEVDVVSITLQVL 94
 Db 12 CYLLVLLRGQTCTSPASPGPSP-----SIQPAQS-----ELIVEAGDTIRLT 57
 Qy 95 VDAPGNISCLVFKHSSLNCQPHFDLQNRGVVSMVLKMTQ-TOAGEYLLFIQSEATNYT 153
 Db 58 CTDPAFVK--WTFE-----ILDVRIENKQSEWIREKAEATHTKYTCVSSGLRSSI 107
 Qy 154 ILFTVSIIRN-TLLYTLRREYFRKMNQDALVCISESVPEPIVWVLCDSQGESCKEESPA 212
 Db 108 YVF--VRDPAVLFLVGLPLFGK-EDNDALVRCPLTDPO-VSNYSLEICDGKSLPTDLKF 162
 Qy 213 V-----VKEEKVLHELFGTDIRCCARNELGRCTRLLFTID-----LNQTPQTLLPOL 260
 Db 163 VNPKAGITIKNVKAYHRLC---IRCAAQREGKWMRSKDTLTKVRAAIAKAIPIVVSYPET 219
 Qy 261 --FLKVGPELWIRCAVHVNHGFLTW-----ELENKALEEGNYFEMS--TYSNTRMIR 311
 Db 220 SHLLKEGDTFTVICTIKVSTSDVSMWIKLNLPQPSKAQVRNWSHQGDNYERQETLT- 278
 Qy 312 ILFAFVSSVARNDTGYTCTSSSKHPSQSALVT---IVGKGFNI---ATNSSEYEDIQYE 365
 Db 279 ----ISSARVNDSGVFCYANNTFGSANVTTLTKVVERGFNIIPVGNIT--VFVTDGE 331
 Qy 366 EFCFSVRFKAYPO-IRCTWTFSRKSPPCQKGLD-----NGYSISKFCNHKH-----QP 413
 Db 332 NVDLVVEFEAYPKPEHQQIYNNRT--PTNRGEDIYKSDNQSNIRYVNEURLTLKGTGEG 389
 Qy 414 GEYIHAENDDAQFTKMTFLNIRKPOVLA--EASASQSCFSDGYPLPSWTWKKCSKDS 471
 Db 390 GTYTLVNSDVSAVTFDVTYVNTKPEILTYDRLMNGRLQCVAAAGPEPTIDWYFCTGAE 449
 Qy 472 PNCTEEITE-GYNNRKANKRVFGQWSSSTLNMSEAIKGLFLVKCCAYNSLGTSCETILN 530
 Db 450 QRCCTVPPVVDVQIQNASVSPGKLVQSSIDSSVFRHNGTVECKASNAVGKS--SAFFN 507
 Qy 531 SPGPPPP-----IQDN-----ISFYATIGVCLLFIIVLTLCHIKYKQFRYESQL 576
 Db 508 ----FAFKGSKSEQIOPHTLFTPLLGIFVVVTAAG--LMGIIVMVL--AYKYLQKPMYEVQW 559
 Qy 577 QMV-QVTSSDNEYFVDPREYEDLKWEFPRENLEFPGKLVGSGAFKVMNATAYGISKT 635
 Db 560 KVEEING---NNYVIIDPTQPYDHWKWEFPNRNLSFGKTLGAGAFKGVVEATAYGLIKS 616
 Qy 636 GVSIOVAVKMLKEKADSSREALMSLKMTQLGSHENIVNLGACTLSGPIYLIFFEYCC 695
 Db 617 DAAMTVAVKMLKPSAHLTEREALMSKLVSLYGLNHNINVLGACTVGGPTLVITEYCC 676
 Qy 696 YGDLNLYLRKREKHFRTWTEIFKEHNFSPYPTFQSHPNSSMPGSR--VOIHPDSDQISG 754
 Db 677 YGDLNLYLRKREKDSF--IPSKQEQADAAALYKNLLHKSKESSCDSSNEYMMDKPGVSYVVP 734
 Qy 755 LHGNSFHS---EDETEYENQKLEBEEDLNVLTFEDLLCFAYQVAKGMEFLFKSCVHRD 811
 Db 735 TKTDKRSARIDSYIERDVTPTAIMEDEL-ALDLEDLLSFSYQVAKGMAPLASKNCIHRD 793

```
QY 812 LAARNVLTHGKVVKICDFGLARDMSNVVVRGNARLPVKWMAPELSFEGYTIKSDV 871
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 794 LAARNILLTHGRITKICDFGLARDIRNDSNVVVKGNARLPVKWMAPEISFNCVTFESDV 853
QY 872 WSYGILWEIFSLGVNYPGIPVDANYPKILQNGKMDQPPYATEEYIIMQSCWAFDSR 931
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 854 WSYGIFLWELFSLGSSPYGPNVDSKFKYKIKEGFRMLSPHEAPAAEYVNMKTCDADPL 913
QY 932 KRSPFNLTSLFLGCOLADAEAMYQNV 958
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 914 KRPTFKOVVQLIEKQISDSSKHIYSNL 940

RESULT 4
O97744 PRELIMINARY; PRT; 964 AA.
AC O97744;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Mast/stem cell growth factor receptor (Fragment).
GN KIT1-0101.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HAMPSHIRE BREED; TISSUE=LEUKOCYTE;
RX MEDLINE=98391767; PubMed=9724328;
RA Marklund S., Kijas J., Rodriguez-Martinez H., Roennstrand L., Funa K.,
RA Moeller M., Edfors-Lilla I., Andersson L.;
RT "Molecular evolution of the dominant white phenotype in the domestic
RT p39.";
RL Genome Res. 8:826-833(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HAMPSHIRE BREED; TISSUE=LEUKOCYTE;
RA Marklund S.;
RL Thesis (1997), Department of Animal Breeding and Genetics,
RL Swedish University of Agricultural Sciences, Uppsala, SWEDEN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR ENBL; AJ223228; CAAL1196.1; -.
DR HSP; P11362; IFGK.
DR InterPro; IPR00719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; rTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00219; TyRc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
KW Transmembrane; Tyrosine-protein kinase.
FT NON TER 964
SQ SEQUENCE 964 AA; 108287 MW; 90E72EDFAB1358B7 CRC64;
```

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Query Match 23.9%; Score 1262.5; DB 6; Length 964;
Best Local Similarity 33.4%; Pred. No. 1.8e-95;
Matches 332; Conservative 169; Mismatches 349; Indels 143; Gaps 36;
QY 47 VKSSSPVMSPESEDLCALRPQSSGTVYEAANAIVEDVSASITQLVLDAPGNISCLMW 106
```

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Db 20 VQTSSQPSV--SPEEL-----SPPSIHPAKS-ELIVSAGDBIRLCTDPGSK--WT 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 107 FKHSLLNCQPHFDLQNRGVSMVLKMTETOAGEVLLPIQSEATNYTILFTVSRN--TL 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 68 FETLG-----QLSENTHAEWIVEKAEAMNTGNYCTNEGGLSSSIYVF---VRDP 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 166 YTLRRPYFRKMENODALYCISEVPEPIVWVLCDSQGESCKEESPAY-----VK 217
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 118 FLVDPPLYGK-EDNDALVRCPLTDPV-VTNSLTGCGCKPLPKDLTFVADPKAGIT 175
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 218 EKVHLELFGTDIRC--CARNELGRE-CTRLFTID-----LNQTPQTTLFQ--L 268
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 KREYHRL-----CLHCSANQGGKSVLSKFTLKVRAAIRAVPVVAVKASYLLREG 229
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 269 WIRCKAVVNHGFGLTWELEN---KALEEGNYFEMSTYSTNTRMIRILFAFVSSVAR 325
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 230 AVMCILIKDVSSVDSMMIRENSQTAQVKRNSWHQGFN----FLQRRLTISSARV 285
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 326 GYITCSSSKHPQSALVT---IVGKGFINA-----TNSSEDEYIDQVEEFCFSVR 373
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 286 GVFMCIYANNTEGSANVTTLLEVVDKGFNIFFPMNTTVFVNDGEDVDL----- 337
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 374 KAYPO-----IRCTWTFSRKFPCEQKGLDNGYSISKFCNHKH-----Q 418
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 338 EAYPKPEHRQWIYMNRTATDKWEDYPKSE-----NESNIRVVSSELHLRLKGT 392
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 419 HAENDDAQFTKMTLNIRRKQVLA--EASASQASCFSDGYPVLPSTWTKCKSDKSP 476
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 393 LVSADNVNSSFVFNYYNTKPEILTHRLMNGMLQCVAAAGPEPTIDMYFCPTQRCS 452
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 477 EI-TEGVNRKANRKVGOWVSSSTLNMSEAIKGLVKKCCAYNSLCTSCETILLNS 535
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 453 PVGPDVQIQNSSVSPFGKLVHSDISYAFKHNGTVECRAYNDVGS--SAFFN--- 506
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 536 PFIQD-----NISFYATIGVCLLFIIVLTLIICHYKKQPRYSQLOMV--QV 584
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 507 AFKEQIHAHTLFTPLLLIGFVIAAGMCIIVMLT---VKYLQKPMYEVQWKVBE 561
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 585 SDNEYFYDFREYVDLKWEPRENLEFGKVLGSCAFKVMNATAYGKTVGTSQVAVK 644
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 562 ---NNYVYIDPTQLPYDHHKWEFPNRNLSFGKTLGAGAFGKWEATAYGLIKSDA 619
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 645 MLKEKADSSEREALMSLKMVTGLSHENIVNLGACLTLSGPIYLIFCYCCYGDLLN 704
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 620 MLKPSAHLTEREALMSLKVLSYLGNNHNIIVNLGACTIGGTLVITEYCCYGDLL 679
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 705 SKREKPHRTWTE-----IFKEHNFSPYTFQSHPNSSM---PGSREVOIHPDSD 755
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 680 RKRDSFICSKQEDHAEALYKNLLHSSKSSCSDSTNEYMDMKPGVSYV-VPTKA 738
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 756 HGNFSHSEDEIEYENQKRLBEEDLNVLTFEDLLCFAYQVAKGMFLEPKSCVHR 815
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 739 RIGSY-----IERDVTPAIMEDDEL-ALDLEDLSSFSYQVAKGMAFLASKNC 792
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 816 NVLVTHGKVVKICDFGLARDIMSDSNVYVRGNARLPVKWMAPELSFEGYTIK 875
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 793 NILTHGRITKICDFGLARDINKDSNVYVKNARLPVKWMAPEISFNCVTFESD 852
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 876 ILLWEIFSLGVNYPGIPVDANFYKLIQNGFMDQPPYATEEYIIMQSCWAFDSR 935
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 853 IFLWELFSLGSSPYGPNVDSKFKYKIKEGFRMLSPHEAPAEYVNMKTCDADPL 912
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 936 FPNLTSFGCOLADAEAMYQNVQDVRVSEC-PH 967
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 913 FKQIVQLIEKQIESTNHIYSN---LANCSPH 941
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
Q9TQ01 PRELIMINARY; PRT; 964 AA.
AC Q9TQ01;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
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RA Marklund S., Kijas J., Rodriguez-Martinez H., Roenstrand L., Funa K.,
RA Moller M., Edfors-Lilja I., Andersson L.;
RT "Molecular evolution of the dominant white phenotype in the domestic
RT pig.";
RL Genome Res. 8:826-833(1998).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AJ223230; CAAL1198.1; -.
DR HSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00219; TyRK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
KW Transmembrane; Tyrosine-protein kinase.
FT NON TER 964 964
SQ SEQUENCE 964 AA; 108287 MW; 1B21292A962E9191 CRC64;

Query Match 23.9%; Score 1261.5; DB 6; Length 964;
Best Local Similarity 33.4%; Pred. No. 2.2e-95;
Matches 332; Conservative 169; Mismatches 349; Indels 143; Gaps 38;

QY 47 VGKSSYPMVSESPELGCALRPOSSGTVYEAAVEVDVSASITQLVLVDAPGNISCLMW 106
DB 20 VOTGSSQPSV--SPEEL-----SPPIHPAKS-ELIVSAGDEIRLCTDPGVK--WT 67

QY 107 FKHSNLNQPHFDLQNRGVSMVLKMTETQAGEYLLFIQSEATNYTLFTVSRN-TLL 165
DB 68 FETLQ-----QLSENTHAEWIVEKAEAMNTGNYTCNEGSLSSIIYVF---VRDPEKL 117

QY 166 YLRRPYRKMNEDALVCISEVPEPIVENVLQDSQESCKEESPAV-----VKKE 217
DB 118 FLVDPPLVYGR-EDNDALVRCPLTQPE-VTNYSLTQCEGKPLPKDLTFVADPKAGITIRNV 175

QY 218 EKVHLHFGTDIRC--CARNELGRE-CTRLFTID----LNQTPQTLTPQ--LFLKVGSEPL 268
DB 176 KREYHRL-----CLHCSANQGGKSVLSKKTLLKYRAAIRAVPVVAVSKASYLLREGSEF 229

QY 269 WIRKXAVHNVHFGLTWLEN---KALEGNYFEMSTYNTNRTMIRILPAFVSSVARNDT 325
DB 230 AVMCILIKDVSSVSDMSWIRENSQTKAQVKRNSHQGFN----FLRQEKLATISSARVND 285

QY 326 GYYTCSSSKHPSQNALVT---IVGKGFINA-----TNSSEDEYIDQVEEFCFSYRF 373
DB 286 GVFWCYANNFTGSANVTTLTLEWDKGFNIFPMNTVTFFVNDGEDVDL-----IVEY 337

QY 374 KAYPO-----IRCTWTFGRKSPPCQKQGLDNGYSISKFCNHHK-----QPGEYIF 418
DB 338 EAYPKPEHROWIYMNRTATDKWEDPKSE-----NESNIRYVSELHLRLKTEGTYTF 392

QY 419 HAENDDAQFTKMTLNIIRKQVLA--BASASQACSFSDGVPLPSWTWKCKSDKSPNCTE 476
DB 393 LVSNADVNSSVTENVYNTKPEILTHRLMGLMCQVAAAGPEPTIDWVFCPTGTCQRCV 452

QY 477 EI-TEGVNRNKRANKRVFGQWSSSTLANSEALKFLVKCCAYNSLGTSCETILLNSPGFF 535
DB 453 PVGPVDVQIQNSSVPFQKLVHSSIDYSAFKHNGTVECRAYNDVGKS--SAFFN----F 506

QY 536 PPIQD-----NISFYATIGVCLLFIIVLTLICHYKKQFRYESQLQWV-QVTGS 584

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DB 507 AFKEQIHATLFTPLLLIGFVIAAGMCMIVMILT-----YKLOKPMYEQWVVEEING- 561
QY 585 SDNEFYVDREYEDLKEWEPRENLEFGKVLGAGFKVMNATAYGISTGVSIOVAVK 644
DB 562 --NNVYVIDPTOLPVDHKWEPNRNLSFGKTLGAGAFKGVVETAYGLIKSDAAMTVAVK 619
QY 645 MLKEKADSSEREAALMSLKMMTQLGSHENIVNLLGACTLSGPIYLIIFYCCYCGDLLNLYR 704
DB 620 MLKPSAHLTEREAALMSLKVLSYLGHNHNIYNLLGACTIGGPTLVITEYCCYCGDLLNPLR 679
QY 705 SKREKFHRTWTE-----IFKEHNPFSFYPTQSHPNSSM---PGSREVOIHPDSQOISGL 755
DB 680 RKDSFICSKQEDHAEALYKNLLHSKSSCSDSNTEYMDMKPGVSYV-VPTKADKRRSA 738
QY 756 HGNSFHSDEIYEYENQKLEBEEDNLVLTFFDLFCFAVOVAKGMEFLFKPSCVHRDLAAR 815
DB 739 RIGSY-----IERDVTPTAIMEDEL-ALDLEDLSFSYQVAKGMAPLASKNCIHRDLAAR 792
QY 816 NVLVTHGKVKICDFGLARDIMSDSNVYVRGNARLPVKWMAPESLPEGIYTIKSDVWSYG 875
DB 793 NILTHGRITKICDFGLARDIKNSNVYVKGARLPVKWMAPESEFNCVYTFESDVWSYG 852
QY 876 ILLWEIFSLGVNPPGIPVDANFYKLIQNGFMDQOPFYATEEIIYIMOSCAWAFDSRRKPS 935
DB 853 IFLWELPSLGSPPGMPVDSKFKYKMKEGPRMLSPERAPVEMYDIMKTCWDADPLKRP 912
QY 936 FPNLTSLFGCOLADAEAMYNQVDRVSEC-PH 967
DB 913 FKQIVQLIEKQISESTNNIYSN-----LANCSPH 941

RESULT 7
Q8WN23 ID Q8WN23 PRELIMINARY; PRT; 979 AA.
AC Q8WN23;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C-KIT.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Zemke D., Yuzbasiyan-Gurkan V.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448148; AAL40833.1; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00410; IG like; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyRK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; UNKNOWN_1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; UNKNOWN_1.
SQ SEQUENCE 979 AA; 109753 MW; 46C30D5DEB8E33D3 CRC64;

Query Match 23.7%; Score 1250.5; DB 6; Length 979;
Best Local Similarity 33.6%; Pred. NO. 1.9e-94;
Matches 334; Conservative 161; Mismatches 345; Indels 153; Gaps 39;

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Db 278 SSARVNDGVMFCYANNVTFGSANVTTLTLEVVVDKGFIFMFMINTVTVFVNDGENVDL----- 333
QY 366 EFCFSVRFKAYPO-IRCTWTFSRKSF--PCEQKGLDNGYSISKFCNKH-----QPGE 415
Db 334 ----IVEYEAPKPEHQOWIYMNRFTFTDKWEDYPKSENESNIRYVSELHLTRLKGTEGT 389
QY 416 YIHAENDDAQFTKMTFLNIRRKQVLA--BASASQASCFSDGYPPLPSWTWKKCSKSPN 473
Db 390 YTELVSNSDVNAALAFNYYNTKPEILTYDRLVNGMLQCVAAGPEPTIDWYFCFGTEQR 449
QY 474 CTEITE-GVMNRKANRKFVQWSSSTLAMSSEAKGLFLVKCCAYNSLGTSCETILLNSP 532
Db 450 CSASVLVDVQTLNSGPPGPKLVQSSIDSSAFKNGTVECKAYNDVGKT--SAYFN-- 505
QY 533 GPPFFIQD-----NISFYATIGVCLLFIVVLTLCHYKYPKRYESQLQWV-QV 581
Db 506 --FAFKGQIHPHTLFTPLLLGCFVIVAGMWCIIVMILT-----YKYLQKPMYEVQMKVVEI 559
QY 582 TGSDDNEYFYVDPREYEDLKWEPRENLEBFGKVLGSGAFGKVMNATAYGISKTVGSIQV 641
Db 560 NG---NNYVYIDPTQLPYDHKWEPNRLSFGKTLGAGAFGKVVVEATAYGLIKSDAAMTV 616
QY 642 AVKMLKEKADSSEREALMSLKMWTQLGSHENIVNLGACTLSGPIVLIIFYCCVGDLLN 701
Db 617 AVKMLKPSAHLTEREALMSLKLUSYLGNGHNIIVNLGACTIGTPTLVITEYCYGDLN 676
QY 702 YLRSKREKPHRTWTE-----IPKEHNFsfYPTQSPHNSM---PGSREVQIHPDSQI 752
Db 677 FLKRKDSFCSKQEDHAEALYENLHLSKSSCSDSTNEYMDMKPGVSYV-VPTKADK 735
QY 753 SLHGNSFHSEDEIYENQKRLBEEEDLVLTFDLCLCFAYQVAKGMFLFKSCVHRDL 812
Db 736 RSVRIGSY-----IERDVTPEIMDEDEL-ALDLEDLLSFSYQVAKGNFLASKNCIHRDL 789
QY 813 AARNVLTHGKVKIKCDPLGARDMSNVYVGRNARLPVKWMAPESLFEGIYTIKSDVW 872
Db 790 AARNILTHGRITKICDFGLARDIKDSDNVYVGRNARLPVKWMAPESLFENCFYTFESDVW 849
QY 873 SYGILLWEISLGNVPYGPVPDANFYKLIQNGFPMQOPFYATBEIYIMOSCAWAFDSRK 932
Db 850 SYGILFELFSLGSPYFGMPVDSKFKYKMKIEGFRMLSPESAHPAEMYDIMKTCWDADPLK 909
QY 933 RPSFNLTSFLGCOLADABEAMYQNV 958
Db 910 RPTPKQIVOLIEKQISESTNHSNL 935

RESULT 9
Q9XS93
ID Q9XS93 PRELIMINARY; PRT; 978 AA.
AC Q9XS93;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KIT.
GN C-KIT.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=CEREBELLUM;
RC London C.A., Galli S.J., Yuuki T., Hu Z.-Q., Helfand S.C.,
RA Geissler E.N.;
RT "Spontaneous canine mast cell tumors express tandem duplications in
the proto-oncogene c-kit.";
RL Exp. Hematol. 0:0-0(1999).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
PROTEIN KINASES.
DR EMBL; AF099030; AAD28369.1; -.
DR HSPB; P11362; 1FGK.
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DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;
KW Receptor; Transferase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 978 AA; 109651 MW; 5AC31ESAC4E9910F CRC64;

Query Match 23.6%; Score 1244; DB 6; Length 978;
Best Local Similarity 33.2%; Pred. No. 6.4e-94;
Matches 330; Conservative 161; Mismatches 346; Indels 158; Gaps 38;

QY 47 VKSSSTPMVSESEDLGALRPOSSGTVYEAAVEVDVASITQLVLDAPGNISCLWV 106
Db 22 VQTGSSQPSVSPGPEPLP-SIHPAKS-----ELIVSVGDELRLSCTDPGVK--WT 69
QY 107 FKH--SSLNCQPHFDLQNRGVVSVMLKMTETQAGEVLLFIOSEATNYTIL-----PT 157
Db 70 FETLGQNLNETH----NEWITE-----KAEAG-----HTGNYTCNRDGLSRSIY 110
QY 158 VSIRN-TLLYTLRPFYFRKMENQDALVCISBPBPPIVWVLCDSQGSCKEESPAV--- 213
Db 111 VFVRDPAKLFLVDLPYLYCK-EGNDTLVRCPLTDPE-VTNSLRGCEGKPLKDLTFVADP 168
QY 214 -----VKEEKVLHELFGTDIRC--CARNELGRE-CTRLFTID-----LNQTTQTLPLQ- 260
Db 169 KAGITIRNVKREYHRL-----CLHCSADQKGRTVLSKFTLKVRAAIRAVPVWSVKTS 222
QY 261 -FLKVGELWIRCKAVHYNHGFLGTWELEN---KALEBGNYPEMSTYSTNRTWIRILPAF 316
Db 223 SLLKEGEAFSVMCFIKDVSSFVDSWIKENSQTNQTSNWHHGDGFPEROEKLI---- 278
QY 317 VSSVARNDTGYITCSSSKHPSQSALVT---IVKGKFINA-----TNSSEDEYIDQY 364
Db 279 ISSARVNDGVMFCYANNVTFGSANVTTLTLEVVVDKGFIFMFMINTVTVFVNDGENVDL--- 335
QY 365 EFCFSVRFKAYPO-IRCTWTFSRKSPCEQKGL---DNGYSISKFCNKH-----QP 413
Db 336 ----IVEYEAPKPEHQOWIYMNRFTFTDKWEDYPKSDNESNI-RYVSELHLTRLKGNEG 389
QY 414 GEYIFHAENDDAQFTKMTFLNIRRKQVLAESAQA--SCFSDGYPLPSWTWKKCSKDS 471
Db 390 GTYTFQVNSDVNSSVTFNVYNTKPEILTHESLNGMLQCVAAGPEPFAVDWYFCPGA 449
QY 472 PNCTEEI-TEGVMNRKANRKFVQWSSSTLAMSSEAKGLFLVKCCAYNSLGTSCETILLN 530
Db 450 QRCVSPGICPMQVQNSLSLSPGKLVQSSIDYSAFKNGTVECRAYNNVGRS--SAPFN 507
QY 531 SPGPPFFIQDN-----ISFYATIGVCLLFIVVLTLCHYKYPKRYESQL 576
Db 508 ----FAFKGSKSEQIHPHTLFTPLLLGCFVIVAGMWCIIVMILT-----YKYLQKPMYEVQW 559
QY 577 QMW-QVTGSSDNEYFYVDPREYEDLKWEPRENLEBFGKVLGSGAFGKVMNATAYGISK 635
Db 560 KVVVEING---NNYVYIDPTQLPYDHKWEPNRLSFGKTLGAGAFGKVVVEATAYGLIKS 616
QY 636 GVSIOVAVKMLKEKADSSEREALMSLKMWTQLGSHENIVNLGACTLSGPIVLIIFYCC 695
Db 617 DAAMTVAVKMLKPSAHLTEREALMSLKLUSYLGNGHNIIVNLGACTIGTPTLVITEYCC 676
QY 696 YGDLNLYRSKREKPHRTWTEIFKEH-NFSFYPTFQSHFNSSMPGMSRVEQIHPDSQISG 754
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Db 677 YGDLNLFRRKDSFICKQK---DHGEVALYKXNLLHSSKSSCSUS-----THEYMDM 726
Qy 755 LHGNSFHSEDEIEYENQKRLKE-----EEDLNVLTFEDLLCFAYQVAKGMEFLE 803
Db 727 KPGDSYVVPTRKDRSRIGSYIERDVTPAIMEDELALDLEDLLSFQYQVAKGMAFLA 786
Qy 804 PKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDSNVVRGNARLPVKWMAPESLFEG 863
Db 787 SKNCIHRDLAARNILLTHGRITKICDFGLARDIKDSDSNVVRGNARLPVKWMAPESEIENC 846
Qy 864 IYTIKSDVWSYGILLWEIFSLGVNVPYGPVDPANFKLIQNGFKMDQPPYATEEIIYIMQ 923
Db 847 VITFESDVWSYGIFLWEIFSLGVSSPYGMPVDSKYKMKKEGFRMLSPHEAPAMTDIMK 906
Qy 924 SCWAFDSRKRPSFNNLTSLFGLCQLADAEAMYQNV 958
Db 907 TCWDADPLKRPSTKQIVOLIEKQISDSNTHIYNSL 941

RESULT 10
Q98SUI PRELIMINARY; PRT; 977 AA.
AC Q98SUI
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Receptor tyrosine kinase fms.
OS Danio nigrofasciatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=144739;
RN [1]
RP MEDLINE=21359118; PubMed=11466528;
RX Parichy D.M., Johnson S.L.;
RA "Zebrafish hybrids suggest genetic mechanisms for pigment pattern
RT diversification in Danio.";
RL Dev. Genes Evol. 211:319-328(2001).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AF324481; AAK15303.1; -.
DR HSP; P11362; IFGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; Ig_c2.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane.
FT VARIANT 60 V -> L.
FT VARIANT 103 103 A -> S.
FT VARIANT 742 742 P -> S.
FT VARIANT 899 899 E -> D.
SQ SEQUENCE 977 AA; 109881 MW; CF54E129FAB10E3E CRC64;

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Query Match 23.3%; Score 1230.5; DB 13; Length 977;
Best Local Similarity 32.8%; Pred. No. 8.4e-93;
Matches 326; Conservative 174; Mismatches 367; Indels 127; Gaps 34;

Qy 71 SSGTVYAAAVEVDYSASITLQVLVDAPGNISCL-WFVKHSSLNCOPHFDLQNGRVVSMV 129
Db 27 NSGAL---AGTDVILDSGSPQLVCEGDPVTFPPVAKH-----KRYTSKEVGKIRSPR 78
Qy 130 ILKMTETQAGEY-LLIQSEATNYTILFTVSRNT-LLY-----TLRPPYFRKWNODAL 182
Db 79 VEKATVDFGTGKVCVYINGSNLAASSVHFVDRSVLFVSPSSLR--VYRK-EGEDLL 135
Qy 183 V-CISESVEP-IVEWLCDSQESCKEESPAVKKBEKV-----HELFOTDIRCCARNE 236
Db 136 LPCL---LTPDATDTFTRMDNGSAAPYGMNATFDRKGLVIRNVHPGFNADYICSAIG 192
Qy 237 LGRECTRLFTIDLNTPOTTLPLFLK-----VGEPLWIRCKAVVNHGFLTWELN 289
Db 193 GAEKVSKIFSIINVIQRLRP-PYVILKRNEYVKLVGERIQISCTTNPNFYINVTWTHSS 251
Qy 290 KALBEGNYFEMSTYSTRMTIRILFAFVSSVARNDTGYTCTSSSKHPSQSALVT---IVG 346
Db 252 KELPKPE--EKSTMEGDLAIESILT-ISSVOLSDTGNITCTQNEAGANSSITQLLAVD 308
Qy 347 KGFY-----NATNSDEYIDQYEEFCFSVRFKAYQIRC-TW---TFSRKSPPCEQ 394
Db 309 EPIRLSPKLSSKLTHRGLSIEVSEGEDVDLGLVLAEPPLTSHETPTSHNASLP--- 365
Qy 395 KGLDNGYSISKFCNHK-----HQPGEYIFHAENDDAQFTKMTLNIIRKPKQ 440
Db 366 -----ENRRYNANDRYEALLFLKRLNFEIIGQVTLNVKNMSKASITFDIKMYTKPV 417
Qy 441 VLAE-ASASQASCFSDGYPSPWTKKCDKSPNCTEEITE-----GVNRRKANRKFVGQW 495
Db 418 ARVKWENVTLSCRSYGVYAPSLILWYQCTGIRTCENTDLOIQTQVTFEPQKESGAV 477
Qy 496 VSSSTLNMSAETKGLVKCCAYNSLGTSCTETLLNSPGPPFPQDNISFYATTG-VCLL 553
Db 478 GVESVLTWGPV-RRMTVVCVAFNLVQGGSDTFSMD-----VSDQIFTSAMCGSTVAMV 529
Qy 554 FIVLTLLICHYKKQPRVESQLQMVQVGTSSDNEYFYVDPREYEDLWKWEPRENLEFG 613
Db 530 VUGLLLIIMYIKQPRYEIRWKIIEAT--NGNNVTDFIDTOLPYNEKWEFPDRDLKLG 587
Qy 614 KVLGSGAFGKVMNATAYGISKTGVSIQVAVKMLKEKADSSEREAALMSELKMTOLGSHEN 673
Db 588 KTLGAGAGKVVETAYGLGKEDNITRVAVKMLKASHPDEREALMSELKILSHLGQHN 647
Qy 674 IVNLLGACTLSGPIYLIFCYCYGDLNLYLRSKREKPHRTWTEIPKEHNFSPYPTFQSH 733
Db 648 IVNLLGACTHGGPVLVITEYCHGDLNLFRLSKAENF-----LNFVMTI---P 692
Qy 734 NSSMP-----GSREVQIHPSDQISGLHGSFHSDEIEYENQKRLKE-----EEDLN 782
Db 693 NFPEPVTDYKKNVSTERMFVRSDSGISSTCSHYLDMRPVTSRPTNSALDPSSDCQEDSW 752
Qy 783 LTFEDLLCFAYQVAKGMEFLEKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDSNY 842
Db 753 LDMDDLRFSSQVAGLDPLAAKNCIHRDVAARNVLNTRVAKICDFGLARDIMSDSNY 812
Qy 843 VVRGNARLPVKWMAPESEFEGYITIKSDVWSYGILLWEIFSLGVNVPYGPVDPANFYKLI 902
Db 813 VVKGNARLPVKWMAPESEFECVYTVQSDVWSYGIMLWEIFSLGKSPYNILVDSKEYKMI 872
Qy 903 QNGFKMDQPPYATEEIIYIMQSCWAFDSRKRPSFNNLTSLFGLCQLADAEAM-----YQNV 958
Db 873 KCGYQMSRPDPAPPMTYIMKMCNLEAERPTFSKISQMIQRMILGETSEQDQTOBYKNI 932
Qy 959 DGRVSECPHYQNRPPFSREMDLGLLSPOAQVED 992
Db 933 PSE-AEVQPLESCDPVKHDESEFTSCPEBED 965

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RESULT 11
O77589 PRELIMINARY; PRT; 945 AA.
AC O77589;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tyrosine kinase receptor homolog (Fragment).
GN KIT.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Lear T.L., Adams M.H., McDowell K.J., Ponce de Leon F.A.,
RA Sullivan N.D., Coogle L., Ferguson E., Chambers T.M., Bailey E.;
RT "Chromosomal location of genes for ESR, ETS2, KIT, MX1 and PGR
RT in the horse, Equus caballus.";
RL Proc. Xth Amer. Coll. Dom. Anim. Cytogenet. Gene Mapp. 0:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
RT "An Equine sequence homologous to the c-KIT-proto-oncogene mapped to
RT chromosome 3q13-21.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
DR EMBL; AF055037; AAC23611.1; -.
DR HSFP; P11362; 1FGK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001824; RTKinaseIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Glycoprotein; Immunoglobulin domain; Kinase; Phosphorylation;
KW Receptor; Transmembrane; Tyrosine-protein kinase.
FT NON_TER 945
SQ SEQUENCE 945 AA; 106143 MW; 7DB424A89DF5C340 CRC64;

Query Match 23.3%; Score 1229; DB 6; Length 945;
Best Local Similarity 32.5%; Pred. NO. 1.1e-92;
Matches 323; Conservative 166; Mismatches 368; Indels 136; Gaps 31;

Qy 47 VKSSSPVWSSPEDLGCALPQSGTYEAAVEVDVSASITLQVLDAPGNISCLWV 106
Db 20 VQTGSSQPSV--SPGEL-----SPPSIHPAKS-ELIVSVGDEIRLLCADFGVK--WT 67
Qy 107 FK-HSSLNCPHFQDLNQRGVSMVILKMTETQAGEYLLFIQSEANTYTLFTVTSIRNTLL 165
Db 68 FETWGLSENTHKE-----WVTEKATNTGTYCTNEGLSSIVF---VRDPAK 116
Qy 166 YTLRRPYFRMKNQDALVCISVPEPIYVWVLCDSQGSCKEESPAV-----VKKE 217
Db 117 LFLFDPSLYGKSSDTLVRCPLTDPE-VTVNSLMACEGKSLPKDLTFVADPRKAGITIRNV 175
Qy 218 EKVHLEFGTDTRCCARNEIGRECTLFID-----LNQTPQTLPO--LFLKVGELPLWR 271
Db 176 KEYHRLC---LRCSADKDGKSVLSNKFLLKVRATRAVFPVSVSKASYLLREGGEFSVT 232

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Qy 272 CKAVVNHGFLTWELNKALEBEGNYFEMSTYSTRNTRILFAFVSSVARNDGTGYTCS 331
Db 233 CLIKDVSSSDVMWIRENSRTKE-QVKSSSSHQGDFNVRQERLTIISPARVNDGVPFCY 291
Qy 332 SSKHPSOSALVT---IVGKGFNA-----TNSSEDEIDQYEEFCFVSVRKAYPQ- 378
Db 292 ANNTFGSANVTTLTLEVDKGCINFPMMNTTVFVNDGENVDL-----IVEYESPKP 343
Qy 379 -----IRCTWTFSRKSFCEQKGLDNGYSISKFNHKK-----QPGEYIIFHAEND 424
Db 344 EHQWIYMNRTSTDKMEDYKSE-----NESNIRYVSELHLTRLKGTGGTYTLVLSNSD 398
Qy 425 AQTYMFTLINRRKPOVLA--EASASQASCFSDGYPDPSTWTKCKSDKSPNCTBEI--TEG 481
Db 399 VDSVTFNVVYNTKPEILTRDLRMNGMLQCVAAGFPEPTIDWYFCPTGEQRCSPFVGPVD 458
Qy 482 VWRKANRKPVGQWSSSTLNMSEAIGFLVKCCAYNSLGTSCETILLNSPGPPFIQDN 541
Db 459 VKIQNSSVSPFGKLVQSSIDYSAFKNGTVECRAYNDVGKSSAFF-----N 505
Qy 542 ISFYATIGVCLLF-----IVLTLILCHYKQFRIESQLQMV--QVTGSSDN 587
Db 506 PAFKEQIHPTLFTPELLIGSVVAGMCMVIMVLTLYKLOKPMYEVQWKVVEEING---N 562
Qy 588 EYFVDFREYDYDLKWEPFRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIOVAVKMLK 647
Db 563 NVYVIDPTQLPYDHKWEPFNRNLSFGKTLGAGAFKVVVEATAYGLIKSDAAMTAVKMLK 622
Qy 648 EKADSSEREALMSLKMTQLGSHENIVNLGACTLSPYILPEYCCYGDLLNLYRSKR 707
Db 623 PSAHLTEREALMSLKLVSYLGNHNVNLGACTVGGFTLVITEYCCYGDLLNLYRRKR 682
Qy 708 EKFRHTWTE-----IPKEHNFYSFPTQSHPNSSM---PGSREVOIHDPDSQISGLHN 758
Db 683 DSFICKQEDHAEALYKYLHLSKSSCNDSTNEYMDMKPGSVYV-VPTKTDKRAARIG 741
Qy 759 SFHSEDEIEYENQKLEEBEEDNLVLTFDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVL 818
Db 742 SY-----IERDVAPSIMEDDEL-ALDLBLLSFSYQVAKGMAFLASKNCKIHRDLAARNIL 795
Qy 819 VTHGKVKIKCDGLARDIMSDSYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILL 878
Db 796 LTHGRITKICDGLARDIKNDNSYVVRGNARLPVKWMAPESLFNCVYTFESDVWSYGIFL 855
Qy 879 WEIFSLGVNPYGPVPDANFYKLIQNGFKMDQPFYATBEIYIMOSCWAFDSRKRPSFPN 938
Db 856 WELFSLGSSPFGMPVDSKFYKMIKEGFRMLSPHAPAEYDIMKTCWDADPLKPTFPKQ 915
Qy 939 LTSFLGCOLADABEAMYQNQDGRVSECPTHYQN 971
Db 916 IVOLIEKQISDSTNQIYSN-----LANCSPROEN 944

RESULT 12
Q98SU3
ID Q98SU3 PRELIMINARY; PRT; 974 AA.
AC Q98SU3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Receptor tyrosine kinase Fms.
GN FMS.
OS Danio dangila.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=127599;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21359118; PubMed=11466528;
RA Parichy D.M., Johnson S.L.;
RT "Zebrafish hybrids suggest genetic mechanisms for pigment pattern
RT diversification in Danio.";

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[illegible]

Db 896 LKRPFTKQIVQVMEQQLSDSK 916

RESULT 14

Q918N6 PRELIMINARY; PRT; 977 AA.

AC Q918N6

DT 01-OCT-2000 (TEMBLrel. 15, Created)

DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)

DE Fms.

GN CSF1R OR FMS.

OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AB;

RA MEDLINE=20323166; PubMed=10862741;

RA Parichy D.M., Ransom D.G., Paw B., Zon L.I., Johnson S.L.;

RT "An orthologue of the kit-related gene fms is required for development

RT of neural crest-derived xanthophores and a subpopulation of adult

RT melanocytes in the zebrafish, *Danio rerio*.";

RL Development 127:3031-3044(2000).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-

CC PROTEIN KINASES.

DR EMBL: AF240639; AAF76872.1; --

DR HSSP; P11362; IFGK.

DR ZFIN; ZDB-GENE-001205-1; csflr.

DR InterPro; IPR000719; Euk.pkinase.

DR InterPro; IPR003598; IG_C2.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR001824; RTKinaseII.

DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00047; ig; 4.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Euk.pkinase; 2.

DR SMART; SM00408; IGC2_1

DR SMART; SM00219; TyrKC; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

DR PROSITE; PS00240; RECEPTOR TYR KIN III; 1.

KW ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;

KW Receptor; Transfrase; Transmembrane; Tyrosine-protein kinase.

FT VARIANT 238 238 N -> K.

FT VARIANT 615 615 V -> M.

FT SEQUENCE 977 AA; 110187 MW; C91A2F339E746A58 CRC64;

Query Match 23.2%; Score 1223.5; DB 13; Length 977;

Best Local Similarity 31.6%; Pred. No. 3.2e-92;

Matches 321; Conservative 170; Mismatches 355; Indels 169; Gaps

Qy 71 SSGVTVEAAAVEDVNSAITLVLDAPGNISCL-WVFKHSSLNCPHFDLQNRGVVSMV 129

Db 27 SSGAL---AGTDVILESGSLQVCEGDGVTFLPLAKH-----KRYISKEVKINSFR 78

Qy 130 ILKMTETQAGEY-LLFIOSEATNYTILFTVSRNT-LLY-----TLRRPYPRKMNQDAL 182

Db 79 VEKTTVDFTCTYKCVVMNGNSNLSSVHFVRDSRVLFVSPSTSLR--YVRK-EGEDLL 135

Qy 183 VCISESVPPIVEWVLCDSQGSCKEESPAVVKKEKVL-----HELFGTDTRCCARNELG 238

Db 136 LPCLLTDPPE-ATDFTPRMDGSAAPYGMNITYDPRKGVLIIRNVHPGFNADYICCARIGGA 194

Qy 239 RECTRLFTIDLNTPTQTLTLPOLFLK-----VGEPLMIRCKAVVNHGFLGTWELENKA 291

Db 195 EKVSFKISINIIQLRFPF-PYVILKRNEVYKVLGRLQISCTTNPNFYINVTWTHSSRM 253

Qy 292 LEEGNYPFEMSTYNTMTIRILFAFVSSVARNDTCYTTCCSSKHPQSALVT---IVKGK 348

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Db 254 LPKAE--EKSTWEGRLAESILT-IPVQLSHNTICTGNEAGANSTTQLLIVVEEP 310
Qy 349 FI-----NATNSEDYEIDQYEEFCFSVRKAYPQIRC-----TWTFSRKSFCEQKG 396
Db 311 YIRLSPKLSKLTHRLGSLIEVSGDDVGLVLEAYPLTSHKWTPTSHNASLP----- 365
Qy 397 LDNGYSISKFNHK-----HQGEYIFHAENDDAQTKMFTLNIRKPKQVL 442
Db 366 -----ENRFFNDRYEAALLLKLNFEEIGQYTLNKNMSKASITFDIMYTKPVAR 419
Qy 443 AE-ASASQSCFSQGYPLPSWTWKCKSDKSPNCTEITE-----GVNWKANRKFVGQWVS 497
Db 420 VKWENVTLSCRSYGPAPSLWYQCTGIRTCPPNTDLQPIQOTVEFKESGAVGV 479
Qy 498 SSTLNMSBAIKGLVKCCAYNSLGTSCETILNLSGPPFPFFODNISFYATIG--VCLIFI 555
Db 480 ESVLTUGFN-RRMTVVCVAFNLVGQSDTFSME-----VSDQIFTSAMCGSTVAMVVL 531
Qy 556 VLTLLICHKYKOPRYESQLQMVQVGTSSDNEYFYVDFREYEDLKWEPFPRENLEFGKV 615
Db 532 GLLLIFMYIKYKQPRYBIRWKIIEAT--NGNNYTFIDPTQLPYNEKWEFPRDKLKLGT 589
Qy 616 LGSAGFQVMNATYGISKTGVSIOAVKMLKEKADSSEREALMSLXOMTOLGSHENIV 675
Db 590 LGAGAFGVKEATAYGLGKEDNITRVAVKMLKASAHDPEREALMSLXILSHLGQHKIV 649
Qy 676 NLGACTLGGPIYLIIFYCCYGDLLNLYRSKREK-----HRT 713
Db 650 NLGACTGGPVLTITECHGDLNLFNRKAEFLNFMTIPNPEPMTDYKNVSTERM 709
Qy 714 W-----TEIFKEHNFSPYTFQSHPNSSMPGSRVQIHDPDQISGLHGNSFHSDEI 766
Db 710 FVRSDGISSTCSHYLDMRPVTSRPTNSALDSSSEQ----- 747
Qy 767 EYENQKLEEDLNLTFFEDLFCAYQVAKGWELEPKSCVHRDLAARNVLVTHGKVVK 826
Db 748 -----EDGWPLDMDDLRFSSQVAGGLDFLAANKCIHRDVAARNVLLTNSRVAK 796
Qy 827 ICDGLARDIMSDSNVYVRGNARLPVKWAPESLFEGLIYTIKSDVMSYGILLWEIFSLGV 886
Db 797 ICDGLARDIMSDSNVYVRGNARLPVKWAPESIFECVYTVGSDVMSYGIMLWEIFSLGK 856
Qy 887 NPYGIPVDANFYKLIQNGFKMDQPFYATEEYIIIMQSCWAFSDRKRSPFNLTSLGQC 946
Db 857 SPYENILVDSKFYKMKICGYQMSRDPFAPPENYTIKMCWNLDAAEPTFSKISQMIQRM 916
Qy 947 LADAEAM-----YQNV-----DGRVSECPHYQNRPF-----SREMDLGLLSP 986
Db 917 LGSETSEQDTQYKNIPTAEAEQQLSCDPVKHEDESFTSCDQEEEDQPLMKP 971

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RESULT 15

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Q9TDT7 PRELIMINARY; PRT; 948 AA.
AC Q9TDT7
ID Q9TDT7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Stem cell factor receptor (Fragment).
GN C-KIT.
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP SEQUENCE FROM N.A.
RA Lawrence S.B., Greenwood P., Tisdall D.J., McNatty K.P., Fidler A.E.;
RT "Partial cDNA sequence of the c-kit homologue of brushtail possum
RT (Trichosurus vulpecula).";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131209; AAF22141.1; -.
DR HSSP; P11362; 1FGK.

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DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00047; Ig_3.
DR Pfam; PF00069; pkinase_1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Euk_pkinase; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW immunoglobulin domain; Receptor; Tyrosine-protein kinase.
FT NON TER 948
SQ SEQUENCE 948 AA; 106323 MW; 708E0258FFC4D07D CRC64;

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Query Match 23.2%; Score 1221; DB 6; Length 948;

Best Local Similarity 33.2%; Pred. No. 4.9e-92;

Matches 319; Conservative 160; Mismatches 363; Indels 118; Gaps 32;

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Qy 67 LRPOSSTVYEAAYVEVDVVSASITLQVLVDAPGNISCL-----WFKHSSLNCQPHFDL 120
Db 24 LQSTSPANYSSPSI---TPARSQLTVNFSGSEIKLSCSDLHFVNWTFENAAHLLE----- 75
Qy 121 QNRGVVSMVLKMTQAGEYLLFIQSEATNYTILFTVSRNTLLYTLRRPYFRKMENQD 180
Db 76 SSRTTETLTTNAQAQDTGRYCTNKGMLSSSIYFVVKPK--ILFLDLRLLYGN-EGSD 132
Qy 181 ALVCSISESVPEIVFW--LCD-----SQGESCKEESPANVVKKEKVLHEL 224
Db 133 ALVNCFTVDPE-VTNFTLRLCDGKPLPKDLTIPIQKGITIKN----VKRSHNKIC--- 184
Qy 225 FGTDIRCCARNELGECTRLFTIDLNOTPQTLTPOL-----FLKVGELWIRCAVHV 277
Db 185 ----FQCSAYQDQGLKLSDRMTLKVRPAQ-SVPEVSLIQTNYLLREGETFOATCMIKDV 239
Qy 278 NHGFGLTWELENKALEEGNYFEMSTYSTNTRMIRILFAFVSSVARNDTGYTSSSK--- 334
Db 240 ASSVVSMMIKDNNRI---STHTQSRHSGDYAYERQDILTISPVRVNDSGVFTCFANNTFG 296
Qy 335 HPSQALVTIVCKGFINA-TNSEDYEIDQYEEFCFSVRKAYPO-----IRCTWTFSR 387
Db 297 PANVTATLKVVEKGFINIPFKMNTTIFINDGENIDLVVEYEAFFKPEHLQWIMNGTVD 356
Qy 388 KGFPCBQKGLDNGYSISKFCNKH-----OPGEYIFHAENDDAQTKMFTLNIRKPK 440
Db 357 KWDDYTKPGSE---STIRYISLHLNRLKGTGGPTTFSVNSDVSSTVTFKYVTKTKE 413
Qy 441 VLAEASASQA--SCFSDGYPLFSWTWKCKSDKSPNCTEITEGVNWKANRKY---FGQW 495
Db 414 ILTSDRLNGLLQCVAAAGFPETIDWYFCPGTEQRCSTSLP--MDVKTNSMLPPFGKI 471
Qy 496 VSSSTLNMSBAIKGLVKCCAYNSLGTSCETILNLSGPPFP--IQNISFYATIGVCLL- 553
Db 472 VVESTIDSSAPRYNGTVECKASNDVG-----KSSAFNFAIKEQITSHTLTFTPLIG 523
Qy 554 FIV-----VLTLLICHKYKQFRYESQLQMV-QVTGSSDNEYFYVDFREYEDLKWEP 606
Db 524 FVVAAGLMCVIILITYKYFQKPMYEVQWKVVEEING---NNVYIDPTQLPYDHWKEFP 580
Qy 607 RENLBFKVLGSGAFQVMNATYGISKTGVSIOAVKMLKEKADSSEREALMSLXOMT 666
Db 581 RNLRFSGKTLGAGAFGVKEATAYGLKSDAAMTAVAKMLKPSAHLTEREALMSLXVLS 640
Qy 667 QLGSHEINVLGACTLSGPIYLIIFYCCYGDLLNLYRSKREKFRHTWTWEIFKEH----N 722
Db 641 YLGNHMNIANLLGACTIGGTTLVITEYCCYGDLLNLRKRDSF-----ICSKHEDHAE 694
Qy 723 FSYFTTFQSHPNSSMPGSR-VQIHDPDQISGLHGNSFHS-----DEIYENQKLEEE 778
Db 695 AALYKNLLQSKSSCDGANEYMDMKFGVSVVVPVTKAEKRGRSARVGYIERDVTVAIMEDD 754

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Qy	779	DLNVLTEEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMS	838
Db	755	EL-ALDIEDLLSPSYQVAKGMSFLASKNCIHRDLAARNILLTHGRITKICDFGLARHIKN	813
Qy	839	DSNYVVEGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNYPYGPVDANF	898
Db	814	DSNYVVKGNARLPVKWMAPEIFNCVYTFESDVWSYGIFLWELFSLGSSPYPGMPVDSKF	873
Qy	899	YKLIQNGFKMDQPEYATEEYIIMQSCWAFDSRKRPGFPNLTSLGCOLADAEAMYNV	958
Db	874	YKMIKEGFRMLSPECAPPMEYINKSCWNEDPLQPTFKLIVOLIEQQQLLSDTNHVYSNI	933

Search completed: May 24, 2003, 16:59:25
Job time : 78.0358 secs

Result No.	Score	Query			DB	ID	Description
		Match	Length	DB			
1	5274	100.0	993	16	AAR67816	Flik2 receptor	
2	5274	100.0	993	16	AAR67536	Human flik-1	
3	5274	100.0	993	17	AAR97419	Murine flik-1	
4	5274	100.0	993	18	AAM19873	Human flik-1	
5	5274	100.0	993	20	AAV08617	Human flik-1	
6	5271	99.9	993	14	AAR37503	Human flik-1	
7	5266	99.8	993	14	AAR44995	Human flik-1	
8	5266	99.8	993	16	AAR75961	Human STR-1	
9	5265	99.8	993	16	AAR81869	Human Flik2	
10	5262	99.8	1167	14	AAR31376	Human flik-1	

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XX 18-JUN-1993; 93US-0080244.
PR 21-JUN-1993; 93US-0081508.
PR 23-NOV-1993; 93US-0157490.
XX
XX (UYPR-) UNIV PRINCETON.
XX
XX Lemischka IR;
XX
XX WPI; 1995-052014/07.
DR N-PSDB; AAQ81013.
XX
XX Ligand for receptor protein tyrosine kinase - useful for the
PT stimulation of primitive haematopoietic stem cells causing
PT proliferation and/or differentiation
XX
XX Disclosure; Fig 1b; 131pp; English.
XX
XX The sequence corresponds to a human Flk2 (fetal liver kinase)
CC receptor protein-tyrosine-kinase, which is expressed in primitive
CC hematopoietic cells but not in mature hematopoietic cells. The
CC protein is useful in isolation of receptor ligands, which have
CC applications in diagnosis of bone marrow disorders, and in
CC stimulating proliferation and/or differentiation of primitive
CC hematopoietic stem cells.
XX
XX Sequence 993 AA;
XX
Query Match 100.0%; Score 5274; DB 16; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPALARDAGTVPLLVVFSGAMIFGTTITNODLPVVKVLINHKNDSSVGKSSSYPMVSESP 60
Db 1 MPALARDAGTVPLLVVFSGAMIFGTTITNODLPVVKVLINHKNDSSVGKSSSYPMVSESP 60
Qy 61 EDLGCALPQSSGTYVEAAAEVDVDSASITLQVLVDAPGNISCLVWFKHSSLNCPHFDL 120
Db 61 EDLGCALPQSSGTYVEAAAEVDVDSASITLQVLVDAPGNISCLVWFKHSSLNCPHFDL 120
Qy 121 QNRGVSMVILKMTQAGEYLLFTQSEATNTYTLFTWSIRNTLLYTLRRPYFRKXENQD 180
Db 121 QNRGVSMVILKMTQAGEYLLFTQSEATNTYTLFTWSIRNTLLYTLRRPYFRKXENQD 180
Qy 181 ALVCISESVPEIWEVLCDGSECKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISESVPEIWEVLCDGSECKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Qy 241 CTRLFTIDLNOTPOTTLPOLFLKVGEPMLWIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
Db 241 CTRLFTIDLNOTPOTTLPOLFLKVGEPMLWIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
Qy 301 STYSTNRTMIRILFAPVSSVARNDGYTCSSSKHPSQSALVTIVGKGFINATNSSEDE 360
Db 301 STYSTNRTMIRILFAPVSSVARNDGYTCSSSKHPSQSALVTIVGKGFINATNSSEDE 360
Qy 361 IDOYEEFCFVRFKAYPQIRCTWTTSRKSFPCEQGLDNGYSISKFCNHKHOPGEYIFHA 420
Db 361 IDOYEEFCFVRFKAYPQIRCTWTTSRKSFPCEQGLDNGYSISKFCNHKHOPGEYIFHA 420
Qy 421 ENDDAQFTKMTLNTIRRKQVLAESAASQSCFSDGYPLPSTWTKCKSDKSPNCTEEITE 480
Db 421 ENDDAQFTKMTLNTIRRKQVLAESAASQSCFSDGYPLPSTWTKCKSDKSPNCTEEITE 480
Qy 481 GVMNRKANRKFQGVSSSTLANSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIOD 540
Db 481 GVMNRKANRKFQGVSSSTLANSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIOD 540
Qy 541 NISFYATIGVCLLFIIVLLTLLCHKYKQFRYESQLOMVQVGTSSDNEYFYVDREYED 600
Db 541 NISFYATIGVCLLFIIVLLTLLCHKYKQFRYESQLOMVQVGTSSDNEYFYVDREYED 600
Qy 601 LKWEFFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIOQAVKMLKEKADSSREALMS 660

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Db 601 LKWEFFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIOQAVKMLKEKADSSREALMS 660
Qy 661 ELKMTOLGSHENIVNLLGACTLSGPIYLIFEYCCYGDLLNLYLRSKREKPHRTWTEIFKE 720
Db 661 ELKMTOLGSHENIVNLLGACTLSGPIYLIFEYCCYGDLLNLYLRSKREKPHRTWTEIFKE 720
Qy 721 HNFSEYPTFQSHPNSSMPGSGREVQIHPDSDQISGLHGNFSHSEDEIEYENOKRLEEBEDL 780
Db 721 HNFSEYPTFQSHPNSSMPGSGREVQIHPDSDQISGLHGNFSHSEDEIEYENOKRLEEBEDL 780
Qy 781 NVLTFEDLLCFAYQVAKGMFLEPKSCVHRDLAARNVLVTHGKVKICDGLADIMSDS 840
Db 781 NVLTFEDLLCFAYQVAKGMFLEPKSCVHRDLAARNVLVTHGKVKICDGLADIMSDS 840
Qy 841 NYVVRGNARLPVKWMAPESLPEGIYTIKSDVWSYGILLWEIFSLGVNPPYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWMAPESLPEGIYTIKSDVWSYGILLWEIFSLGVNPPYPGIPVDANFYK 900
Qy 901 LIQNGFKMDQPFYATEEIIIMQSCWAFDSKRKPSFNLTSFLGCOLADABEAMYQNVGD 960
Db 901 LIQNGFKMDQPFYATEEIIIMQSCWAFDSKRKPSFNLTSFLGCOLADABEAMYQNVGD 960
Qy 961 RVSECPHTYQNRPFPSREMDLGLSPQAQVEDS 993
Db 961 RVSECPHTYQNRPFPSREMDLGLSPQAQVEDS 993

RESULT 2
AAR67536
ID AAR67536 standard; Protein; 993 AA.
XX
XX AC AAR67536;
XX
XX DT 04-JUL-1995 (first entry)
XX
XX DE Human flk-2.
XX
XX KW Fetal liver kinase-2; flk-2; protein tyrosine-kinase receptor;
KW hematopoiesis; stem cell.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT Peptide 1..27
FT Domain 28..543
FT FT /label= Extracellular_receptor_domain
FT FT /label= 544..563
FT FT /label= Transmembrane_region
FT FT /label= 564..993
FT FT /label= Intracellular_catalytic_domain
XX
XX US5367057-A.
XX
XX PN 22-NOV-1994.
XX
XX PD 02-APR-1991; 91US-0679666.
XX
XX PF 02-APR-1991; 91US-0679666.
XX
XX PR 02-APR-1991; 91US-0679666.
XX
XX PR 28-JUN-1991; 91US-0728913.
XX
XX PR 15-NOV-1991; 91US-0793065.
XX
XX PR 24-DEC-1991; 91US-0813593.
XX
XX PR 26-JUN-1992; 92US-0906397.
XX
XX PR 12-NOV-1992; 92US-0975049.
XX
XX PR 19-NOV-1992; 92US-0977451.
XX
XX PR 30-APR-1993; 93US-0055269.
XX
XX (UYPR-) UNIV PRINCETON.
XX
XX PI Lemischka IR;
XX
XX WPI; 1995-005894/01.
DR

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DR N-PSDB; AAQ79069.
XX Murine flk-2 receptor protein tyrosine kinase - used to stimulate
PT proliferation and/or stimulation of primitive mammalian
PT haematopoietic stem cells in vitro or in vivo.
XX
XX Disclosure; Fig. 2A-1F; 69pp; English.
XX cDNAs encoding receptor protein tyrosine-kinases, mouse fetal liver
CC kinase-2 (flk-2), human flk-2 and mouse flk-1 are given in AAQ79068-70,
CC respectively, and the deduced amino acid sequences in AAQ7535-37,
CC respectively.
XX
XX Sequence 993 AA;
SQ

Query Match 100.0%; Score 5274; DB 16; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVPLLVFSGAMIFGTTTNDLPVVKVILNHKNDSSVGKSSYPMVSESP 60
Db 1 MPALARDAGTVPLLVFSGAMIFGTTTNDLPVVKVILNHKNDSSVGKSSYPMVSESP 60
Qy 61 EDLGCALRQSSGTVYEAAREVDVSASTLQVLVDAPGNISCLVFKHSSLNCOPHPDL 120
Db 61 EDLGCALRQSSGTVYEAAREVDVSASTLQVLVDAPGNISCLVFKHSSLNCOPHPDL 120
Qy 121 QNRGVSVVILKMTQAGEYLLFTQSEATNYTILFTVSIIRNTLLYLRPPYFRKMNQD 180
Db 121 QNRGVSVVILKMTQAGEYLLFTQSEATNYTILFTVSIIRNTLLYLRPPYFRKMNQD 180
Qy 181 ALVCISESVPEIPEVWVLCDGSGESKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISESVPEIPEVWVLCDGSGESKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Qy 241 CTRLETDLNTQPTTLQPLFKVCEPLWIRCKAVHNGFGLTWELNKALEEGNYFEM 300
Db 241 CTRLETDLNTQPTTLQPLFKVCEPLWIRCKAVHNGFGLTWELNKALEEGNYFEM 300
Qy 301 STYSNTRTWIRLPAFVSSVARNDGYTTCSSSKHPSQSALVTIVGKGFINATNSSEYD 360
Db 301 STYSNTRTWIRLPAFVSSVARNDGYTTCSSSKHPSQSALVTIVGKGFINATNSSEYD 360
Qy 361 IDQYEEFCFVRKAYPOIRCTWTFSRSPCEQKGLONGYSISKFNHKGQGEYIFHA 420
Db 361 IDQYEEFCFVRKAYPOIRCTWTFSRSPCEQKGLONGYSISKFNHKGQGEYIFHA 420
Qy 421 ENDDAQFTKMTFNIRRPQVLAESASQSCFSDGYPLPSWTWKCDKSPNCTEEITE 480
Db 421 ENDDAQFTKMTFNIRRPQVLAESASQSCFSDGYPLPSWTWKCDKSPNCTEEITE 480
Qy 481 GWNKKAIRKVFQWVSSSTLNSBAIKGLVKCCAYNSLGTSCETILLNSPGPPPIOD 540
Db 481 GWNKKAIRKVFQWVSSSTLNSBAIKGLVKCCAYNSLGTSCETILLNSPGPPPIOD 540
Qy 541 NISFYATIGVCLLFIVLTLCHYKQFRYESQLQWQVQTGSSDNEYFYVDPREYED 600
Db 541 NISFYATIGVCLLFIVLTLCHYKQFRYESQLQWQVQTGSSDNEYFYVDPREYED 600
Qy 601 LKWEFPRENLEFGKVLGSGAFKVNATAYGISTGVSTQAVKMLKEKADSSEREAALS 660
Db 601 LKWEFPRENLEFGKVLGSGAFKVNATAYGISTGVSTQAVKMLKEKADSSEREAALS 660
Qy 661 ELKMMTQLGSHENIVNLLGACTLSGPYLIPEYCCVGDLLNLRKREKPHRTWTPEIKE 720
Db 661 ELKMMTQLGSHENIVNLLGACTLSGPYLIPEYCCVGDLLNLRKREKPHRTWTPEIKE 720
Qy 721 HNFSPYPTFQSHPNSSMPGSRVQIHPSDQISGLHNSFHSDEIEYENQKRLBEEDL 780
Db 721 HNFSPYPTFQSHPNSSMPGSRVQIHPSDQISGLHNSFHSDEIEYENQKRLBEEDL 780
Qy 781 NVLTPEDLICFAYQVAKGMEFLPKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Db 781 NVLTPEDLICFAYQVAKGMEFLPKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840

Db 781 NVLTPEDLICFAYQVAKGMEFLPKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Qy 841 NYVVRGNARLPVKWNPAPESLPBEGIYTIKSDVMSYGILLWEISLGVNYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWNPAPESLPBEGIYTIKSDVMSYGILLWEISLGVNYPGIPVDANFYK 900
Qy 901 LIQNGFKMDQPEYATEEYIIIMOSCAFDSPKRPSPNLTSLGCOLADAEEAMYQNVDS 960
Db 901 LIQNGFKMDQPEYATEEYIIIMOSCAFDSPKRPSPNLTSLGCOLADAEEAMYQNVDS 960
Qy 961 RVSECPHTYQNRPRPSREMDLCLLSLPSQAQVEDS 993
Db 961 RVSECPHTYQNRPRPSREMDLCLLSLPSQAQVEDS 993

RESULT 3
AAR97419
ID AAR97419 standard; Protein; 993 AA.
XX AAR97419;
XX 11-DEC-1996 (first entry)
XX Murine foetal liver kinase 2.
XX Murine; foetal liver kinase 2; flk-2; protein tyrosine kinase;
KW monoclonal; antibody; extracellular domain; receptor assay;
KW haematopoietic stem cell; ligand; stimulation; proliferation;
KW differentiation; treatment; anaemia; bone marrow damage;
KW cancer chemotherapy; radiation.
XX Mus musculus.
XX Key Location/Qualifiers
FT Peptide 1..27
FT Peptide /label= sig_peptide
FT Peptide 28..993
FT Domain /label= mat_peptide
FT Domain 28..544
FT Domain /label= extracellular_domain
FT Domain 545..564
FT Domain /label= transmembrane_domain
FT Domain 565..993
FT Domain /label= intracellular_domain
XX US5548065-A.
XX 20-AUG-1996.
XX 02-APR-1991; 91US-0679666.
XX 19-NOV-1992; 92US-0977451.
XX 02-APR-1991; 91US-0679666.
XX 28-JUN-1991; 91US-0728913.
XX 15-NOV-1991; 91US-0793065.
XX 24-DEC-1991; 91US-0813593.
XX 26-JUN-1992; 92US-0906397.
XX 12-NOV-1992; 92US-0975049.
XX 30-APR-1993; 93US-0055269.
XX 31-OCT-1994; 94US-0252517.
XX (UYPR-) UNIV PRINCETON.
XX Lemischka IR;
XX WPI; 1996-392678/39.
XX N-PSDB; AAT38734.
XX Anti-foetal liver kinase 2 (flk-2) antibodies - useful in assays,
PT for isolating haematopoietic stem cells expressing receptor and for
PT obtaining ligands
XX Claim 1; Columns 39-48; 50pp; English.
PS

XX The present sequence is murine foetal liver kinase 2 (flk-2),
 CC a protein tyrosine kinase. Isolated antibodies, pref. monoclonal,
 CC raised against the extracellular portion of flk-2 can be used to
 CC assay for flk receptors on the surface of primitive haematopoietic
 CC stem cells, and to isolate positive cells. The antibodies can also
 CC be used as, or to obtain ligands, which stimulate the proliferation
 CC and/or differentiation of stem cells. The ligands can be used, e.g.
 CC for treating anaemia, or bone marrow damage resulting from cancer
 CC chemotherapy, or radiation.
 XX Sequence 993 AA;
 SQ

Query Match 100.0%; Score 5274; DB 17; Length 993;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVPLLVVSAMIFGTITNODLPVVKVCLVNHQNDSSVGKSSSYPMVSESP 60
 Db 1 MPALARDAGTVPLLVVSAMIFGTITNODLPVVKVCLVNHQNDSSVGKSSSYPMVSESP 60

Qy 61 EDLGCALRQSSGTYEAAAEVVDVSASITLQVLVDAPGNISCLWVFKHSSLNCOHPFDL 120
 Db 61 EDLGCALRQSSGTYEAAAEVVDVSASITLQVLVDAPGNISCLWVFKHSSLNCOHPFDL 120

Qy 121 QNRGVSVMLKMTETQAGEYLLFIQSEATNYTILFTVSIIRNTLLYLRRPYFRKMNQD 180
 Db 121 QNRGVSVMLKMTETQAGEYLLFIQSEATNYTILFTVSIIRNTLLYLRRPYFRKMNQD 180

Qy 181 ALVCISESPVPIVEWVLCDQSGESCKEESPAVVKKEKVLHELFGTDIRCARNELGRE 240
 Db 181 ALVCISESPVPIVEWVLCDQSGESCKEESPAVVKKEKVLHELFGTDIRCARNELGRE 240

Qy 241 CTRFTIDLNTPTQTLFQKVEPLWIRCKAVVNHGGLTWELNKALEEGNYFEM 300
 Db 241 CTRFTIDLNTPTQTLFQKVEPLWIRCKAVVNHGGLTWELNKALEEGNYFEM 300

Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTCTSSSKHPSQSALVTIVGKGFINATNSSEDE 360
 Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTCTSSSKHPSQSALVTIVGKGFINATNSSEDE 360

Qy 361 IDQVEEFCFVRKAYPOIRCTWTSRSPFCQKGLDNGYSISKFCNHKQPGYIYFHA 420
 Db 361 IDQVEEFCFVRKAYPOIRCTWTSRSPFCQKGLDNGYSISKFCNHKQPGYIYFHA 420

Qy 421 ENDDAQFTKMTLNRKPOVLAEASQSCFSDGYPPLPSWTWKCKSDKSPNCTEEITE 480
 Db 421 ENDDAQFTKMTLNRKPOVLAEASQSCFSDGYPPLPSWTWKCKSDKSPNCTEEITE 480

Qy 481 GWNKRKANRKFVGQWVSSSTLNMSEAIKGLVKKCAVNSLGTSCETILLNSPGPPFIQD 540
 Db 481 GWNKRKANRKFVGQWVSSSTLNMSEAIKGLVKKCAVNSLGTSCETILLNSPGPPFIQD 540

Qy 541 NISFYATIGVCLLFIIVLTLLICHYKQFRYESQLOVQVGTGSSDNEYFYVDREYED 600
 Db 541 NISFYATIGVCLLFIIVLTLLICHYKQFRYESQLOVQVGTGSSDNEYFYVDREYED 600

Qy 601 LKWEPPRENLEFGKVLGSGAFCKVNNATAYGISTKTVSIOAVKMLKEKADSSEREALMS 660
 Db 601 LKWEPPRENLEFGKVLGSGAFCKVNNATAYGISTKTVSIOAVKMLKEKADSSEREALMS 660

Qy 661 ELKMMTQLGSHENIVMLGACTLSGPYILFIYCCYGDLLNLYRSKREKFRHTWTWIFKE 720
 Db 661 ELKMMTQLGSHENIVMLGACTLSGPYILFIYCCYGDLLNLYRSKREKFRHTWTWIFKE 720

Qy 721 HNFSPYPTFQSHNPSMPCGSRVQIHPSDQISGLHGNFSFHEDIEYENQKRLSEEDL 780
 Db 721 HNFSPYPTFQSHNPSMPCGSRVQIHPSDQISGLHGNFSFHEDIEYENQKRLSEEDL 780

Qy 781 NVLTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHCKVKIKICDFGLARDIMSDS 840
 Db 781 NVLTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHCKVKIKICDFGLARDIMSDS 840

Qy 841 NYVVRGNARLPKWMAPESLFEGLYTIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYK 900
 Db 841 NYVVRGNARLPKWMAPESLFEGLYTIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYK 900

Qy 901 LIQNGFKMDQPFYATEEYIIIMQSCWAFDSRKRSPFNLTSLFLGCOLADAEAMYQNVGD 960
 Db 901 LIQNGFKMDQPFYATEEYIIIMQSCWAFDSRKRSPFNLTSLFLGCOLADAEAMYQNVGD 960

Qy 961 RVSECPHTYQNRPRPFSREMDLGLLSPOAQVEDS 993
 Db 961 RVSECPHTYQNRPRPFSREMDLGLLSPOAQVEDS 993

RESULT 4
 AAW19873
 ID AAW19873 standard; Protein; 993 AA.
 XX
 AC AAW19873;
 XX DT 19-AUG-1997 (first entry)
 XX Human flk-2 receptor.
 XX Human; fetal liver kinase 2; flk2; receptor protein tyrosine kinase;
 KW ptk; liver; spleen; thymus; adult; brain; bone marrow; primitive portion;
 KW haematopoietic hierarchy; extracellular domain; soluble form; ligand;
 KW proliferation; differentiation; mammalian; haematopoietic stem cell;
 KW macrocytic anaemia; aplastic anaemia; cancer; radiation; mouse.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..27
 FT Protein /note= "Signal peptide"
 FT Protein 28..993
 FT Protein /note= "Mature flk-2"
 XX USS621090-A.
 XX PN 15-APR-1997.
 XX PD 02-APR-1991; 91US-0679666.
 XX PF 26-JUN-1992; 92US-0906397.
 XX PR 02-APR-1991; 91US-0679666.
 XX PR 28-JUN-1991; 91US-0728913.
 XX PR 15-NOV-1991; 91US-0793065.
 XX PR 24-DEC-1991; 91US-0813593.
 XX (UYPR-) UNIV PRINCETON.
 XX Lemischka IR;
 XX WPI; 1997-235228/21.
 XX DR N-ESDB; AAT72117.
 XX Protein containing the extracellular domain of human flk-2 - used
 PT for identification of primitive haematopoietic cell proliferation
 PT and differentiation stimulatory ligands, e.g. for treating anaemia
 XX Claim 1; Fig 1B; 55pp; English.
 XX This sequence represents human fetal liver kinase 2 (flk2). flk-2 is
 CC a receptor protein tyrosine kinase (ptk) and is important in transducing
 CC putative self-renewal signals from the environment. flk-2 is expressed
 CC in fetal liver, spleen, fetal thymus, adult brain and adult bone marrow,
 CC and it is thought that flk-2 is expressed in the entire primitive portion
 CC of the haematopoietic hierarchy. The invention concerns a recombinant
 CC nucleic acid, preferably mRNA, which encodes a protein containing only
 CC the extracellular domain of human flk-2 and lacking the flk-2 intra-
 CC cellular catalytic domain. The resultant protein represents a soluble
 CC form of flk-2 which is used to isolate specific ligands for flk-2. These
 CC ligands can be used to stimulate proliferation and/or differentiation of

CC mammalian haematopoietic stem cells, in vivo or in vitro, e.g. for
CC treatment of macrocytic or aplastic anaemia or bone marrow damage caused
XX by cancer treatment or radiation.

SQ Sequence 993 AA;

```
Query Match      100.0%; Score 5274; DB 18; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVPLLVVFSAMIFGTITNQLPVKCVLINHKNNDSSVGKSSSPMYVSESP 60
Db 1 MPALARDAGTVPLLVVFSAMIFGTITNQLPVKCVLINHKNNDSSVGKSSSPMYVSESP 60

Qy 61 EDLGCALRQSSGTYVEAAAEVDVSASITLQVLDVDPAGNISCLVDFKHSLLNCQPHFDL 120
Db 61 EDLGCALRQSSGTYVEAAAEVDVSASITLQVLDVDPAGNISCLVDFKHSLLNCQPHFDL 120

Qy 121 QNRGVVSVILKMTQAGEYLLFQSEATNTYTLFTVSRINTLYTLRRPYFRKMNOD 180
Db 121 QNRGVVSVILKMTQAGEYLLFQSEATNTYTLFTVSRINTLYTLRRPYFRKMNOD 180

Qy 181 ALVCISSEVPEPIVWLVCDGSCSKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISSEVPEPIVWLVCDGSCSKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240

Qy 241 CTRLEFDLNOTPOTTLFLKVGLEPLWIRKCAVHVNHGFLTWELNKALEEGNYFEM 300
Db 241 CTRLEFDLNOTPOTTLFLKVGLEPLWIRKCAVHVNHGFLTWELNKALEEGNYFEM 300

Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTCSSSKHPSQSAVTIIVKGFINATNSSEDEYE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTCSSSKHPSQSAVTIIVKGFINATNSSEDEYE 360

Qy 361 IDQYEEFCFVRKAPQIRCTWTSRKSFPCEQKGLDNGYSISKFCNHKHQPGEYIFHA 420
Db 361 IDQYEEFCFVRKAPQIRCTWTSRKSFPCEQKGLDNGYSISKFCNHKHQPGEYIFHA 420

Qy 421 ENDDAQFTKMTLNTRRKPOVLAESAQSCFSGYPLPSWTWKCKDKNPCNTEITE 480
Db 421 ENDDAQFTKMTLNTRRKPOVLAESAQSCFSGYPLPSWTWKCKDKNPCNTEITE 480

Qy 481 GWNKRNKRVFGQWSSSTLNMSEAIKGLVKCCAYNSLGTSCETILLNSPGPRPFID 540
Db 481 GWNKRNKRVFGQWSSSTLNMSEAIKGLVKCCAYNSLGTSCETILLNSPGPRPFID 540

Qy 541 NISFYATIGVCLLFIWLTLLIHKYKQFRYESQLQWQVGTSSDNEYFYVDREYED 600
Db 541 NISFYATIGVCLLFIWLTLLIHKYKQFRYESQLQWQVGTSSDNEYFYVDREYED 600

Qy 601 LKWEFPRENLEFGKLGSAFGKVNATAYGSKTGVSTQVAVKMLKEKADSSREALMS 660
Db 601 LKWEFPRENLEFGKLGSAFGKVNATAYGSKTGVSTQVAVKMLKEKADSSREALMS 660

Qy 661 ELKMTQLGSHENIIVNLGACTLSGPVILIPEYCCVGDLLNLRKREKPHRTWTEIFKE 720
Db 661 ELKMTQLGSHENIIVNLGACTLSGPVILIPEYCCVGDLLNLRKREKPHRTWTEIFKE 720

Qy 721 HNFSPYPTFQSHPNSSMPGSRVQIHPSDQISGLHGNFSHSEDEIEYENQKLEEEEDL 780
Db 721 HNFSPYPTFQSHPNSSMPGSRVQIHPSDQISGLHGNFSHSEDEIEYENQKLEEEEDL 780

Qy 781 NVLTPEDLCCFAYQAKWMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Db 781 NVLTPEDLCCFAYQAKWMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840

Qy 841 NVVVRGNARLPVKWMAPSLEGIYITIKSDVMSYGILLWEIFSLGNVPYPGIPVDANFYK 900
Db 841 NVVVRGNARLPVKWMAPSLEGIYITIKSDVMSYGILLWEIFSLGNVPYPGIPVDANFYK 900

Qy 901 LTQNGFKMDQPPYATEEYIIMQSCWAFDSRKRFPNLTSLFGCOLADAEAMQNVNDG 960
Db 901 LTQNGFKMDQPPYATEEYIIMQSCWAFDSRKRFPNLTSLFGCOLADAEAMQNVNDG 960
```

Qy 961 RVSECHPTTYQNRPPFSREMDLGLLSPOAQVEDS 993
Db 961 RVSECHPTTYQNRPPFSREMDLGLLSPOAQVEDS 993

RESULT 5

AAV08617
ID AAY08617 standard; Protein; 993 AA.

XX AAY08617;

XX 05-AUG-1999 (first entry)

XX Human flk-2 protein.

XX Human; flk-2; flk-1; cell isolation; fetal liver kinase; receptor;
KW monoclonal; polyclonal; antibody; tyrosine kinase.

XX Homo sapiens.

XX US5912133-A.

XX 15-JUN-1999.

XX 10-FEB-1998; 98US-0021324.

XX 19-NOV-1992; 92US-0977451.

XX 02-APR-1991; 91US-0679666.

XX 28-JUN-1991; 91US-0728913.

XX 15-NOV-1991; 91US-0793065.

XX 24-DEC-1991; 91US-0813593.

XX 26-JUN-1992; 92US-0906397.

XX 12-NOV-1992; 92US-0975049.

XX 30-APR-1993; 93US-0055269.

XX 31-OCT-1994; 94US-0252498.

XX 15-FEB-1996; 96US-0601891.

XX (UYPR-) UNIV PRINCETON.

XX Lemischka IR;

XX WPI: 1999-357194/30.

XX N-PSDB; AAX77515.

XX Isolating hematopoietic cells expressing fetal liver kinase 1

XX receptors

XX Disclosure; Fig 1b; 59pp; English.

XX This invention describes a novel method of isolating cells expressing

XX fetal liver kinase 1 (flk-1) receptors on their surface and comprises

XX binding the cells to a polyclonal or monoclonal antibody specific to

XX the FLK-1 receptor and isolating the cells that have bound to the

XX antibody. The method can be used to isolate hematopoietic stem cells in

XX any mammal but preferably a rat, mouse, rabbit or human. The proteins of

XX the invention belong to the receptor protein family. This sequence

XX represents the human flk-2 protein which is used in the method of the

XX invention.

SQ Sequence 993 AA;

Query Match 100.0%; Score 5274; DB 20; Length 993;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVPLLVVFSAMIFGTITNQLPVKCVLINHKNNDSSVGKSSSPMYVSESP 60

Db 1 MPALARDAGTVPLLVVFSAMIFGTITNQLPVKCVLINHKNNDSSVGKSSSPMYVSESP 60

Qy 61 EDLGCALRQSSGTYVEAAAEVDVSASITLQVLDVDPAGNISCLVDFKHSLLNCQPHFDL 120

Db 61 EDLGCALRQSSGTYVEAAAEVDVSASITLQVLDVDPAGNISCLVDFKHSLLNCQPHFDL 120

QY 121 QNRGVSNVILKMTETQAGEYLLFIQSEATNYTLFTVSIINTLLYTLRRYPFRMENQD 180
DB 121 QNRGVSNVILKMTETQAGEYLLFIQSEATNYTLFTVSIINTLLYTLRRYPFRMENQD 180
QY 181 ALVVCISSEVPEPIVWVLCDSQGSCKEESPAVVKKEKVLHELFGTDIRCARNELGRE 240
DB 181 ALVVCISSEVPEPIVWVLCDSQGSCKEESPAVVKKEKVLHELFGTDIRCARNELGRE 240
QY 241 CTRLFTIDLNTPTOTLPLQFLKGEPLWIRCKAVHNVHGFGLTWELNKALEBGNFYEM 300
DB 241 CTRLFTIDLNTPTOTLPLQFLKGEPLWIRCKAVHNVHGFGLTWELNKALEBGNFYEM 300
QY 301 STYSTNRTMIRILPAFVSSVARNDTGYTSCSSKHPQSALVTIVGKGFINATNSSDEYE 360
DB 301 STYSTNRTMIRILPAFVSSVARNDTGYTSCSSKHPQSALVTIVGKGFINATNSSDEYE 360
QY 361 IDQYEEFCFSVRFKAYPOIRCTWTFRSKSPCEQKGLDNGYSISKFCNHKHPQGEYIFHA 420
DB 361 IDQYEEFCFSVRFKAYPOIRCTWTFRSKSPCEQKGLDNGYSISKFCNHKHPQGEYIFHA 420
QY 421 ENDDAQFTKMTLIRRPQVLASASQASCFSDGYPLPWTWKKCSKSPNCTEETE 480
DB 421 ENDDAQFTKMTLIRRPQVLASASQASCFSDGYPLPWTWKKCSKSPNCTEETE 480
QY 481 GWNKRNKRVFGQVSSSTLMNSEAIKGFVLVCKCAYNSLGTSCETILLNSPGPPFIQD 540
DB 481 GWNKRNKRVFGQVSSSTLMNSEAIKGFVLVCKCAYNSLGTSCETILLNSPGPPFIQD 540
QY 541 NISFYATIGVCLLFTVLTLLIHKYKQFYESQLQVQVGTSSSDNEYFYVDREYEYD 600
DB 541 NISFYATIGVCLLFTVLTLLIHKYKQFYESQLQVQVGTSSSDNEYFYVDREYEYD 600
QY 601 LKWEFFRENLEFGLVGSAGFKVNNATAYGISTKGVSIQVAVKMLKEKADSSEREALMS 660
DB 601 LKWEFFRENLEFGLVGSAGFKVNNATAYGISTKGVSIQVAVKMLKEKADSSEREALMS 660
QY 661 ELKMTQLGSHENIVNLLGACTLSGPIYLIPEYCCYDGLLNLRLSKREKFRHTWTEIFKE 720
DB 661 ELKMTQLGSHENIVNLLGACTLSGPIYLIPEYCCYDGLLNLRLSKREKFRHTWTEIFKE 720
QY 721 HNFSPYPTFQSHPNSSMGREVOIHPDSQISGLHNSFHSDEIEYENQKLEBEDL 780
DB 721 HNFSPYPTFQSHPNSSMGREVOIHPDSQISGLHNSFHSDEIEYENQKLEBEDL 780
QY 781 NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
DB 781 NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
QY 841 NYVVRGNARLPVKWMAPELSLFEIYTIKSDVMSYGILLWEIFSLGWNYPGIPVDANFYK 900
DB 841 NYVVRGNARLPVKWMAPELSLFEIYTIKSDVMSYGILLWEIFSLGWNYPGIPVDANFYK 900
QY 901 LIQNGFKMDQPFYATEEYIIMQSCWAFDSRKRPFNLTSLFGQLADAEAMQNVNDG 960
DB 901 LIQNGFKMDQPFYATEEYIIMQSCWAFDSRKRPFNLTSLFGQLADAEAMQNVNDG 960
QY 961 RVSECPHTYQNRPPFSEMDLGLLSPQAQVEDS 993
DB 961 RVSECPHTYQNRPPFSEMDLGLLSPQAQVEDS 993
RESULT 6
ID AAR37503 standard; Protein; 993 AA.
XX AAR37503;
AC AAR37503;
XX 19-OCT-1993 (first entry)
DT Human flk-2.
XX Murine; receptor; protein; tyrosine kinase; ptk; flk-2; primitive;
KW

KW henatopoietic cell; mature; family; conserved; region;
KW catalytic domain; c-kit; fetal liver kinase; fik; fetal; spleen;
KW thymus; adult; brain; bone marrow; multipotential; CFU-Blast colony;
KW hierarchy; transduction; T-lymphoid; lineage.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1...27
FT /note= "Hydrophobic leader sequence"
FT Protein 28..993
FT /note= "Mature murine flk-2"
FT Domain 28..543
FT /note= "Extracellular receptor domain"
FT Region 544..563
FT /note= "Transmembrane region"
FT Domain 564..983
FT /note= "Intracellular catalytic domain"
XX W09310136-A.
XX 27-MAY-1993.
XX 16-NOV-1992; 92WO-US09893.
XX 15-NOV-1991; 91US-0793065.
XX (UYPR-) UNIV PRINCETON.
XX Lemischka IR;
XX WPI; 1993-182479/22.
XX N-PSDB; RAAQ40915.
XX Totipotent haematopoietic stem cell receptors, their ligands and
XX DNA sequences - for treating anaemia(s) and bone marrow damage
XX due to e.g. cancer chemotherapy or radiotherapy
XX Claim 39; Fig 1b; 127pp; English.
XX This sequence represents the human receptor protein tyrosine kinase
XX (pTK), flk-2. The nucleic acid encoding this receptor is expressed
XX in primitive hematopoietic cells and not in mature hematopoietic
XX cells. Members of this family of pTK's can be recognised by the
XX conserved amino acid regions in the catalytic domain. This family
XX of pTK's also contains c-kit. These new receptors are termed fetal
XX liver kinases (flk's) after the tissue in which they were discovered.
XX flk-2 is also expressed in fetal spleen, fetal thymus, adult brain
XX and adult bone marrow. flk-2 is expressed in individual multipotential
XX CFU-Blast colonies capable of generating numerous multilineage colonies
XX upon replating. It is likely therefore, that flk-2 is expressed in
XX the entire primitive portion of the hematopoietic hierarchy. This is
XX consistent with flk-2 being important in transducing putative self-
XX renewal signals from the environment. flk-2 is the first receptor
XX pTK known to be expressed in the T-lymphoid lineage.

Query Match 99.9%; Score 5271; DB 14; Length 993;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 992; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVVKVILNHKNDSVSGKSSYPMVSESP 60
DB 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVVKVILNHKNDSVSGKSSYPMVSESP 60
QY 61 EDLGCALRPQSSGTVYVAAAEEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQHPFDL 120
DB 61 EDLGCALRPQSSGTVYVAAAEEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQHPFDL 120
QY 121 QNRGVSNVILKMTETQAGEYLLFIQSEATNYTLFTVSIINTLLYTLRRYPFRMENQD 180
DB 121 QNRGVSNVILKMTETQAGEYLLFIQSEATNYTLFTVSIINTLLYTLRRYPFRMENQD 180

Qy 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHFGTDIRCCARNELGRE 240
 Db 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHFGTDIRCCARNELGRE 240
 Qy 241 CTRLTIDLNQTPOTTLPOLFLKVGEPWIIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
 Db 241 CTRLTIDLNQTPOTTLPOLFLKVGEPWIIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
 Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTSCSSKHPSQSALVTIVGKGFINATNSSEDE 360
 Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTSCSSKHPSQSALVTIVGKGFINATNSSEDE 360
 Qy 361 IDQYEEFCFSVRKAYPOIRCTWTFSRKSPCEQKGLDNGYSISKFCNHKQPGPFIYIHA 420
 Db 361 IDQYEEFCFSVRKAYPOIRCTWTFSRKSPCEQKGLDNGYSISKFCNHKQPGPFIYIHA 420
 Qy 421 ENDDAQFTKMTLIRRKPOVLAAASQASCFSDGYPLPSMTWKCKSDKSPNCTEEITE 480
 Db 421 ENDDAQFTKMTLIRRKPOVLAAASQASCFSDGYPLPSMTWKCKSDKSPNCTEEITE 480
 Qy 481 GWNRKANRKFVGVWSSSTLNMSEAIGFLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
 Db 481 GWNRKANRKFVGVWSSSTLNMSEAIGFLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
 Qy 541 NISFYATIGVCLLFIVLTLIICHKYKQFYESQLOVQVGTGSSDNEYFYVDFREYED 600
 Db 541 NISFYATIGVCLLFIVLTLIICHKYKQFYESQLOVQVGTGSSDNEYFYVDFREYED 600
 Qy 601 LKWEFPRENLEFGKVLGSGAGFKVMNATAYGISKTGVSIOAVKMLKEKADSSEREALMS 660
 Db 601 LKWEFPRENLEFGKVLGSGAGFKVMNATAYGISKTGVSIOAVKMLKEKADSSEREALMS 660
 Qy 661 ELKMTQLGSHENIVNLGACTLSGPYLIIEYCCYGDLLNVLRSKRKFHRTWTEIFKE 720
 Db 661 ELKMTQLGSHENIVNLGACTLSGPYLIIEYCCYGDLLNVLRSKRKFHRTWTEIFKE 720
 Qy 721 HNFSPYPTFQSHPNSSMPGSRVQIHPDSQISGLHGNSPHSEDEIYENQKRLSEEDL 780
 Db 721 HNFSPYPTFQSHPNSSMPGSRVQIHPDSQISGLHGNSPHSEDEIYENQKRLSEEDL 780
 Qy 781 NVLTFEDLLCFAYQVAKGMEFLKSCVHRDLAARNVLVTHGVKVKICDFGLARDIMSDS 840
 Db 781 NVLTFEDLLCFAYQVAKGMEFLKSCVHRDLAARNVLVTHGVKVKICDFGLARDIMSDS 840
 Qy 841 NYVVRGNARLPVKWAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYK 900
 Db 841 NYVVRGNARLPVKWAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYK 900
 Qy 901 LIQNGFKMDQPFYATEEIIYIMQSCWAFDSRKRPSFPNLTSLGCOLADAEAMYQNVDG 960
 Db 901 LIQNGFKMDQPFYATEEIIYIMQSCWAFDSRKRPSFPNLTSLGCOLADAEAMYQNVDG 960
 Qy 961 RVSECPHTYQNRPFPSREMDLGLLSPQAEVDS 993
 Db 961 RVSECPHTYQNRPFPSREMDLGLLSPQAEVDS 993

RESULT 7
 AAR44995
 ID AAR44995 standard; Protein; 993 AA.
 XX
 AC AAR44995;
 XX
 XX 27-JUN-1994 (first entry)
 XX
 DE Human flk-2 receptor protein tyrosine kinase.
 XX
 KW Receptor protein tyrosine kinase; ptk family; foetal liver kinase;
 KW flk1; primitive; totipotent; haematopoietic cell; stem cell;
 KW proliferation; stromal cell.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH 1..27
 FT /label= signal sequence
 FT /note= "hydrophobic leader"
 FT Protein 28..993
 FT /label= flk-2
 FT /note= "mature protein"
 FT 28..544
 FT /label= extracellular_domain
 FT Region 545..563
 FT /label= transmembrane_region
 FT Domain 564..993
 FT /label= intracellular_catalytic_domain
 XX
 PN US5270458-A.
 XX
 PD 14-DEC-1993.
 XX
 PF 02-APR-1991; 91US-0679666.
 XX
 PR 02-APR-1991; 91US-0679666.
 PR 28-JUN-1991; 91US-0728913.
 PR 15-NOV-1991; 91US-0793065.
 PR 24-DEC-1991; 91US-0813593.
 PR 26-JUN-1992; 92US-0906397.
 PR 12-NOV-1992; 92US-0975049.
 PR 19-NOV-1992; 92US-0977451.
 XX
 PA (UYPR-) UNIV PRINCETON.
 XX
 PI Lemischka IR;
 XX
 DR WPI; 1993-405021/50.
 DR N-PSDB; AAQ53503.
 XX
 PT Isolated nucleic acid molecules of hematopoietic stem cell
 PT receptor flk-2 - encoding mammalian receptor protein tyrosine
 PT kinases expressed in primitive haematopoietic cells
 PS Disclosure; Fig 1b; 60pp; English.
 XX
 CC Nucleic acid sequences coding for murine flk-2 and specified
 CC subfragments of it are claimed. The human flk-2 coding sequence
 CC (i.e. AAQ53503) is also disclosed. The murine and human flk-2
 CC polypeptides represent a new class of receptor protein tyrosine
 CC kinases which are expressed only in primitive haematopoietic cells.
 XX
 SQ Sequence 993 AA;
 Query Match 99.8%; Score 5266; DB 14; Length 993;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 992; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MPALARDAGTVPLLVVFSAMIFGTTITNODLPVIKCVLINHKNDSSVGKSSYPMVSESP 60
 Db 1 MPALARDAGTVPLLVVFSAMIFGTTITNODLPVIKCVLINHKNDSSVGKSSYPMVSESP 60
 Qy 61 EDLGCALRQSSGTVYEAAREVDVVSASITLQVLVDAPGNISCLWVFKHSSLNCQHPFDL 120
 Db 61 EDLGCALRQSSGTVYEAAREVDVVSASITLQVLVDAPGNISCLWVFKHSSLNCQHPFDL 120
 Qy 121 QNRGVSVVILKMTQAGEVLLFIQSEATNYTLFTVTSIRNTLLVTLRRPYFRKMENOD 180
 Db 121 QNRGVSVVILKMTQAGEVLLFIQSEATNYTLFTVTSIRNTLLVTLRRPYFRKMENOD 180
 Qy 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHFGTDIRCCARNELGRE 240
 Db 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHFGTDIRCCARNELGRE 240
 Qy 241 CTRLTIDLNQTPOTTLPOLFLKVGEPWIIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
 Db 241 CTRLTIDLNQTPOTTLPOLFLKVGEPWIIRCKAVVNHGFGLTWELENKALEEGNYFEM 300

Qy	301	STYSTNRTMIRILILPAFVSSVARNDGTYYTCSSSHKPSQSLVTVIGKGFINATNSSDEYE	360
Db	301	STYSTNRTMIRILILPAFVSSVARNDGTYYTCSSSHKPSQSLVTVIGKGFINATNSSDEYE	360
Qy	361	IDQYEEFCFSVRKAYPOIRCTWTFSRKSPCEOKGLDNGYSISKFCNKHQPGGEYIFHA	420
Db	361	IDQYEEFCFSVRKAYPOIRCTWTFSRKSPCEOKGLDNGYSISKFCNKHQPGGEYIFHA	420
Qy	421	ENDDAQTKMFTLNIRRKPOVLAEASASQSCFSDGYPLPSWTWKCKSDKSPNCTEITE	480
Db	421	ENDDAQTKMFTLNIRRKPOVLAEASASQSCFSDGYPLPSWTWKCKSDKSPNCTEITE	480
Qy	481	GVNWRKANRVFGQWSSSTLNMSSEALIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD	540
Db	481	GVNWRKANRVFGQWSSSTLNMSSEALIKGLVKCCAYNSLGTSCETILLNSAGPPFIQD	540
Qy	541	NISFYATIGVCLLFIIVLTLILCHYKKQRYESQLOQVQVGTSSDNEYFYVDPREYED	600
Db	541	NISFYATIGVCLLFIIVLTLILCHYKKQRYESQLOQVQVGTSSDNEYFYVDPREYED	600
Qy	601	LKWEFFPRENLEFGVLGSGAFKVMNATAYGISKTGYSIQVAVKMLKEKADSSREALMS	660
Db	601	LKWEFFPRENLEFGVLGSGAFKVMNATAYGISKTGYSIQVAVKMLKEKADSSREALMS	660
Qy	661	ELKWMVQLGSHENIVNLGACTLSGPIYLIFPEYCCYGDLLNLYLRSKREKPHRTWTEIFKE	720
Db	661	ELKWMVQLGSHENIVNLGACTLSGPIYLIFPEYCCYGDLLNLYLRSKREKPHRTWTEIFKE	720
Qy	721	HNFSFYFTQSHPNSSMPGSRVQIHDPDSQISGLHGNSFSEDEIIEYENOKRLEBEDL	780
Db	721	HNFSFYFTQSHPNSSMPGSRVQIHDPDSQISGLHGNSFSEDEIIEYENOKRLEBEDL	780
Qy	781	NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVVICDFGLARDINSDS	840
Db	781	NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKVVICDFGLARDINSDS	840
Qy	841	NYVVRGNARLPVKWMAPESLFEGYITTKSDVMSYIGILLWEIFSLGVNYPGIPVDANFYK	900
Db	841	NYVVRGNARLPVKWMAPESLFEGYITTKSDVMSYIGILLWEIFSLGVNYPGIPVDANFYK	900
Qy	901	LIQNGFMDQPFYATEEIIYIIIMQSCWAFDSRKRSFNLTSFLGCOLADAEAMYQNVVDG	960
Db	901	LIQNGFMDQPFYATEEIIYIIIMQSCWAFDSRKRSFNLTSFLGCOLADAEAMYQNVVDG	960
Qy	961	RVSECPHTYQNRPFPSREMDLGLLSPQAQVEDS	993
Db	961	RVSECPHTYQNRPFPSREMDLGLLSPQAQVEDS	993

RESULT 8
AAR75961 ID AAR75961 standard; Protein: 993 AA.
XX AC AAR75961;
XX AC AAR75961;
XX AC AAR75961;
DT 29-DEC-1995 (first entry)
XX DE Human STK-1.
XX KW STK-1; receptor PTK; protein tyrosine kinase.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT Peptide 1..23
FT FT /label= signal
FT FT /note= "unique PTK receptor sequence"
FT FT Cleavage-site 25..26
FT FT Domain 35..524
FT FT /note= "part of extracellular domain contg.
FT FT 22 Cys residues marked on Fig. 1".
FT Modified-site 43..45

FT	Modified-site	/label= potential N-linked glycosylation site
FT	100..102	
FT	Modified-site	/label= see above
FT	151..153	
FT	Modified-site	/label= see above
FT	250..252	
FT	Modified-site	/label= see above
FT	306..308	
FT	Modified-site	/label= see above
FT	323..325	
FT	Modified-site	/label= see above
FT	351..353	
FT	Modified-site	/label= see above
FT	354..356	
FT	Modified-site	/label= see above
FT	473..475	
FT	Modified-site	/label= see above
FT	502..504	
FT	Modified-site	/label= see above
FT	542..562	
FT	Region	/label= transmembrane spanning region
FT	708..782	
FT	Region	/label= kinase insert region
FT	617..622	
FT	Domain	/label= ATP binding domain
FT	835..840	
FT	Domain	/label= WMAPES motifs
FT	808..813	/note= "cytoplasmic domain"
FT	Peptide	/note= "used to design PCR oligos"
FT	870..875	
FT	Peptide	/note= "used to design PCR oligos"
FT	XX	
PN	WO9519175-A.	
XX	20-JUL-1995.	
XX	06-JAN-1995;	95WO-US00176.
XX	14-JAN-1994;	94US-0183211.
XX	(UYJO) UNIV JOHNS HOPKINS.	
PA	(UYPE-) UNIV PENNSYLVANIA.	
XX	Civin CI, Gewirtz AM, Small D;	
XX	WPI; 1995-263709/34.	
DR	N-PSDB; AAQ91356.	
XX	Artificial STK-1 gene and gene-specific anti-sense oligo:nucleotide -	
PT	used to treat neoplastic diseases and as bone marrow purging agents for	
PT	treating leukaemia and neoplasma	
XX	Disclosure; Fig 1; -66pp; English.	
XX	The STK-1 gene encodes a receptor PTK which is expressed in	
CC	proliferating hematopoietic stem cells but not in quiescent stem	
CC	cells. The STK-1 gene is also expressed in certain malignant cells	
CC	of non-hematopoietic origin. An antisense oligo specific for STK-1	
CC	is an oligo having a sequence (i) capable of forming a stable	
CC	triplex with a portion of the STK-1 gene, or (ii) capable of forming	
CC	a stable duplex with a portion of an mRNA transcript of the STK-1	
CC	gene. Antisense oligos capable of forming a stable duplex with a	
CC	portion of a STK-1 mRNA transcript are given in AAQ91536 FT and in	
CC	AAQ91537 and AAQ91538. The antisense oligos of the invention are useful	
CC	in the treatment of hematologic malignancies characterised by	
CC	STK-1 expression. Several of the conserved domains of PTKs	
CC	including the ATP binding domain and the WMAPES motifs are	
CC	found in the STK-1 protein (see AAR75961 FT).	
XX	Sequence	993 AA;
SQ	Query Match	99.8%; Score 5266; DB 16; Length 993;

		Best Local Similarity 99.9%; Pred. No. 0;		Matches 992; Conservative 0; Mismatches 1; Indels 0; Gaps 0;						
Qy	1	MPALARDAGTVP	LLVVFSA	MI	FGTITNQDLPV	KVCLV	LNHNKNDSSV	GKSSYP	PMVSESP	60
Db	1	MPALARDAGTVP	LLVVFSA	MI	FGTITNQDLPV	KVCLV	LNHNKNDSSV	GKSSYP	PMVSESP	60
Qy	61	EDLGCALR	POSSGTYE	AAAEV	DVSASIT	LQVLVD	APGNISCL	WVFKH	SLNCQPHFDL	120
Db	61	EDLGCALR	POSSGTYE	AAAEV	DVSASIT	LQVLVD	APGNISCL	WVFKH	SLNCQPHFDL	120
Qy	121	QNRGVSW	VLKMTET	QAGEV	LLFIQ	SEATNT	YTLFTV	SIRNT	LYTLRRPYFR	180
Db	121	QNRGVSW	VLKMTET	QAGEV	LLFIQ	SEATNT	YTLFTV	SIRNT	LYTLRRPYFR	180
Qy	181	ALVCISES	VPPIV	EWVLCD	SQGES	CKEES	PAVVK	KEE	KVLHELFGTD	240
Db	181	ALVCISES	VPPIV	EWVLCD	SQGES	CKEES	PAVVK	KEE	KVLHELFGTD	240
Qy	241	CTRFLTID	NQTP	QTTLP	QFLK	VGEP	LWIRCK	AVHVN	HGFLTW	300
Db	241	CTRFLTID	NQTP	QTTLP	QFLK	VGEP	LWIRCK	AVHVN	HGFLTW	300
Qy	301	STYSTN	RTMIR	ILF	AFVSS	VARND	GYT	TCSS	KHPQS	360
Db	301	STYSTN	RTMIR	ILF	AFVSS	VARND	GYT	TCSS	KHPQS	360
Qy	361	IDQVEE	FCFS	VR	KAYP	QIR	CTW	TSR	KSP	420
Db	361	IDQVEE	FCFS	VR	KAYP	QIR	CTW	TSR	KSP	420
Qy	421	ENDDAQ	TQM	PTL	NI	RK	PQV	LA	ASASQ	480
Db	421	ENDDAQ	TQM	PTL	NI	RK	PQV	LA	ASASQ	480
Qy	481	GVNRKANR	KVFG	OW	SS	TL	NM	SE	AIK	540
Db	481	GVNRKANR	KVFG	OW	SS	TL	NM	SE	AIK	540
Qy	541	NISFYAT	IGV	CLL	FI	VL	TL	LI	CH	600
Db	541	NISFYAT	IGV	CLL	FI	VL	TL	LI	CH	600
Qy	601	LKWEF	PRE	N	LE	F	G	V	L	660
Db	601	LKWEF	PRE	N	LE	F	G	V	L	660
Qy	661	ELKMT	Q	L	G	S	H	E	N	720
Db	661	ELKMT	Q	L	G	S	H	E	N	720
Qy	721	HNFS	F	Y	P	T	F	Q	S	780
Db	721	HNFS	F	Y	P	T	F	Q	S	780
Qy	781	NVL	T	F	E	D	L	C	F	840
Db	781	NVL	T	F	E	D	L	C	F	840
Qy	841	NYVR	G	N	A	R	L	P	K	900
Db	841	NYVR	G	N	A	R	L	P	K	900
Qy	901	LIQNG	F	K	M	D	Q	P	F	960
Db	901	LIQNG	F	K	M	D	Q	P	F	960
Qy	961	RVSE	C	P	T	Y	Q	N	R	993
Db	961	RVSE	C	P	T	Y	Q	N	R	993

RESULT 9

AAR81869		AAR81869 standard; Protein; 993 AA.	
XX	AC	AAR81869;	
XX	DT	19-MAR-1996 (first entry)	
XX	DE	Human Flk2/flt3 tyrosine kinase receptor.	
XX	KW	Tyrosine kinase receptor; flk2; flt3; agonist; monoclonal antibody; haematopoiesis; hypoplasemia; anaemia; thrombocytopenia; stem cell.	
XX	OS	Homo sapiens.	
XX	PN	WO9527062-A1.	
XX	PD	12-OCT-1995.	
XX	PF	23-MAR-1995; 95WO-US03718.	
XX	PR	04-APR-1994; 94US-0222299.	
XX	PA	(GETH) GENENTECH INC.	
XX	PI	Bennett BD, Broz SD, Matthews W, Zeigler FC;	
XX	DR	WPI; 1995-358636/46.	
XX	DR	N-PSDB; AAT00802.	
XX	PT	Agonist antibody which binds to flk2-flt3 tyrosine kinase receptor - enhances proliferation of haematopoietic stem cells, in the treatment of hypoplasia, anaemia, etc.	
XX	PS	Disclosure; Page 44-47; 59pp; English.	
XX	CC	DNA (AAT00801) coding for murine stem cell tyrosine kinase receptor flk2 (also called flt3) (AAR81868) was obtd. by RT-PCR amplification of RNA isolated from mid-gestation mouse foetal livers using primers based on the murine flt3 sequence, and subcloning of the product into pRK5.1. An flk2/flt3 extracellular domain-IgG1 Fc fusion protein was constructed and used to raise agonist antibodies able to bind to, and activate, flk2/flt3. The human flk2/flt3 receptor gene (AAT00802) and amino acid sequence (AAR81869) are also given.	
Qy	Sequence 993-AA;		
Qy	Query Match	99.8%;	Score 5265; DB 16; Length 993;
Qy	Best Local Similarity	99.9%;	Pred. No. 0;
Qy	Matches 99;	Conservative 0; Mismatches 1;	Indels 0; Gaps 0;
Qy	1	MPALARDAGTVP	LLVVFSA
Qy	1	MPALARDAGTVP	LLVVFSA
Qy	61	EDLGCALR	POSSGTYE
Qy	61	EDLGCALR	POSSGTYE
Qy	121	QNRGVSW	VLKMTET
Qy	121	QNRGVSW	VLKMTET
Qy	181	ALVCISES	VPPIV
Qy	181	ALVCISES	VPPIV
Qy	241	CTRFLTID	LNQTP
Qy	241	CTRFLTID	LNQTP
Qy	301	STYSTN	RTMIR
Qy	301	STYSTN	RTMIR

Query Match 99.8%; Score 5265; DB 16; Length 993;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 361 IDQEEFCFSVRKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQPGGEYIFHA 420
 Db 361 IDQEEFCFSVRKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQPGGEYIFHA 420
 Qy 421 ENDDAQFTKMTNIRKPKQVLASASQSCFSDGYPPLSWTWKCKSDKSPNCTEITE 480
 Db 421 ENDDAQFTKMTNIRKPKQVLASASQSCFSDGYPPLSWTWKCKSDKSPNCTEITE 480
 Qy 481 GVMNRKANRVFGQWSSSTLMSSEALIGFLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
 Db 481 GVMNRKANRVFGQWSSSTLMSSEALIGFLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
 Qy 541 NISFYATIGVCLLFIIVLTLIICHYKQFYESQLOQVQVGTSSDNEYFYVDREYEYD 600
 Db 541 NISFYATIGVCLLFIIVLTLIICHYKQFYESQLOQVQVGTSSDNEYFYVDREYEYD 600
 Qy 601 LKWEFFRENLEFGKVGSGAFKVMNATAYGISKTGVSIOVAVKMLKEKADSSREALMS 660
 Db 601 LKWEFFRENLEFGKVGSGAFKVMNATAYGISKTGVSIOVAVKMLKEKADSSREALMS 660
 Qy 661 ELKMTQLGSHENIVNLGACTLSGPYILIPEYCCYGDLLNLYLSKREKPHRTWTEIFKE 720
 Db 661 ELKMTQLGSHENIVNLGACTLSGPYILIPEYCCYGDLLNLYLSKREKPHRTWTEIFKE 720
 Qy 721 HNFSPYPTFQSHPNSSMPGSRVQIHPDSQIISGLHNSFHSDEIEYENOKRLEEEEDL 780
 Db 721 HNFSPYPTFQSHPNSSMPGSRVQIHPDSQIISGLHNSFHSDEIEYENOKRLEEEEDL 780
 Qy 781 NVLTFEDLLCFAYQAKGMELEFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDS 840
 Db 781 NVLTFEDLLCFAYQAKGMELEFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDS 840
 Qy 841 NYVVRGNARLPVKWAPPSLEGIYTIKSDVWSYGILLWEIFSLGVNYPYGPVDANFYK 900
 Db 841 NYVVRGNARLPVKWAPPSLEGIYTIKSDVWSYGILLWEIFSLGVNYPYGPVDANFYK 900
 Qy 901 LIQNGFKMDQPFYATEEYIIIMQSCWAFDSRKRPSFNLTSFLGCOLADAEAMYQNVVDG 960
 Db 901 LIQNGFKMDQPFYATEEYIIIMQSCWAFDSRKRPSFNLTSFLGCOLADAEAMYQNVVDG 960
 Qy 961 RVSECPHTYQNRPFPSREMDLGLLSPQAQVEDS 993
 Db 961 RVSECPHTYQNRPFPSREMDLGLLSPQAQVEDS 993

RESULT 10
 AAR31376
 XX ID AAR31376 standard; Protein; 1167 AA.
 XX AC AAR31376;
 XX XX
 XX DT 25-JUN-1993 (first entry)
 XX DE Human flk-2.
 XX XX
 KW Human; receptor; protein; tyrosine kinase; ptk; primitive; mammalian;
 KW hematopoietic cell; pbc; mature; mhc; fetal; liver kinase 2; flk-2;
 KW liver; spleen; thymus; adult; brain; marrow; thymocyte; subset;
 KW multipotential; T-lymphoid; lineage.
 XX OS Homo sapiens.
 XX XX
 PH Key Location/Qualifiers
 FT Misc-difference 1013 /note= "Nonsense mutation"
 FT Misc-difference 1038 /note= "Nonsense mutation"
 FT Misc-difference 1042 /note= "Nonsense mutation"
 FT Misc-difference 1057 /note= "Nonsense mutation"
 FT Misc-difference 1102 /note= "Nonsense mutation"

FT Misc-difference 1117 /note= "Nonsense mutation"
 FT Misc-difference 1127 /note= "Nonsense mutation"
 FT Misc-difference 1127 /note= "Nonsense mutation"
 XX W093003049-A.
 XX PN 07-JAN-1993.
 XX PD 26-JUN-1992; 92WO-US05401.
 XX PF 28-JUN-1991; 91US-0728913.
 XX PR 15-NOV-1991; 91US-0793085.
 XX PR 24-DEC-1991; 91US-0813593.
 XX PR 02-APR-1992; 92WO-US02750.
 XX (UYPR-) UNIV PRINCETON.
 XX PA Lemischka IR;
 XX PI WPI; 1993-036323/04.
 XX DR N-PSDB; AAQ35250.
 XX DX Nucleic acid encoding receptor protein tyrosine kinase - allows
 XX PT development of ligands to stimulate proliferation and/or
 XX PT differentiation of mammalian haematopoietic stem cells
 XX PS Claim 9; Fig 1b; 78pp; English.
 XX CC This sequence represents a human receptor protein tyrosine kinase
 CC which belongs to a new functional class of protein tyrosine kinases
 CC (ptks). ptk in this class are expressed in primitive mammalian
 CC hematopoietic (pbc) cells but not in mature hematopoietic cells (mhc).
 CC This protein is an example of a receptor ptk and is called fetal liver
 CC kinase 2 (flk-2). flk-2 is expressed in fetal liver, spleen and thymus,
 CC and adult brain and marrow. Expression of flk-2 mRNA occurs in the
 CC most primitive thymocyte subset, which is believed to be uncommitted.
 CC Therefore, thymocytes expressing flk-2 may be multipotential. flk-2
 CC is the first receptor tyrosine kinase known to be expressed in the
 CC T-lymphoid lineage.
 XX SQ Sequence 1167 AA;
 Query Match 99.8%; Score 5262; DB 14; Length 1167;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 991; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVPLLVFSAMIFGTITNODLPVVKVNLNHNKNDSSVGKSSSYPMVSESP 60
 Db 20 MPALARDAGTVPLLVFSAMIFGTITNODLPVVKVNLNHNKNDSSVGKSSSYPMVSESP 79
 Qy 61 EDLGCALRPQSSGTVEAAAEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCPHFDL 120
 Db 80 EDLGCALRPQSSGTVEAAAEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCPHFDL 139
 Qy 121 QNRGVSVMLKMTETQAGEYLLFIQSEATNTYTLFTVSIRNTLYTLRRPYFRKXNQD 180
 Db 140 QNRGVSVMLKMTETQAGEYLLFIQSEATNTYTLFTVSIRNTLYTLRRPYFRKXNQD 199
 Qy 181 ALVCISESVPEPIVENVLDCSGESCKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
 Db 200 ALVCISESVPEPIVENVLDCSGESCKESPAVVKKEKVLHELFGTDIRCCARNELGRE 259
 Qy 241 CTRLTIDINOTPOTTLPOLFLKVGEPWIRCKAVVNHGFLTWELNKALEEGNYPFM 300
 Db 260 CTRLTIDINOTPOTTLPOLFLKVGEPWIRCKAVVNHGFLTWELNKALEEGNYPFM 319
 Qy 301 STYSTNRTMIRILFAFVSSVARNNDGYTTCSSSKHPSQSALVTIIVKGFINATNSEDYE 360
 Db 320 STYSTNRTMIRILFAFVSSVARNNDGYTTCSSSKHPSQSALVTIIVKGFINATNSEDYE 379
 Qy 361 IDQEEFCFSVRKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQPGGEYIFHA 420


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Db 380 IDQVEEFCFSVRKAYPQIRCTWTSRKSFPCEQGLDNGYSISKFCNKHQGPGEYIFHA 439
Qy 421 ENDDAQFTQKFTLNIRRKPOVLAPASASQSCFSDGYPLPSWTWKCKSDKSPNCTEETE 480
Db 440 ENDDAQFTQKFTLNIRRKPOVLAPASASQSCFSDGYPLPSWTWKCKSDKSPNCTEETE 499
Qy 481 GWNRKANRKFVGQWVSSSTLNMSAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Db 500 GWNRKANRKFVGQWVSSSTLNMSAIKGLVKCCAYNSLGTSCETILLNSAGPPFIQD 559
Qy 541 NISFYATIGVCLLFIWLTLLIICHYKKQFRYESQLOMQVQVTSQSDNBYFYVDREYED 600
Db 560 NISFYATIGVCLLFIWLTLLIICHYKKQFRYESQLOMQVQVTSQSDNBYFYVDREYED 619
Qy 601 LKWEFPRENLEFGKVLGSAFGKVMNATAYGISKTGVSQVAVKMLKEKADSSREALMS 660
Db 620 LKWEFPRENLEFGKVLGSAFGKVMNATAYGISKTGVSQVAVKMLKEKADSSREALMS 679
Qy 661 ELKQMTQLGSHENIVNLGACTLSGPIYLIPEYCCYGDLLNLYLSKREKPHRTWTEIFKE 720
Db 680 ELKQMTQLGSHENIVNLGACTLSGPIYLIPEYCCYGDLLNLYLSKREKPHRTWTEIFKE 739
Qy 721 HNFSPYPTFQSHPNSSMPGSRVQIHDPDSDOIISGLHNSFHSDEIEYENOKRLEEREDL 780
Db 740 HNFSPYPTFQSHPNSSMPGSRVQIHDPDSDOIISGLHNSFHSDEIEYENOKRLEEREDL 799
Qy 781 NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Db 800 NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 859
Qy 841 NYVVRGNARLPVKWMAPESLPEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK 900
Db 860 NYVVRGNARLPVKWMAPESLPEGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK 919
Qy 901 LIQNGKMDQPFYATEEYIIMQSCWAFDSRKRPSFPNLTSLGCOLADABEAMYQNVDG 960
Db 920 LIQNGKMDQPFYATEEYIIMQSCWAFDSRKRPSFPNLTSLGCOLADABEAMYQNVDG 979
Qy 961 RVSECPHTYQNRPFPSREMDLGLLSPQAQVEDS 993
Db 980 RVSECPHTYQNRPFPSREMDLGLLSPQAQVEDS 1012

RESULT 11
AAW63588
ID AAW63588 standard; Protein; 983 AA.
XX
AC AAW63588;
XX
DT 12-OCT-1998 (first entry)
XX
DE Human receptor type protein kinase FLT3 protein SEQ ID NO:19.
XX
KW Human; receptor type protein kinase; FLT3; diagnosis; leukaemia;
KW membrane-vicinal region; tyrosine kinase; juxtamembrane region.
XX
OS Homo sapiens.
XX
PN WO9817808-A1.
XX
PD 30-APR-1998.
XX
PF 13-OCT-1997; 97WO-JP03667.
XX
PR 18-OCT-1996; 96JP-0297329.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
PI Yokota S;
XX
WPI; 1998-362333/31.
DR N-ESDB; AAV39041.
DR
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XX Nucleic acid sequences encoding receptor type protein kinase -
PT useful for diagnosing adult acute leukaemia of, e.g. FAB sub-classes
PT M2
XX
PS Claim 6; Page 45-50; 80pp; Japanese.
XX
CC New nucleic acid sequences have been isolated which encode receptor type
CC protein kinases (especially a tyrosine kinases) having tandem repeats in
CC the juxtamembrane region. Also described in the present invention are:
CC (1) any one of 10 amino acid (aa) sequences (AAW63580 to AAW63589)
CC representing FLT3 juxtamembrane receptor type protein kinases found in
CC leukaemia patients of FAB subclass M2, M4 or M5 (nucleic acid sequences
CC encoding the proteins are given in AAV39028 to AAV39042); (2) antibodies
CC recognising the kinases or their portions including the tandem repeat
CC region; (3) nucleic acid sequences hybridising with the nucleic acids;
CC (4) a method for detecting the nucleic acid sequences in human tissue
CC samples by: (i) extracting nucleic acid; (ii) amplifying the kinase
CC gene, and (iii) determining the size of the gene for comparing the size
CC of the normal gene not containing tandem repeats, and (5) kits for
CC carrying out the detection. The products and methods may be used for
CC diagnosing adult acute leukaemia of FAB subclasses M2, M4 and M5.
XX
SQ Sequence 983 AA;

Query Match 97.8%; Score 5159; DB 19; Length 983;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 973; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy 1 MPALARDAGTVPLLVFSAIFGTITNODLPVICKVLINHKNDSSVGKSSSPVWVSESP 60
Db 1 MPALARDAGTVPLLVFSAIFGTITNODLPVICKVLINHKNDSSVGKSSSPVWVSESP 60
Qy 61 EDLGCALRQSSGTVYEAADVVDVSASITLQVLVDAPGNI SCLVWFKHSSLNCQPHFDL 120
Db 61 EDLGCALRQSSGTVYEAADVVDVSASITLQVLVDAPGNI SCLVWFKHSSLNCQPHFDL 120
Qy 121 QNRGVSVVILKMTETQAGEYLLFIQSEATNTYTLFTVSRNTLLYTLRRPFRKMNOD 180
Db 121 QNRGVSVVILKMTETQAGEYLLFIQSEATNTYTLFTVSRNTLLYTLRRPFRKMNOD 180
Qy 181 ALVCISESVPEPIVEWVLCDQSOGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Db 181 ALVCISESVPEPIVEWVLCDQSOGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
Qy 241 CTRLFTIDLNTQPTTLPLQFLKVGELPWRCKAVVNHGFGLTWELENKALEEGNYFEM 300
Db 241 CTRLFTIDLNTQPTTLPLQFLKVGELPWRCKAVVNHGFGLTWELENKALEEGNYFEM 300
Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTCCSSKHPQSALVTIVGKGFINATNSSEDEYE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTCCSSKHPQSALVTIVGKGFINATNSSEDEYE 360
Qy 361 IDQVEEFCFSVRKAYPQIRCTWTSRKSFPCEQGLDNGYSISKFCNKHQGPGEYIFHA 420
Db 361 IDQVEEFCFSVRKAYPQIRCTWTSRKSFPCEQGLDNGYSISKFCNKHQGPGEYIFHA 420
Qy 421 ENDDAQFTQKFTLNIRRKPOVLAPASASQSCFSDGYPLPSWTWKCKSDKSPNCTEETE 480
Db 421 ENDDAQFTQKFTLNIRRKPOVLAPASASQSCFSDGYPLPSWTWKCKSDKSPNCTEETE 480
Qy 481 GWNRKANRKFVGQWVSSSTLNMSAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Db 481 GWNRKANRKFVGQWVSSSTLNMSAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Qy 541 NISFYATIGVCLLFIWLTLLIICHYKKQFRYESQLOMQVQVTSQSDNBYFYVDREYED 600
Db 541 NISFYATIGVCLLFIWLTLLIICHYKKQFRYESQLOMQVQVTSQSDNBYFYVDREYED 600
Qy 601 L-----KWEFPRENLEFGKVLGSAFGKVMNATAYGISKTGVSQVAVKMLKEKA 650
Db 601 LKWEFPRENLEFGKVLGSAFGKVMNATAYGISKTGVSQVAVKMLKEKA 660
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QY 651 DSSREALMSLKMOTQSGSHENIVNLLGACTLGGPIYLIPEYCCYCDLLNLYRSKREKF 710
 DB 661 DSSREALMSLKMOTQSGSHENIVNLLGACTLGGPIYLIPEYCCYCDLLNLYRSKREKF 720
 QY 711 HRTWTETFEKHNFSFYPTFQSHNSMPSGSRVQIHPDSDQISGLHNSPHSEDELEYEN 770
 DB 721 HRTWTETFEKHNFSFYPTFQSHNSMPSGSRVQIHPDSDQISGLHNSPHSEDELEYEN 780
 QY 771 QKLEEEEDLNVLTFEDLLCFAYQVAKGMFEFLFKSCVHRDLAARNVLVTHGKVKICDF 830
 DB 781 QKLEEEEDLNVLTFEDLLCFAYQVAKGMFEFLFKSCVHRDLAARNVLVTHGKVKICDF 840
 QY 831 GLARDIMSDSNVYVGNARLPVKWMAPESLFEGITYIKSDVMSYGILLWEIFSLGNVYP 890
 DB 841 GLARDIMSDSNVYVGNARLPVKWMAPESLFEGITYIKSDVMSYGILLWEIFSLGNVYP 900
 QY 891 GIPVDANFYKLIQNGFKMDQPFYATEEIIYIMOSWAFDSRKRPSPNLTSLGCOLADA 950
 DB 901 GIPVDANFYKLIQNGFKMDQPFYATEEIIYIMOSWAFDSRKRPSPNLTSLGCOLADA 960
 QY 951 EEMAYQNVDCRVSECPHTYQNR 973
 DB 961 EEMAYQNVDCRVSECPHTYQNR 983

RESULT 12
 AA63587
 ID AA63587 standard; Protein; 986 AA.
 XX
 AC AA63587;
 DT 12-OCT-1998 (first entry)
 XX
 DE Human receptor type protein kinase FLT3 protein SEQ ID NO:18.
 XX
 KW Human; receptor type protein kinase; FLT3; diagnosis; leukaemia;
 XX membrane-vicinal region; tyrosine kinase; juxtamembrane region.
 OS Homo sapiens.
 XX
 XX WO9817808-A1.
 XX
 PD 30-APR-1998.
 XX
 PF 13-OCT-1997; 97WO-JP03667.
 XX
 PR 18-OCT-1996; 96JP-0297329.
 XX
 PA (TAKI) TAKARA SHUZO CO LTD.
 XX
 PI Yokota S;
 XX
 DR WPI; 1998-362333/31.
 DR N-PSDB; AAV39040.
 XX
 XX Nucleic acid sequences encoding receptor type protein kinase -
 PT useful for diagnosing adult acute leukaemia of, e.g. FAB sub-classes
 PT M2
 XX
 PS Claim 6; Page 40-45; 80pp; Japanese.
 XX
 CC New nucleic acid sequences have been isolated which encode receptor type
 CC protein kinases (especially a tyrosine kinases) having tandem repeats in
 CC the juxtamembrane region. Also described in the present invention are:
 CC (1) any one of 10 amino acid (aa) sequences (AAW63580 to AAW63589)
 CC representing FLT3 juxtamembrane receptor type protein kinases found in
 CC leukaemia patients of FAB subclasses M2, M4 or M5 (nucleic acid sequences
 CC encoding the proteins are given in AAV39028 to AAV39042); (2) antibodies
 CC recognising the kinases or their portions including the tandem repeat
 CC region; (3) nucleic acid sequences hybridising with the nucleic acids;
 CC (4) a method for detecting the nucleic acid sequences in human tissue
 CC samples by: (i) extracting nucleic acid; (ii) amplifying the kinase
 CC gene, and (iii) determining the size of the gene for comparing the size

CC of the normal gene not containing tandem repeats, and (5) kits for
 CC carrying out the detection. The products and methods may be used for
 CC diagnosing adult acute leukaemia of FAB subclasses M2, M4 and M5.
 XX
 SQ Sequence 986 AA;
 Query Match 97.8%; Score 5157.5; DB 19; Length 986;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 973; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
 QY 1 MPALARDAGTVPLLVVFSAMIFGTITNODLPVTKVLINHKNDSSVGKSSSYPMWSESP 60
 DB 1 MPALARDAGTVPLLVVFSAMIFGTITNODLPVTKVLINHKNDSSVGKSSSYPMWSESP 60
 QY 61 EDLGCALRPOSSGTVYEAATAVEVDVSASITLQVLVDPAGNISCLWVPKHSNLCOPHFDL 120
 DB 61 EDLGCALRPOSSGTVYEAATAVEVDVSASITLQVLVDPAGNISCLWVPKHSNLCOPHFDL 120
 QY 121 QNRGVSMVILKMTETQAGEYLLFIQSEATNYTLFTVSRNTLLYTLRRPYFRMENQD 180
 DB 121 QNRGVSMVILKMTETQAGEYLLFIQSEATNYTLFTVSRNTLLYTLRRPYFRMENQD 180
 QY 181 ALVCISESVPEPIVEWVLCDQSGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
 DB 181 ALVCISESVPEPIVEWVLCDQSGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
 QY 241 CTRLFTIDLNQTPQTLPLQFLKVGEPILWIRCKAVHNVHGFGLTWELNKALEBGNYP 300
 DB 241 CTRLFTIDLNQTPQTLPLQFLKVGEPILWIRCKAVHNVHGFGLTWELNKALEBGNYP 300
 QY 301 STYSTNRTMIRILPAFVSSVARNDTGYTCTSSSKHPQSALVTIVGKFINATNSSEDE 360
 DB 301 STYSTNRTMIRILPAFVSSVARNDTGYTCTSSSKHPQSALVTIVGKFINATNSSEDE 360
 QY 361 IDQYEEFCFSVRKAYPOIRCTWTFSRKSPCEQGLDNGYSISKFCNHKHOPGEYIFHA 420
 DB 361 IDQYEEFCFSVRKAYPOIRCTWTFSRKSPCEQGLDNGYSISKFCNHKHOPGEYIFHA 420
 QY 421 ENDDAQFTKMTLNIIRKQVLAESASQASCFSDGYPLPSWTWKCKSDKSPNCTEETITE 480
 DB 421 ENDDAQFTKMTLNIIRKQVLAESASQASCFSDGYPLPSWTWKCKSDKSPNCTEETITE 480
 QY 481 GWNRKANRKFVGQWVSSTLWSEAIKGLVKCAYNSLGTSCETILLNSPGPPPTQD 540
 DB 481 GWNRKANRKFVGQWVSSTLWSEAIKGLVKCAYNSLGTSCETILLNSPGPPPTQD 540
 QY 541 NISFYATIGVCLLFIVLTLIICHYKKOPRYESQLOQWQVQVGTSSDNEFYFV 592
 DB 541 NISFYATIGVCLLFIVLTLIICHYKKOPRYESQLOQWQVQVGTSSDNEFYFV 600
 QY 593 -----DPREYEDLKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIVAVKMLK 647
 DB 601 LKWEFDREYEDLKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIVAVKMLK 660
 QY 648 EKADSSREALMSLKMOTQSGSHENIVNLLGACTLGGPIYLIPEYCCYCDLLNLYRSKR 707
 DB 661 EKADSSREALMSLKMOTQSGSHENIVNLLGACTLGGPIYLIPEYCCYCDLLNLYRSKR 720
 QY 708 EKFHRTWTEIFEKHNFSFYPTFQSHNSMPSGSRVQIHPDSDQISGLHNSPHSEDEITE 767
 DB 721 EKFHRTWTEIFEKHNFSFYPTFQSHNSMPSGSRVQIHPDSDQISGLHNSPHSEDEITE 780
 QY 768 YENQKLEEEEDLNVLTFEDLLCFAYQVAKGMFEFLFKSCVHRDLAARNVLVTHGKVKI 827
 DB 781 YENQKLEEEEDLNVLTFEDLLCFAYQVAKGMFEFLFKSCVHRDLAARNVLVTHGKVKI 840
 QY 828 CDFGLARDIMSDSNVYVGNARLPVKWMAPESLFEGITYIKSDVMSYGILLWEIFSLGNV 887
 DB 841 CDFGLARDIMSDSNVYVGNARLPVKWMAPESLFEGITYIKSDVMSYGILLWEIFSLGNV 900
 QY 888 PYPGIPVDANFYKLIQNGFKMDQPFYATEEIIYIMOSWAFDSRKRPSPNLTSLGCOL 947
 DB 901 PYPGIPVDANFYKLIQNGFKMDQPFYATEEIIYIMOSWAFDSRKRPSPNLTSLGCOL 960

Qy 948 ADABEAMYQNDGRVSECPHTYQNR 973
 Db 961 ADABEAMYQNDGRVSECPHTYQNR 986

RESULT 13

AAW63589
 ID AAW63589 standard; Protein; 986 AA.

XX AAW63589;

DT 12-OCT-1998 (first entry)

XX Human receptor type protein kinase FLT3 protein SEQ ID NO:20.

XX Human; receptor type protein kinase; FLT3; diagnosis; leukaemia;
 KW membrane-vicinal region; tyrosine kinase; juxtamembrane region.

XX Homo sapiens.

PN WO9817808-A1.

XX 30-APR-1998.

XX 13-OCT-1997; 97WO-JP03667.

XX 18-OCT-1996; 96JP-0297329.

XX (TAKI) TAKARA SHUZO CO LTD.

XX Yokota S;

XX WPI; 1998-362333/31.

DR N-PSDB; AAV39042.

XX Nucleic acid sequences encoding receptor type protein kinase -

PT useful for diagnosing adult acute leukaemia of, e.g. FAB sub-classes

PT M2

XX Claim 6; Page 50-55; 80pp; Japanese.

XX New nucleic acid sequences have been isolated which encode receptor type
 CC protein kinases (especially a tyrosine kinases) having tandem repeats in
 CC the juxtamembrane region. Also described in the present invention are:
 CC (1) any one of 10 amino acid (aa) sequences (AAW63580 to AAW63589)
 CC representing FLT3 juxtamembrane receptor type protein kinases found in
 CC leukemia patients of FAB subclass M2, M4 or M5 (nucleic acid sequences
 CC encoding the proteins are given in AAV39028 to AAV39042); (2) antibodies
 CC recognising the kinases or their portions including the tandem repeat
 CC region; (3) nucleic acid sequences hybridising with the nucleic acids;
 CC (4) a method for detecting the nucleic acid sequences in human tissue
 CC samples by: (i) extracting nucleic acid; (ii) amplifying the kinase
 CC gene, and (iii) determining the size of the gene for comparing the size
 CC of the normal gene not containing tandem repeats, and (5) kits for
 CC carrying out the detection. The products and methods may be used for
 CC diagnosing adult acute leukaemia of FAB subclasses M2, M4 and M5.

XX Sequence 986 AA;

Query Match 97.8%; Score 5157.5; DB 19; Length 986;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 973; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 MPALARDAGTPLLIVVFSAMIFGITITNODLPVVKVLINHKNDSSVGKSSYPVWVSESP 60
 Db 1 MPALARDAGTPLLIVVFSAMIFGITITNODLPVVKVLINHKNDSSVGKSSYPVWVSESP 60
 Qy 61 EDLGCALRQSSGTVEAAAEVVDVSASITLQVLVDAPGNISCLVFKHSSLNCPHFDL 120
 Db 61 EDLGCALRQSSGTVEAAAEVVDVSASITLQVLVDAPGNISCLVFKHSSLNCPHFDL 120
 Qy 121 QNRGVSVMLKWTQTQAGEVLLFTQSEATNTYILFTVTSIRNTLLTYLRRPFRKMNQD 180

Db 121 QNRGVSVMLKWTQTQAGEVLLFTQSEATNTYILFTVTSIRNTLLTYLRRPFRKMNQD 180
 Qy 181 ALVCISESVPEPIVEWVLCDSSQESCKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
 Db 181 ALVCISESVPEPIVEWVLCDSSQESCKESPAVVKKEKVLHELFGTDIRCCARNELGRE 240
 Qy 241 CTRLEFDINQTPOTTLQPLFKVGEPLWIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
 Db 241 CTRLEFDINQTPOTTLQPLFKVGEPLWIRCKAVVNHGFGLTWELENKALEEGNYFEM 300
 Qy 301 STYSTNRTMIRILPAFVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360
 Db 301 STYSTNRTMIRILPAFVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360
 Qy 361 IDQYEEFCFSVRFKAYPOIRCTWTFSRKSFPCEQKGLDNGYSISKFCNHKHPGEYIFHA 420
 Db 361 IDQYEEFCFSVRFKAYPOIRCTWTFSRKSFPCEQKGLDNGYSISKFCNHKHPGEYIFHA 420
 Qy 421 ENDDAQFTMTFLNIRRKPOVLAEASASQASCFSDGYPLPSWTWKKCSDKSPNCTEITE 480
 Db 421 ENDDAQFTMTFLNIRRKPOVLAEASASQASCFSDGYPLPSWTWKKCSDKSPNCTEITE 480
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 Qy 541 NISFYATIGVCLLFIIVLTLLIICHYKKQFRYESQIQMVQVT-----GSSDN 587
 Db 541 NISFYATIGVCLLFIIVLTLLIICHYKKQFRYESQIQMVQVTGSSDNEYFYVDFRGSND 600
 Qy 588 EYFYVDPREYEDLKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTVSIQVAVKMLK 647
 Db 601 EYFYVDPREYEDLKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTVSIQVAVKMLK 660
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 Qy 708 EKFHRTWTETPKHEHNFSPYPTFQSHPNSSMPGSRREVQIHPDSQISGLHGNSPHSEDEIE 767
 Db 721 EKFHRTWTETPKHEHNFSPYPTFQSHPNSSMPGSRREVQIHPDSQISGLHGNSPHSEDEIE 780
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 Db 781 YENQKRLSEEDLNVLTPEDLFCPAYQVAKGMFLEFKSCVHRDLAARNVLTGHKVKVI 840
 Qy 828 CDFGLARDIMSDSNVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVN 887
 Db 841 CDFGLARDIMSDSNVVRGNARLPVKWMAPESLFEGIYTIKSDVMSYGILLWEIFSLGVN 900
 Qy 888 PYPGIPVDANFYKLIQNGPKMDQPPFYATEEIIYIMQSCWAFDSRKRPSPNLTSPFLGCQL 947
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 Db 961 ADAEEAMYQNVDGRVSECPHTYQNR 986

RESULT 14

AAW63586

ID AAW63586 standard; Protein; 994 AA.

XX AAW63586;

DT 12-OCT-1998 (first entry)

XX Human receptor type protein kinase FLT3 protein SEQ ID NO:17.

XX Human; receptor type protein kinase; FLT3; diagnosis; leukaemia;
 KW membrane-vicinal region; tyrosine kinase; juxtamembrane region.

XX

OS Homo sapiens.
 XX PN WO9817808-A1.
 XX PD 30-APR-1998.
 XX PF 13-OCT-1997; 97WO-JP03667.
 XX PR 18-OCT-1996; 96JP-0297329.
 XX PR (TAKI) TAKARA SHUZO CO LTD.
 XX PA Yokota S;
 XX PI WPI; 1998-362333/31.
 XX DR N-PSDB; AAV39039.
 XX DR Nucleic acid sequences encoding receptor type protein kinase -
 PT useful for diagnosing adult acute leukaemia of, e.g. FAB sub-classes
 PT M2
 XX Claim 6; Page 34-39; 80pp; Japanese.
 XX CC New nucleic acid sequences have been isolated which encode receptor type
 CC protein kinases (especially a tyrosine kinases) having tandem repeats in
 CC the juxtamembrane region. Also described in the present invention are:
 CC (1) any one of 10 amino acid (aa) sequences (AAW63580 to AAW63589)
 CC representing FLT3 juxtamembrane receptor type protein kinases found in
 CC leukaemia patients of FAB subclass M2, M4 or M5 (nucleic acid sequences
 CC encoding the proteins are given in AAV39028 to AAV39042); (2) antibodies
 CC recognising the kinases or their portions including the tandem repeat
 CC region; (3) nucleic acid sequences hybridising with the nucleic acids;
 CC (4) a method for detecting the nucleic acid sequences in human tissue
 CC samples by: (i) extracting nucleic acid; (ii) amplifying the kinase
 CC gene, and (iii) determining the size of the gene for comparing the size
 CC of the normal gene not containing tandem repeats, and (5) kits for
 CC carrying out the detection. The products and methods may be used for
 CC diagnosing adult acute leukaemia of FAB subclasses M2, M4 and M5.
 XX CC
 XX SQ Sequence 994 AA;
 Query Match 97.7%; Score 5153.5; DB 19; Length 994;
 Best Local Similarity 97.9%; Pred. No. 0;
 Matches 973; Conservative 0; Mismatches 0; Indels 21; Gaps 1;
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 DB 1 MPALARDAGTVPLLVVFSAAMIFGTTITNODLPVVKVLINHKNDSSVGKSSSYPMVSESP 60
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 DB 61 EDLGCALRPQSSGTYVEAAAEVDVVSASITLQVLVDAPGNISCLWVFKHSSLNCOQPHFDL 120
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 DB 301 STYSTNRTMIRILFAFVSSVARNDGTTCSSKHPQSALVTIIVKGFINATNSESDEYE 360
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 DB 541 NISFYATIGVCLLFIIVVLTLLIHKYKQFRYESQLOLQWQVTGSSDNEYFYVDREY 600
 QY 598 -----EYDLKWEFPRENLEFGKVLGSGAGFGKVMNATAYGISKTGYSI 639
 DB 601 LKWEFPRENLEFGKVLGSEYDLKWEFPRENLEFGKVLGSGAGFGKVMNATAYGISKTGYSI 660
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 DB 661 QVAVKMLKEKADSSEREAALMSLKMWTQOLGSHENIVNLLGACTLSGPIYLLIFEYCCYGD 720
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 QY 820 THGKVKICDPGLARDIMSDSNVYVVRGNARLPVKWAPESLFEGIYTIKSDVWSYGILLW 879
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 QY 880 EIFSLGVNPEGIPVDANFYKLIQNGFKMDQFPYATEBIYIIMQSCWAFDSRKRSPFN 939
 DB 901 EIFSLGVNPEGIPVDANFYKLIQNGFKMDQFPYATEBIYIIMQSCWAFDSRKRSPFN 960
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 DB 961 TSFLGCOLADAEAEAMYQNVDRVSECPHTYQNR 994
 RESULT 15
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 ID AAR81868 standard; Protein; 1000 AA.
 XX AC AAR81868;
 XX AC
 DT 29-FEB-1996 (first entry)
 XX Flk2/Flt3 tyrosine kinase receptor.
 DE Tyrosine kinase receptor; flk2; flt3; agonist; monoclonal antibody;
 KW haematopoiesis; hypoplasia; anaemia; thrombocytopenia; stem cell.
 XX Mus sp.
 FH Key Location/Qualifiers
 FT Domain 1..542
 FT /label= Extracellular_domain
 XX WO9527062-A1.
 FN 12-OCT-1995.
 XX 23-MAR-1995; 95WO-US03718.
 XX 04-APR-1994; 94US-0222299.
 XX (GETH) GENENTECH INC.
 XX Bennett BD, Broz SD, Matthews W, Zeigler FC;
 XX WPI; 1995-358636/46.

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:59:30 ; Search time 41.0207 Seconds

(without alignments)
2400.704 Million cell updates/sec

Title: US-09-919-408-4

Perfect score: 5274

Sequence: 1 MPALARDAGTVPLLVFSAM.....PFSREMDLGLSPQAQVEDS 993

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	4429.5	84.0	992	10	US-09-872-136-2
5	1266	24.0	975	9	US-10-192-867-2
6	1251	23.7	976	9	US-10-099-895-32
7	1251	23.7	976	9	US-10-192-867-4
8	1216.5	23.1	972	10	US-09-944-807-10
9	1166.5	22.1	1088	9	US-09-961-403-4
10	1166	22.1	1089	9	US-09-955-363-36
11	1166	22.1	1089	10	US-09-769-987-2
12	1166	22.1	1089	10	US-09-919-497-90
13	1166	22.1	1089	10	US-09-866-510-2
14	1163	22.1	1089	10	US-09-866-510-10
15	1162	22.0	1089	10	US-09-866-510-4
16	1161	22.0	1089	10	US-09-866-510-8
17	1160	22.0	1089	10	US-09-866-510-6
18	1086.5	20.6	1090	10	US-09-866-510-14
19	1086.5	20.6	1106	9	US-09-955-363-2

20	1086.5	20.6	1106	10	US-09-866-510-22	Sequence 22, Appl
21	1082.5	20.5	1106	10	US-09-866-510-16	Sequence 16, Appl
22	1081.5	20.5	1106	10	US-09-866-510-20	Sequence 20, Appl
23	1080.5	20.5	1106	10	US-09-866-510-18	Sequence 18, Appl
24	990	18.8	1338	9	US-10-059-585-44	Sequence 44, Appl
25	957	18.1	386	9	US-09-939-833-6	Sequence 6, Appl
26	957	18.1	386	10	US-09-939-754-6	Sequence 6, Appl
27	957	18.1	386	10	US-09-939-832-6	Sequence 2, Appl
28	951.5	18.0	1356	9	US-10-022-939-2	Sequence 2, Appl
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30	950.5	18.0	1356	9	US-09-969-037-7	Sequence 7, Appl
31	934	17.7	1367	10	US-09-766-678-2	Sequence 2, Appl
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34	907.5	17.2	1363	9	US-09-375-248-19	Sequence 19, Appl
35	904.5	17.2	1298	10	US-09-982-610-33	Sequence 33, Appl
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37	902.5	17.1	1368	9	US-10-105-901-34	Sequence 34, Appl
38	902	17.1	1362	9	US-10-105-901-33	Sequence 33, Appl
39	880.5	16.7	1363	9	US-10-105-901-32	Sequence 32, Appl
40	859.5	16.3	367	9	US-09-939-833-9	Sequence 9, Appl
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43	846	16.0	367	9	US-09-939-833-12	Sequence 12, Appl
44	846	16.0	367	10	US-09-939-754-12	Sequence 12, Appl
45	846	16.0	367	10	US-09-939-832-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-919-408-4

; Sequence 4, Application US/09919408

; Patent No. US20020072077A1

; GENERAL INFORMATION:

; APPLICANT: Lemischka, Ihor R.

; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL RECEPTORS AND THEIR LIGANDS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ImClone Systems Incorporated

; STREET: 180 Varick Street

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10014

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/919,408

; FILING DATE: 31-Jul-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/977,451

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 07/906,397

; FILING DATE: 26-JUN-1992

; APPLICATION NUMBER: US PCT/US92/05401

; FILING DATE: 26-JUN-1992

; APPLICATION NUMBER: TW 81102961

; FILING DATE: 15-APR-1992

; APPLICATION NUMBER: US PCT/US92/02750

; FILING DATE: 02-APR-1992

; APPLICATION NUMBER: US 07/813,593

; FILING DATE: 24-DEC-1991

; APPLICATION NUMBER: US 07/793,065

; FILING DATE: 15-NOV-1991

; APPLICATION NUMBER: US 07/728,913

; FILING DATE: 28-JUN-1991

APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-919-408-4

Query Match 100.0%; Score 5274; DB 10; Length 993;
Best Local Similarity 100.0%; Pred No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPALARDAGTVPLLVVFSAMIPTITNODLPVVKCVLINHKNDSSVGKSSSYPMVSESP 60
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RESULT 2
US-09-872-136-4
Sequence 4, Application US/09872136
Patent No. US20020119545A1
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/872,136
FILING DATE: 01-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/208,786
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/021,324
FILING DATE: <Unknown>
APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-872-136-4

Query Match 100.0%; Score 5274; DB 10; Length 993;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPALARDAGTVPVLLVFSAMIFGTITNQDLPVICKVLINHKNDSSVGKSSYPMTSESP 60
DB 1 MPALARDAGTVPVLLVFSAMIFGTITNQDLPVICKVLINHKNDSSVGKSSYPMTSESP 60
QY 61 EDLGCALRQSSGTVEAAAVEVDVSGASITLQVLVDAPGNISCLVFPKHSGLNCQPHFDL 120
DB 61 EDLGCALRQSSGTVEAAAVEVDVSGASITLQVLVDAPGNISCLVFPKHSGLNCQPHFDL 120
QY 121 QNRGVVSMILKMTQAGBYLLFIQSEATNYTILFTVSRNTLLYTLRPPYFRKMNQD 180
DB 121 QNRGVVSMILKMTQAGBYLLFIQSEATNYTILFTVSRNTLLYTLRPPYFRKMNQD 180
QY 181 ALVCISESVPEPIVWVLCDSQESCKEESPAVVKKEKVLHFGTDIRCCARNELGRE 240
DB 181 ALVCISESVPEPIVWVLCDSQESCKEESPAVVKKEKVLHFGTDIRCCARNELGRE 240
QY 241 CTRLFTIDLNTQPTTLPLQFLKVGEPWLIRCKAVHNVHGFGLTWELNKALEEGNYFEM 300
DB 241 CTRLFTIDLNTQPTTLPLQFLKVGEPWLIRCKAVHNVHGFGLTWELNKALEEGNYFEM 300
QY 301 STYSTNRTMIRILFAFVSSVARNDTGYTCTSSKHPQSQALVTIVGVKGFNATNSSEDEYE 360
DB 301 STYSTNRTMIRILFAFVSSVARNDTGYTCTSSKHPQSQALVTIVGVKGFNATNSSEDEYE 360
QY 361 IQYEBFCFSVRKAPQIRCTWTFERKSPCEOKGLDNGYSISKFNHKGHPGEYIFHA 420
DB 361 IQYEBFCFSVRKAPQIRCTWTFERKSPCEOKGLDNGYSISKFNHKGHPGEYIFHA 420
QY 421 ENDDAQFTKMTFLNIRRKQVLAESAASQASCFSDGYPPLSPWTKKCDKSPNCTEITE 480
DB 421 ENDDAQFTKMTFLNIRRKQVLAESAASQASCFSDGYPPLSPWTKKCDKSPNCTEITE 480
QY 481 GWNRKANRKFQGVVSSSTLNMSSEAIKGPLVKCCAYNSLGTSCETILLNSPGFPFIQD 540
DB 481 GWNRKANRKFQGVVSSSTLNMSSEAIKGPLVKCCAYNSLGTSCETILLNSPGFPFIQD 540
QY 541 NISFYATIGVCLLFIYVLTLLICHKYKOPRYESQLOMVOVTGSSDNEYFYVDFREYED 600
DB 541 NISFYATIGVCLLFIYVLTLLICHKYKOPRYESQLOMVOVTGSSDNEYFYVDFREYED 600
QY 601 LKWEFPRENLEFGKVLGSAFGKVMNATAYGSKTGVSIQVAVKMLKEKADSSEREAALMS 660
DB 601 LKWEFPRENLEFGKVLGSAFGKVMNATAYGSKTGVSIQVAVKMLKEKADSSEREAALMS 660
QY 661 ELKMMTOLGSHENIVNLLGACTLSGPIYLIFFEYCCYGDLLNLYLRSKREKPHRTWTEIFKE 720
DB 661 ELKMMTOLGSHENIVNLLGACTLSGPIYLIFFEYCCYGDLLNLYLRSKREKPHRTWTEIFKE 720
QY 721 HNFSPYFTQSHNSMPGSRVQIHPDSQIISGLHNSFHSDEDETEYENQKLEBEEDL 780
DB 721 HNFSPYFTQSHNSMPGSRVQIHPDSQIISGLHNSFHSDEDETEYENQKLEBEEDL 780
QY 781 NVLTPEDLCLCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHGVKVKICDFGLARDIMSDS 840
DB 781 NVLTPEDLCLCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHGVKVKICDFGLARDIMSDS 840
QY 841 NYVVRGNARLPVKWMAPESLFEGITYIKSDVMSYGILLMEIFSLGVNYPGIPVDANFYK 900
DB 841 NYVVRGNARLPVKWMAPESLFEGITYIKSDVMSYGILLMEIFSLGVNYPGIPVDANFYK 900

QY 901 LIQNGFKMDQFFYATEEIIYIMQSCWAFDSRKRPSPNLTSLFLGCOLADAEAEAMYQNVDG 960
DB 901 LIQNGFKMDQFFYATEEIIYIMQSCWAFDSRKRPSPNLTSLFLGCOLADAEAEAMYQNVDG 960
QY 961 RVSECPHTYQNRPPFRPMDLGLLSPQAQVEDS 993
DB 961 RVSECPHTYQNRPPFRPMDLGLLSPQAQVEDS 993

RESULT 3
US-09-919-408-2
; Sequence 2, Application US/09919408
; Patent No. US20020072077A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ibor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/919,408
; FILING DATE: 31-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,451
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-919-408-2

Query Match 84.0%; Score 4429.5; DB 10; Length 992;
Best Local Similarity 84.1%; Pred. No. 1.7e-288;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

QY 1 MPALA-RDAGTVPLLVVFGAMIFGTITNODLPVVKVLINKNNDSSVGKSSYPMVSES 59
Db 1 MPALAQRSDRRLLLVLSVMILETVNODLPVVKVLISHENNGSSAGPSSYRVRGS 60
QY 60 PEDLGCALRPQSSGTVYEAADVEVDVSASITLQVLVDAPGNISCLWVKHSSLNCPHF 119
Db 61 PEDLQCTPRQSGTVYEAATVEAESGSIITLQVLATPGDLSCLWVKHSSLCQPHFD 120
QY 120 LQNRGVVSVILKMTQTQAGEYLLFTQSEATNTILFTVSRINTLLYTLRPPFRKME 179
Db 121 LQNRGIVSMAILNVTETQAGEYLLHTQSEBRANYTLFTVNRDQTLVLRPPFRKME 180
QY 180 DALVCISESVPEPIVEMVLCDSEKESPAVVKKEKVLHFGTDIRCCARNELGR 239
Db 181 DALLCISEGVPETVEMVLCDSEKESPAVVKKEKVLHFGTDIRCCARNELGR 240
QY 240 ECTRLFTIDNQTPTLQFLKVGPELWIRCKAVHNVHFGTGLTWELNKALEEGNYFE 299
Db 241 ECTKLTIDNQAQSTLQFLKVGPELWIRCKAVHNVHFGTGLTWELNKALEEGSYFE 300
QY 300 MSTYSTNTRMIRILPAFVSSVARNDTGYTCSKSKHPSQSALVTIVGKFINATNSSEDY 359
Db 301 MSTYSTNTRMIRILAFVSSVGRNDGYTCSKSKHPSQSALVTILEKGFINATSSQEEY 360
QY 360 EIDQYEERCFSVRFKAYPOIRCTWTESRKFCEQKGLDNGYSISKPCNHKHOPGEVIPH 419
Db 361 EIDPYEKFCFSVRFKAYPRIRCTWTIFQSAFCEQKGLDNGYSISKPCDHKNKPGYIFY 420
QY 420 AENDDAQFTKMTLNIRRPQVLAEASASQSCFSGDYPPLPSWTWKCKSKSPNCTEET 479
Db 421 AENDDAQFTKMTLNIRKPKQVLANASASQSCSDGYPPLPSWTWKCKSKSPNCTEET 480
QY 480 EGVNRKANRKYFGQVSSSTLNMSEAIKGLVKCCAYNSLGTSCETILNLSGPPFFIQ 539
Db 481 EGVNRKANRKYFGQVSSSTLNMSEAGLLVKCCAYNSMGTSCTIFLNSGPPFFIQ 540
QY 540 DNISFATIGVCLLFTVILTLILCHYKQFPRYESOLQVQVGTSSDNEYFYVDREY 599
Db 541 DNISFATIGLCLPFTVILTLILCHYKQFPRYESOLQVQVGTSSDNEYFYVDREY 600
QY 600 DLKWFPPRENLEFGKVLGSAFGKVNATAYGSKTGVSIQVAVKMLKEKADSSEREALM 659
Db 601 DLKWFPPRENLEFGKVLGSAFGKVNATAYGSKTGVSIQVAVKMLKEKADSSEREALM 660
QY 660 SELKMTQLGSHENIYNLLGACTLSPYILIPYCCYGLDNLNLRKREKPHRTWTEIFK 719
Db 661 SELKMTQLGHNDIYNLLGACTLSPYILIPYCCYGLDNLNLRKREKPHRTWTEIFK 720
QY 720 EHNFSYPTFQSHNSMFGSREVQIHDPDSQISGLHNSFHSDEIEYENQRL--EE 777
Db 721 EHNFSYPTFQSHNSMFGSREVQIHDPDSQISGLHNSFHSDEIEYENQRLAEE 780
QY 778 EDNLVLTFFEDLLCFAYQVAKGMFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIM 837
Db 781 EDNLVLTFFEDLLCFAYQVAKGMFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIL 840
QY 838 SDSNYVVRGNARLPVKWAPESLFEIGYTIKSDVMSYGILLWEIFSLGNVPYFGIPVDAN 897
Db 841 SDSNYVVRGNARLPVKWAPESLFEIGYTIKSDVMSYGILLWEIFSLGNVPYFGIPVDAN 900
QY 898 FYKLQNGKMQPPFVATETIYIMQSCWAFDSRKRPSFNLTSFLGCQLADAEEMYNQ 957
Db 901 FYKLQSGKMQPPFVATETIYIMQSCWAFDSRKRPSFNLTSFLGCQLADAEEMAC-- 957
QY 958 VDRVSECPTHYQNRPPFREMDELGLLSPQAOVE 991
Db 958 ----IRTSIHLKQAAPOQRG--GLRAQSPORQVK 986

RESULT 4

US-09-872-136-2

; Sequence 2, Application US/09872136

; Patent No. US20020119545A1

GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL RECEPTORS AND THEIR LIGANDS

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/872,136
FILING DATE: 01-Jun-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/208,786
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/021,324
FILING DATE: <Unknown>
APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992

APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991

ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-872-136-2

Query Match 84.0%; Score 4429.5; DB 10; Length 992;
Best Local Similarity 84.1%; Pred. No. 1.7e-288;
Matches 836; Conservative 57; Mismatches 90; Indels 11; Gaps 4;

QY 1 MPALA-RDAGTVPLLVVFGAMIFGTITNODLPVVKVLINKNNDSSVGKSSYPMVSES 59
Db 1 MPALAQRSDRRLLLVLSVMILETVNODLPVVKVLISHENNGSSAGPSSYRVRGS 60
QY 60 PEDLGCALRPQSSGTVYEAADVEVDVSASITLQVLVDAPGNISCLWVKHSSLNCPHF 119
Db 61 PEDLQCTPRQSGTVYEAATVEAESGSIITLQVLATPGDLSCLWVKHSSLCQPHFD 120
QY 120 LQNRGVVSVILKMTQTQAGEYLLFTQSEATNTILFTVSRINTLLYTLRPPFRKME 179

Db	121	LONGIYSMALNVTETQAGEYLLHIOSEBANYTLFTVNVRTQYLVRPYPFRXQEQ	180
Qy	180	DALVCISSEYPEVIEVWVLCDOSGESCKEBSPAVKKEKVLHELFGTDIRCCARNELCR	239
Db	181	DALLCISEGYPEPVIEVWVLCSHRESCKEGBPAVKKEKVLHELFGTDIRCCARNALCR	240
Qy	240	ECTRLFTIDLNQTPQTTLPOLFUKVGEPLWIRKCAVHVNHGFLGTWELENKALEEGNYPE	299
Db	241	ECTKLFTIDLNQAPQSTLPOLFUKVGEPLWIRKCAIHVNHGFLGTWELEDKALEEGSYPE	300
Qy	300	MSYVSTNRWTIRLLFAPVSSVARNDGYVYCSSSKHPSQSALVTIVKGFINATNSSEY	359
Db	301	MSYVSTNRWTIRLLAFVSSVGRNDGYVYCSSSKHPSQSALVTILKEGINATSSQEEY	360
Qy	360	EIDOEYEFCSVRFKAPQIRCTWTSRKSFPCEQKGLDNGYISIKFCHNHKGPGYIEFH	419
Db	361	EIDOPYEKFCSVRFKAPYRIRCTWIFSQA5FPCEQRLDGYISIKFCHKNKPGYIEY	420
Qy	420	AENDDAQFTKMFINTIRPKQVLAESASQA5CFSDGYPLPSWTWKCKSDK5PNCTEET	479
Db	421	AENDDAQFTKMFINTIRPKQVLANASQA5C5SDGYPLPSWTWKCKSDK5PNCTEEP	480
Qy	480	EGVWNKANKRVQGWYSSETLNM5SAIKGFLVKCCAYNSLGTSCETILLNSPGPEPFIQ	539
Db	481	EGVWNKANKRVQGWSSSTLNM5SAGKLLVKCCAYNSMGTSCTIFLNSPGPEPFIQ	540
Qy	540	DNISFYATIGVCLLFIYVLTLILCHYKKOFRYESQLQVQVTS5SDNEFYFYVDFREY	599
Db	541	DNISFYATIGLCPFIYVLVLIVLCHYKKOFRYESQLQVQVTS5PLDNEYFYVDFREY	600
Qy	600	DLKWEPPRENLEPKVLGSGAFKQVMNATAYGTSKTVSIOAVKMLKEKADSSREBALM	659
Db	601	DLKWEPPRENLEFKVLGSGAFGRVMNATAYGTSKTVSIOAVKMLKEKAD5CKEALM	660
Qy	660	SELKMWTLQSGHENIVNLGACLTSGPIYLIPEVCCVGDLLNLYRSKRKEPRTWTEIPK	719
Db	661	SELKMWTLGHNDIVNLGACLTSGPIYLIPEYCCVGDLLNLYRSKRKEPRTWTEIPK	720
Qy	720	EHNFSFYPTQSHPN5MPSREVQIHPDSQDLSGLHGNSFH5DEIEYENQKRL--BEE	777
Db	721	EHNFS5YPTFOAH5NSMPSREVQIHPDLPDLSGFGNGSIH5DEIEYENQKRLAEBEE	780
Qy	778	EDNLVITFEDLLCFAYQVAKGM5FLBPK5CVHRDLDARNVLVTHGKVKICDFGLARDIM	837
Db	781	EDNLVITFEDLLCFAYQVAKGM5FLBPK5CVHRDLDARNVLVTHGKVKICDFGLARDIL	840
Qy	838	SDNSYVVRGNARLPVKWMAPE5LFEGIYTIKSDVWSYGLILLMEIFSLGVNYPGIPVDAN	897
Db	841	SDSYVVRGNARLPVKWMAPE5LFEGIYTIKSDVWSYGLILLMEIFSLGVNYPGIPVDAN	900
Qy	898	FYKLIQNGFKMDQPFYATEBIYTIMOSCAFD5RKRKPSFPNLT5FLGCQLADAEAMYNQ	957
Db	901	FYKLIQSGFKMEQPFYATEGIYFVMO5CAFD5RKRKPSFPNLT5FLGCQLAEBEAC---	957
Qy	958	VDRGV5ECPHYQNRPPFR5MDLGLLSPOAQVE	991
Db	958	-----IRTSIHLPKQAAFPQORG--GLRAQSPORQVK	986

RESULT, T 5

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US-10-192-867-2
;
; Sequence 2, Application US/10192867
; Publication No. US2003008466A1
;
; GENERAL INFORMATION:
;
; APPLICANT: BLUME-JENSEN, Peter
;
; APPLICANT: HUNTER, Tony
;
; TITLE OF INVENTION: SYSTEM AND METHOD FOR CONTROLLING MALE FERTILITY
;
; FILE REFERENCE: SALKINS.002C1
;
; CURRENT APPLICATION NUMBER: US/10/192,867
;
; CURRENT FILING DATE: 2002-07-08
;
; PRIOR APPLICATION NUMBER: US 60/175,625
;
; 2000-01-11

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; PRIOR APPLICATION NUMBER: PCT/US01/00573
; 2001-01-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO 2
; LENGTH: 975
; TYPE: PR1
; ORGANISM: MUS MUSCULUS
US-10-192-867-2

Query Match          24.0%; Score 1266; DB_9; Length 975;
Best Local Similarity 33.2%; Pred. No. 1.2e-76;
Matches 336; Conservative 173; Mismatches 330; Indels 172; Gaps 41;

QY   35 CVLHNKNNDSVCKSSYPMVSESPEDLGALRPQSSGTYEAAAADVVSASITIQVL 94
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   12 CULLVLRGGTATSQSASGEPSPP-----SHPAQS-----ELIVEAGDTLL-- 54

QY   95 VDAPGNISCL-----WVKHSSLNCPHFDLQNRGVSMVILKMTTOAGEYLFIQSE 148
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   55 -----SLTCIDPDPRVRTFK-----TYFN-----EMVENKKNEWIQ-EKAE 89

QY   149 ATNYTLIPTSIRNTL-----LYLTRRPFYRKMNODALVCISESVPEPIVE 195
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   90 ATR-TGTYTCSNGLTSIIYFVRDPAPKLFLVGLPLFGK-EDSDALVRCPLTDPO-VSN 146

QY   196 WVLCDOSGESCKESPAV-----VKKEKVLIHELFGTDIRCARNELGRECTRL-- 244
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   147 YSLIECDGKSULTDITVPNPKGATIKNVKRAYHRLC---VRCAAQ----RDGTWLUSD 199

QY   245 -FTIDLNQ-----PQTLPQI---FLKYGEPLWIRCKAVHNHGFLTW-----E 286
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   200 KFTLKVREAIKAIPVSVPETSHLLKGDPTVVCTIKDVSTSVNSMWLKNWPOPQHIAQ 259

QY   287 LENKALEEGNYFMSTYSTWRMIRILFAFVSSVARNDTGYYTSCSKHPQSALVT--- 343
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   260 VKHNSWRHGDG---NYEROETLT-----ISSARVDGSGVFMCYANNTFGSANVTTLK 309

QY   344 IVKGFINATN-SSEDYEIDOEFEFCFSVRFKAYPO-IRCTWTFSRKSFFCEOKGLD--- 398
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   310 VVEKGFINISPVKNTTVFVTDGENVDLVBYEAYPKPEHOQMIMNKRT---SANKGRDYVK 367

QY   399 -NGVISISKFNCHKH-----QPGEYIFHAENDDAQTKMTNLIRKPOVLA--EASAS 448
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   368 SDNKSNIYVQLRLTRLKTEGGTYTFVLSNDSASVTFVYVNTKPELLIVDRLING 427

QY   449 QASCFSGYPLPWTKWKCKSDKSPNCTEEITE-GVNRRKANRKVFGQWVSSSTLNMSAI 507
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   428 MLQCVAEGFEPTIDWFYCTGAECQRCTTPVSVDVQVNVSVSPFGKLVVQSSIDS SVFR 487

QY   508 KGFLVKCCAVNSLGTSCETILLNSPGFPF---IQDN-----ISPATIGVCLLFIV 557
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   488 HNGTVECKANDVKGS--SAFFN----FAPKQIOAHTLFTPLLIGHVVAAGANGIIVMV 541

QY   558 LTLILICHKYKQFRYSLOQW-QVTGSSDNEYFYVDFREYEDLKWEPRENLEFGKVL 616
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   542 LT---XYILOKPMYEQWVVEING---NNVIYIDPTQLPYDHKWEPFNRNLSFGKTL 594

QY   617 GSAGFGKMVNATAYGISTGVSTQVAVMKLKEKADSSERREALMSELKMMTOLGSHENIVN 676
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   595 GAGAFGRWEATAYGLIKSDAAATVAVMKLKPSAHLTEREALMSELKVLSTYLCNMHNVN 654

QY   677 LLGACTLSGPILIYEFCCYCGDLLNVLRSKEXF-----HRTWEIFKHNHSFYPTFO 730
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   655 LLGACTVGGBPLVITYCCYCGDLLNFLRRKRDSFI FSKOEOEAALYKXNLLHSTEPSCD 714

QY   731 SHPNSSM---PGSREVOIHDPDSQISGLCHNSPHSEDEIEYENOKLEEBEDLNVLTFED 787
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   715 S-SNEYMMDKPGVSIV-VPTKTDKRSARDSY-----IERDVTYPAIMDEL-DLDLD 766

QY   788 LLCFAVOAKGMFEFLFKSCVHRDLAARNVLVTHGKVVKICDFGLARDINSDSNVYVRGN 847
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB   767 LLSFSYOAKAMAFKASKNCIHRDLAARNILLPHGITTKICDEFGIARDINDSNVYVKG 826

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Qy 848 ARLPVKWMAPESLPGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYKLIQNGPK 907
Db 827 ARLPVKWMAPESIFSCVYTFESDVMSYGIFLWELFSLGSSPYGPMVDKSFYKMIKEGFR 886
Qy 908 MDQPYVATEEIIYIIMQSCWAFSDSRKRPSPNLTSLFGCOLADAEAMYNQV 958
Db 887 MVSPEHAPAEYDMVKTCWDADPLKRPPTKQVVQVQLIEKQISDSTKHYSNL 937

RESULT 6
US-10-099-895-32
; Sequence 32, Application US/10099895
; Patent No. US2002017166A1
; GENERAL INFORMATION:
; APPLICANT: BERNDT, Michael C
; APPLICANT: STOMSKI, Frank C
; APPLICANT: LOPEZ, Angel F
; APPLICANT: GUTHRIDGE, Mark A
; TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR
; FILE REFERENCE: 3991/OK379
; CURRENT APPLICATION NUMBER: US/10/099,895
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/AU00/01118
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 32
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-099-895-32

Query Match 23.7%; Score 1251; DB 9; Length 976;
Best Local Similarity 32.7%; Pred. No. 1.2e-75;
Matches 324; Conservative 166; Mismatches 352; Indels 148; Gaps 34;

Qy 47 VKSSSYPMVSSPEDLGCALRPQSSGTVEAAAEVDVYSASITLQVLVDAPGNISCLW 106
Db 20 VOTGSSQPSVSPG-EPSPPSIHPKSDLI-----VRGDEIRLLCTDPPGVK--WT 67
Qy 107 FXHSSLNCQPHDLQNRGVVSVILKWTQAGEYLLFIQSEATN---YTILFTVSIRNT 163
Db 68 FE-----ILDETENKQNEWIT-EKAEATNTGKYCTNKHGLSNS 106
Qy 164 L-----LYTLRPFYFRKMNODALVCISSEVPEPIVWVLCDSQGSCKEE----- 209
Db 107 IYVVRDPAKFLVDRSLYCK-EDNTLVRCPLTDPE-VTNYSKGCQCKPLPKDLRFIP 164
Qy 210 ----SPAVVKEEKLHELFGTDIRCCARNELGRECTRLFTIDL----NQTPQTLPQ--L 260
Db 165 DPKAGIMIKSVKRAYHRLC---LHCSVDQBGKSVLSEKFLKVRPAKAVPVVSVSKASY 221
Qy 261 FLKVGEPILRCKAVNVHGFGLTWLEN---KALEEGNYFEMSTYSTNPTMIRILPAFV 317
Db 222 LLREGSEFTVCTIKDVSSSVSTKRENSQTKLQEKYNSWHHGFDFNYERQAT-----LTI 277
Qy 318 SSVARNDTGYTCSSSKHPSQSALVT---IVGKGFINA-----TNSSEYEDIQYE 365
Db 278 SSARVNDSGVFMFCYANNITGSAVNTTILEVVDKGFINIPMINTTVFVNDGENVDL---- 333
Qy 366 EPCFSVRFKAYPO-ICTWTFRSKSP--PCEQKGLONGYISIFCNHKL-----OPGE 415
Db 334 ----IVEVEAFKPEHQOQIMYNNRTFTDKWEDYPKSESNIRYVSELHLTRLKGTGGT 389
Qy 416 YIFHAENDAAQFTKMTLAIIRRPQVLA---EASASQASCFSDGVPPLPSWTWKCSKSPN 473
Db 390 YTFVLSNDSVNAIAFNVVYNTPEILTYDRLVNGMLQCVAAGFPPEPTIDWYFCPGTEQR 449
Qy 474 CTBEITE-GVNNRKNRKFQGVWSSSTLANSBAIKGFLVKCAYNSLGTSCETILLNSP 532
Db 450 CSASVLVDVQTLNNSGPPFGKLVQSSIDSASFANGKINGTVECKAYNDVGKT--SAYFN-- 505
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Qy 533 GPFPFIQDN-----ISFYATIGVCLLFIIVVLTLLICHKYKKOFRYSQLOM 578
Db 506 --FAFGKNGKQIHPHTLFTPLLIGFVIVAGMCIIVMLT-----YKLOKQMEYQWKV 559
Qy 579 V-QVTSSDNSEYFYVDREYEDLKWEPFRENLEFGKVLGSGAFKQWMTATAYGISKTV 637
Db 560 VEEING---NNYVIDPTQLPYDHKEWEPFNRNLSFGKTLGAGAFGVVEATAYGLIKSDA 616
Qy 638 STOVAVKMLKEKADSSEREALMSLKMMTQOLGSHENIVNLLGACTLSGPIYLIFEYCCY 697
Db 617 AMTVAVKMLKPSAHLTEREALMSLKVLISYLGNNHWNIVNLLGACTLGGTTLVITECCY 676
Qy 698 DLLNLYLRKREKFRHTWTE-----IFKEHNFSPYPTFOSHPNSSM---PGSREVOIHED 748
Db 677 DLLNFERKRDSDFCISKQEDHAAALYKNLLHSESSCSDSTNEYMDMPGVSYV-VPTK 735
Qy 749 SDQISGLHSGNSPHSEDEIEYENQKLEBEDLNVTTFEDLLCFAYQVAKGMFLEFKSCV 808
Db 736 ADKRRSVRIGSY-----IERDVTPAIMDEDEL-ALDLELLSFSYQVAKGMFLASKNCI 789
Qy 809 HRDLAARNVLVTHGVKVICDFGLARDIMSDSNVYVGRNARLPVKWMAPESLPEGIYTIK 868
Db 790 HRDLAARNILLTHGRITTKICDFGLARDIKDSDNYVYVGNARLPVKWMAPESEIFNCVY 849
Qy 869 SDVWSYGILLWEIFSLGVNYPGIPVDANFYKLIQNGFKMDOPFYATEEIIYIIMQSCWAF 928
Db 850 SDVWSYGIFLWELFSLGSSPYGPMVDKSFYKMIKEGFRMLSPHEHAPAEYDMIMKTCWDA 909
Qy 929 DSRKRPSPFNLTSLFGCOLADAEAMYNQV 958
Db 910 DPLKRPPTFKQIVQLIEKQISESTNHIYSNL 939

RESULT 7
US-10-192-867-4
; Sequence 4, Application US/10192867
; Publication No. US20030084466A1
; GENERAL INFORMATION:
; APPLICANT: BLUME-JENSEN, Peter
; APPLICANT: HUNTER, Tony
; TITLE OF INVENTION: SYSTEM AND METHOD FOR CONTROLLING MALE FERTILITY
; FILE REFERENCE: SALKINS.002C1
; CURRENT APPLICATION NUMBER: US/10/192,867
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: US 60/175,625
; PRIOR APPLICATION NUMBER: PCT/US01/00573
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 976
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-192-867-4

Query Match 23.7%; Score 1251; DB 9; Length 976;
Best Local Similarity 32.7%; Pred. No. 1.2e-75;
Matches 324; Conservative 166; Mismatches 352; Indels 148; Gaps 34;

Qy 47 VKSSSYPMVSSPEDLGCALRPQSSGTVEAAAEVDVYSASITLQVLVDAPGNISCLW 106
Db 20 VOTGSSQPSVSPG-EPSPPSIHPKSDLI-----VRGDEIRLLCTDPPGVK--WT 67
Qy 107 FXHSSLNCQPHDLQNRGVVSVILKWTQAGEYLLFIQSEATN---YTILFTVSIRNT 163
Db 68 FE-----ILDETENKQNEWIT-EKAEATNTGKYCTNKHGLSNS 106
Qy 164 L-----LYTLRPFYFRKMNODALVCISSEVPEPIVWVLCDSQGSCKEE----- 209
Db 107 IYVVRDPAKFLVDRSLYCK-EDNTLVRCPLTDPE-VTNYSKGCQCKPLPKDLRFIP 164
Qy 210 ----SPAVVKEEKLHELFGTDIRCCARNELGRECTRLFTIDL----NQTPQTLPQ--L 260
Db 165 DPKAGIMIKSVKRAYHRLC---LHCSVDQBGKSVLSEKFLKVRPAKAVPVVSVSKASY 221
Qy 261 FLKVGEPILRCKAVNVHGFGLTWLEN---KALEEGNYFEMSTYSTNPTMIRILPAFV 317
Db 222 LLREGSEFTVCTIKDVSSSVSTKRENSQTKLQEKYNSWHHGFDFNYERQAT-----LTI 277
Qy 318 SSVARNDTGYTCSSSKHPSQSALVT---IVGKGFINA-----TNSSEYEDIQYE 365
Db 278 SSARVNDSGVFMFCYANNITGSAVNTTILEVVDKGFINIPMINTTVFVNDGENVDL---- 333
Qy 366 EPCFSVRFKAYPO-ICTWTFRSKSP--PCEQKGLONGYISIFCNHKL-----OPGE 415
Db 334 ----IVEVEAFKPEHQOQIMYNNRTFTDKWEDYPKSESNIRYVSELHLTRLKGTGGT 389
Qy 416 YIFHAENDAAQFTKMTLAIIRRPQVLA---EASASQASCFSDGVPPLPSWTWKCSKSPN 473
Db 390 YTFVLSNDSVNAIAFNVVYNTPEILTYDRLVNGMLQCVAAGFPPEPTIDWYFCPGTEQR 449
Qy 474 CTBEITE-GVNNRKNRKFQGVWSSSTLANSBAIKGFLVKCAYNSLGTSCETILLNSP 532
Db 450 CSASVLVDVQTLNNSGPPFGKLVQSSIDSASFANGKINGTVECKAYNDVGKT--SAYFN-- 505
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Db 165 DPKAGIMIKSVKRAYHRLC---LHCSVDQEGKSVLSEKFLKVRPAKAVPVVSVSKASY 221
Qy 261 FLKVGEPMLIRKAVVNHGFLTWLEN---KALBEGNYFEMSTYSTNRTMIRILPAFV 317
Db 222 LLREGEFTVCTIKDVSSSVYSTKRENSQTLQEKYNSWHHGDYFNERQAT---LTI 277
Qy 318 SSVARNDTGYTCSSSKHPSQSALVT---IVGKGFNA-----TNSSEDEYIDOYE 365
Db 278 SSARNVDSGVFWYANNTGSAVNTTILEVVDKGFNIFPMINTVTFVNDGENVDL--- 333
Qy 366 EFCFSVRKAYPO-IRCTWTFRSKF--PCEQKGLDNGYSISKFCNHK-----QPGE 415
Db 334 ----IVEYEAFKPEHQOIMYNRTTDFKWDYPKSENEINIRYVSELHLTRLKGTGGT 389
Qy 416 YLFAENDAOFTQMTLIRKPOVLA--EASASQASCFSDGYPLPSWTWKCSKSPN 473
Db 390 YTLVNSDVNAIAFNVVYNTKPEILTYDLRVNGLQCVAAQFPPEPTIDYFCPGTEQR 449
Qy 474 CTEETE-CVMNRKANRKYFGOWSSSTLNMSAIGFLVKCCAYNSLGTSCETILLNSP 532
Db 450 CSASLPVVDQTLNNSGPPFGKLVQSSIDSSAFKNGTVECKAYINDVGT--SAYFN-- 505
Qy 533 GPFPTQDN-----ISFVATIGVCLLFIVLVTLILCHIKKQFYESQLOM 578
Db 506 --FAFGANKEQIHPHTLPTLLIGFVIVAGVMCIIVILT---YKLOKPMYEQWKV 559
Qy 579 V-OVTGSSONEYVDREYEDLKWEPRENLEFGKVLGSGAFGKVMNATAYGISKTGV 637
Db 560 VEEING--NNYVYIDPTQLPYDHKWEFPNRLSFGKTLGAGAFKVEATAYGLIKSDA 616
Qy 638 STQAVKMKLEKADSSERALSSELKQMTOLGSHENIVNLLGACTLSGPIYLIFFECYCG 697
Db 617 AMTAVKMLKPSAHLTEREALMSLVLYLGNHMINVLLGACTIGGPTLVITEYCCYG 676
Qy 698 DLLNLVRSKREKFRHTWTE-----IFKEHNFSTYTFQSHPNSSM---PGSREVOIHPD 748
Db 677 DLLNLFRRKRDSCQEDHAEALYKMLLHSEKSCSDSTNEYMDMKPGVSIV-VPTK 735
Qy 749 SQOISGLHNSHSEDEIEYENOKRLEEEDNLVLTEDLLCFAYQVAKMEFLFKSCV 808
Db 736 ADKRSVRIGSY-----IERDVTPIAMEDDEL-ALDIEDLLSFYSQVAKMAFLSKNCI 789
Qy 809 HRDLAARNVLVTHGKVKICDFGLARDIMSDSNVYVRGNARLPVKWMAPELFEGIYTK 868
Db 790 HRDLAARNLLTHGRITKICDFGLARDIKNDSNYVYVGNARLPVKWMAPESEIFCYTTE 849
Qy 869 SDVWSYGILLWEIFSLGVNYPGIPVDANFYKLIQNGFKMDQPFYATEEYIIMQSCWAF 928
Db 850 SDVWSYGIFLWELFSLGSSPYGMPVDKSFYKMIKEGFRMLSPHAPAEYDIMKTCWDA 909
Qy 929 DSRKPSFPNLTSLFGLCQCLADAEAMQNV 958
Db 910 DPLKPTFKQIQLIEKQISESTNHIYSNL 939

RESULT 8

US-09-944-807-10
; Sequence 10, Application US/09944807
; Patent No. US2002011949A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082_00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10

; LENGTH: 972
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-944-807-10

Query Match 23.1%; Score 1216.5; DB 10; Length 972;
Best Local Similarity 32.8%; Pred. No. 2.5e-73;
Matches 325; Conservative 156; Mismatches 316; Indels 195; Gaps 33;

Qy 75 VYEAAVEVDV--SASITQLVLDAPGNISCLWFKHSLNCOPHFLQNRGVVSMWLK 132
Db 22 VIEPSVPELVKFGATVTLRCV---GNGSVWDGPPS-----PHMTLYSDGSSILSTN 72
Qy 133 MTE-----TOAGEYL-----LFIQSEATNTILFTVSIIRNTLLTLRPPYFRKM 176
Db 73 NATFQNTGYRCTEPGDPGLGSAIHLIVKDPARPNNVL-----AQEVVVF----- 118
Qy 177 ENODALV-CISESVPEPIVEMWLCDQSGESCKEESPAVVKKEK-----VLHE--- 223
Db 119 EDODALLPCL---LTDPVLE-----AGSLVVRGRPLMRHTNYSFSPWHGFTIHRAKF 169
Qy 224 LFTDTRCARNELGRECTRLFTIDLNQTPQTLT-----QLFLKVGEPMLTRCK 273
Db 170 IQSODYQCSALMG-GR---KWSISIRLKVKQVIPGPPALTLPVPAELVLRIGEAAQIVCS 225
Qy 274 AVHNVHGFLTWELNKALEEGNYFEMSTYSTNRTMIRILFAFVSSVARNDTGYTTCSS 333
Db 226 ASSVDYVDFVLOHNNTKLA---IPOQSDPHNNRYQ-KVLTLLNDQVDFOHAGNYSVAS 281
Qy 334 ---KHPQSALVTIVGKGFINATNSSED---YEIDQYEEFCFSVRKAYPOIR-CTWTF 385
Db 282 NVGKHI-STSMFRVVEYAYLNL--SSEQNLIOEVTVGEGLNLKMWVEAIPGLOCFNWTY 338
Qy 386 SRKSFCEQKGLDNGYSISKFCNHKQP-----GYEIF 418
Db 339 -----LGPFSHQPEKPLANATTQTYRHTFTLSLPLKPSAGRYSF 381
Qy 419 HAENDAOQTKMFTLINRKPOVLAEASQAS-----CFSDGYPLPSWTWKKSDKSPNC 474
Db 382 LARNPGMRALTFELTRYPEVSVIWTFTINGSGTLTCAASGYPOPNVTWLQCSGHTDRC 441
Qy 475 TEEITEGVN---RKANRKYFGOWSSSTLNMSAIGFLVKCCAYNSLGTSCETILLN 530
Db 442 DEAQVLQVDDPYPEVLSQEPFHKTVTQSLLTVEHNOTYECRAHNSVSGSSWAFPI 501
Qy 531 SPGPFPIQDNISFYATIGVC---LLFIVVLTLLICHYKKQFYESQLOMVQVTSDDN 587
Db 502 SAGATHPPDEFLFTPVVVACHSIMALLLLLLLYKKQKPKYQVRWKIIE--SYEGN 559
Qy 588 EYFYVDFREYEDLKWEPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIOQAVKMLK 647
Db 560 SYTFIDPTQLPYNEKWEFPNRLNLOFGKTLGAGAFKVEATAFGLGKEDAVLKVAVKMLK 619
Qy 648 EKADSSERALSSELKQMTOLGSHENIVNLLGACTLSGPIYLIFFECYCGDILLNLSKR 707
Db 620 STAHADKEALMSSELKIMSHLGOHENIVNLLGACTGGPVLVITEYCCYGDLLNFLRKA 679
Qy 708 E-----KFRHTWTEIFKEHNFSTYTFQSHPNSSMPGSRVQIHP 747
Db 680 EAMLGPSLSPGQDPGCVDYKNIHLEKKVVRDSGSF-----SQGVDTYV 724
Qy 748 DSDQISGLHNSHSEDEIEYENOKRLEEEDNLVLTEDLLCFAYQVAKMEFLFKSC 807
Db 725 EMRPVSTNSDSF-SEQDLKDGRPLE-----LRDLLHFSQVAGMAFLASKNC 774
Qy 808 VHRDLAARNVLVTHGKVKICDFGLARDIMSDSNVYVRGNARLPVKWMAPESEFEGIYTI 867
Db 775 IHRDVAARNVLLTNGHVAKIGDFGLARDIMSDSNVYVGNARLPVKWMAPESEIFDCVYV 834
Qy 868 KSDVWSYGILLWEIFSLGVNYPGIPVDANFYKLIQNGFKMDQPFYATEEYIIMQSCWA 927
Db 835 QSDVWSYGILLWEIFSLGILNYPGILVNSKIFYKLVDKQYQMAQPAFAPKNIYSIMOACWA 894

Qy 928 FDSRKRPSPFNLTSTFLGCQL-ADAEEMYQN^V 958
:
Dp 895 LEPTHRPTEFOOICSFLOEOAOCEDRRERDYTNL 926

RESULT. T 9

```

US-09-961-403-4
; Sequence 4, Application US/09961403
; Publication No. US20030077589A1
; GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLT
; APPLICANT: WINTERHAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTTI, SIMONE
; TITLE OF INVENTION: METHOD FOR IN VITRO D
; FILE REFERENCE: SCH-1789
; CURRENT APPLICATION NUMBER: US/09/961,403
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-403-4

```

Query Match	22.1%	Score 1166.5;	DB 9;	Length 1088;
Best Local Similarity	30.4%	Pred. No. 6.3e-70;		
Matches 336;	Conservative 165;	Mismatches 365;	Indels 241;	Gaps 36;

Qy	12	PLLVFSAMIFG--TITNQDLPIV-----KCVLINHKNNSSVGKSS-----SYPMVSES	59
Db	6	PAFLVLGLLTGLSLILCOLSLILPENEKVVQLNSSFSLRCFGESEVSWQYPMSEE	65
Qy	60	PEDLGICALRPQSSG--TVVEAAAVEVDVSASITLQVLVDAPGNTSCLWFKVHSHLNCOP	116
Db	66	SSDVETRIEENNSGLFVTVLEVSS-----ASAHT-----GLTYCYNNHTQTEEN---	110
Qy	117	HFPLQNRGV-----VSMVILKMTETOAGEYLLFIQSEATNYTILFTVSIIRNTLLVTL	168
Db	111	--ELEGRHIVYVDPDPAFVPLGMT-----DYLIVIVE-----	141
Qy	169	RRPYFRXNENQDALVCISEVPPVEVWVLCDSQG-----ESCKE	208
Db	142	-----DDCSAIIPCRTTDPETPV--TLHNSGVPVPSYDSRQFNGCTFTVGPYIC--	189
Qy	209	ESPAVVKKEKVLHELPGTDIRCCARNELGRECTRLFTTILDLNQTPTTLPQLFVKVGRPL	268
Db	190	EATVKGKKFQTIIPFNVALK-----ATSELDLEWALKTV-----YKSGETI	231
Qy	269	WIRCKAVHVNHGFLTW-----ELENKA---LEEGNYFEMSTYSTNRTMIRILFAF-VSSV	320
Db	232	VVTC-AVFENNEVDLQWTPGEVKGKGIWLEB-----IKVPSIKLVTVTLTVEA	280
Qy	321	ARNDTGYTCSKK-----HPSOSALVTIVKGKFINATNSEDYE-IDOYEFECFSVRFK	374
Db	281	TVKDSGDGYECAAQATREVAKEMKKVTISVHEKGFBIKPTFSOLEAVNLIHVKHFVFEVR	340
Qy	375	AYPOICRTWTFSRKSFPCEQKGLDNGYSI-----KFCNHKHO-PGEYIF	418
Db	341	AYPPPRISLWKNLUTL-----IENLTETTDVEKIQEIRYSKULIIRAKEDSGHYTI	394
Qy	419	HAENDDAQTKMFTLINIRRKPOVL-----ABASASQSCFSDGYPLPSWTWKCSDKS	471
Db	395	VAQNEDAVKSVTFELLTQVPSSILDLVDDHHGTTGGQTVRCRTAEGTLPDIEWMICKD-I	453
Qy	472	PNCTEETTEGVWNRKANRKYFGQWVS-----STLANSBAIKFLVKCCAY	517
Db	454	KKCNNETS--WTLIANN-----VSNIIITEHSRDRSTVEGRVTFEAKVEETIAVRCLAK	504

REFERENCE/DOCKET NUMBER: 990008.446C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-955-363-36

Query Match 22.1%; Score 1166; DB 9; Length 1089;
Best Local Similarity 30.3%; Pred. No. 6.8e-70;
Matches 336; Conservative 165; Mismatches 365; Indels 242; Gaps 36;
QY 12 PLLVFSAMIFG---TITNQLPVI-----KCVLINHKNDSSVGKSS---SYPMVSES 59
DB 6 PAFVLGCLLTGLSLILCOLSILPNEKVVQLNSFSRLCFGESEVSWQYPMSEEE 65
QY 60 PEDLGCALRPQSSG---TVYEAADVDSASITLQVLVDAPGNISCLWVFKHSLNCQP 116
DB 66 SSDVEIRNEENSGLFVTVLVSS---ASAHT-----GLYTCYNNHTQTEEN--- 110
QY 117 HFDLQNRGV-----VSMVILKMTETQAGEYLLFIQSEATNYTILFTVSIRNTLLYTL 168
DB 111 --ELEGRIHYIYVDPDPAFVPLGWT-----DYLIVVE----- 141
QY 169 RRPYFRKMENQDALVCISESVPEPIVWVLCDSQG-----ESCKE 208
DB 142 -----DDDSAIIPCRITTDPTPV--TLHNSGVVPASVDSRQGFNGFTVGPYIC-- 189
QY 209 ESPAVVKEEKVHELPGTDIRCCARNELGECRLTIDLNQTPQTLQFLKVGEP 268
DB 190 EATVKGKKFQITPNNVYALK--ATSELDLEMAKTV-----YKSGETI 231
QY 269 WIRCKAVHVNHGFLTW-----ELENKA--LEEGNYFEMSTYSTNRTMIRILFAF-VSSV 320
DB 232 VVTC-AVFNNVVDLQWYGEVKGKGITILEE-----IKVPSIKLIVTLTVPEA 280
QY 321 ARNDTGYTCSSK-----HPSQALVTIVGKGFINATNSSEDE-IDQYEEFCFSVRFK 374
DB 281 TVKSDGYECAARQATREVEMKKTIVSVEHKGFIETKPTFSQLEAVNLHEVHFVVEVR 340
QY 375 AYPQIRCTWTFSRKSPCEOKGLDNGVIS-----KFCNKHQ-PGEYIF 418
DB 341 AYPPIPRISLKNLTL-----IENLTETTDVEKIOEIRYRSKLILIRAKEEDSGHYTI 394
QY 419 HAENDDAQFTKMTLIRKPOVL-----AEASASQASCFSDGYPLPSWTWKCKSDKS 471
DB 395 VAQNEADVKSFTFELLTQVPSSILDLVDHGHSTGGQTVRECTAGTLPDPIEWICKD-I 453
QY 472 PNCTEITEGVWNRKANRVFGOWSS-----STLNMSEAIKGLVKKCAV 517
DB 454 KCKNNETS---WTILANN-----VSNILTEIHSRDRSTVEGRVTFKAVETIAVRLAK 504
QY 518 NSLGTSCETILNSPGFPFIQNIISFYATIGVCLLFIIVVLTLLIHKYKKQFYESQLQ 577
DB 505 NLLGAENRELKLV-----PTLSRELVAARVLLVIVLIVVIVVWVWVWVWVWVWVWV 560
QY 578 MYQVGTSSDNEYFYVDREYVDLKEFFRENLEFGKVLGSGAGFKVMNATAGISKTGV 637
DB 561 VTESTSPDGEHYIYVDPMLQPLDSRVEFRDGLVGLVSGAGFKVVEGTAYGLRSQP 620
QY 638 SIQVAVKMLKADSSERELMSKMTQOLGSHENIVNLLGACTLSGPTYLIFEYCCYG 697
DB 621 VMKVAVKMLKPTARSEKQALMSKIMTHLGLPHLIVNLLGACTSGPIIITEYCFYG 680
QY 698 DLLNLYRSKREKF-----HRTWTEIFKEHNFSFYPTFOSHNP 734
DB 681 DLVNVLHKNRDSFLSHHPEKPKKELDI FGLNPADESTRSVILSFFENNGDYMDMKADIT 740

QY 735 SSMPGSRVQIHPDSDDTISGLHGN--SPHSEDEIEYENQKLEEBEDLNVLTFFDLCLCA 792
DB 741 QYVPMLEKESKYSYDIQSLYDRPASVKKKSMLDSE-VKNLLSDNSEGLTLLDLLSFT 799
QY 793 YQVAKGMEFLFEKSCVHRDLAARNVLYTHGKVVKICDFGLARDIMSDSNVYVGRNARLPV 852
DB 800 YQVARGMEFLASKCNVHRDLAARNVLLAQQKIVKICDFGLARDIMHDSNYSYKSGSTFLPV 859
QY 853 KWMAPESLEFEGIVTIKSDVMSYGILLWEIFSLGVNVPYIGIPVDANFYKLIQNGFKMDQPF 912
DB 860 KWMAPESIFDNLYTTLSDVMSYGILLWEIFSLGGTTPYFGMVVDSTFYNKIKSGYRMAKPD 919
QY 913 YATEEIIYIMOSWAFDSRKRPSFNLTSFLGCOLADAEAEAMYQNV--DGRVSECPH--- 967
DB 920 HATSEVEIIMVKWNSPEKRPSEYHLSEIVENLLPGQYKKSIEKIHLDFLKSDHPAVAR 979
QY 968 -----TYQNRPRPFSREMDLGL 983
DB 980 MRVSDNAYIGVTYKNEEDKLKDWEGGL 1007

RESULT 11

US-09-769-987-2
; Sequence 2, Application US/09769987
; Patent No. US20020055129A1
; GENERAL INFORMATION:
; APPLICANT: Matsui, Toshimitsu
; APPLICANT: Aaronson, Stuart A.
; TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Recept.
; FILE REFERENCE: 14014.0266U2
; CURRENT APPLICATION NUMBER: US/09/769,987
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 08/460,656
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: US 08/439,095
; PRIOR FILING DATE: 1995-05-11
; PRIOR APPLICATION NUMBER: US 07/915,884
; PRIOR FILING DATE: 1992-07-20
; PRIOR APPLICATION NUMBER: US 07/308,282
; PRIOR FILING DATE: 1989-02-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. US20020055129A1e =
; OTHER INFORMATION: synthetic construct
US-09-769-987-2

Query Match 22.1%; Score 1166; DB 10; Length 1089;
Best Local Similarity 30.3%; Pred. No. 6.8e-70;
Matches 336; Conservative 165; Mismatches 365; Indels 242; Gaps 36;

QY 12 PLLVFSAMIFG---TITNQLPVI-----KCVLINHKNDSSVGKSS---SYPMVSES 59
DB 6 PAFVLGCLLTGLSLILCOLSILPNEKVVQLNSFSRLCFGESEVSWQYPMSEEE 65
QY 60 PEDLGCALRPQSSG---TVYEAADVDSASITLQVLVDAPGNISCLWVFKHSLNCQP 116
DB 66 SSDVEIRNEENSGLFVTVLVSS---ASAHT-----GLYTCYNNHTQTEEN--- 110
QY 117 HFDLQNRGV-----VSMVILKMTETQAGEYLLFIQSEATNYTILFTVSIRNTLLYTL 168
DB 111 --ELEGRIHYIYVDPDPAFVPLGWT-----DYLIVVE----- 141
QY 169 RRPYFRKMENQDALVCISESVPEPIVWVLCDSQG-----ESCKE 208
DB 142 -----DDDSAIIPCRITTDPTPV--TLHNSGVVPASVDSRQGFNGFTVGPYIC-- 189

Qy	209	ESPAVWKEEKVJHELFGTDIRCARNELGRCTRULTIDLNQTPOTTLPOULFKVGEPL	266
Db	190	EATVKGKFQIPENVYALK-----ATSELDLEALKTV-----YKSGETI	231
Qy	269	WIRCKAVVHVHGFCLTW-----ELENKA---LESGNYFEMSTYSTNRTMIRLLPAP-VSSV	320
Db	232	VVTC-AVFNEVVDLQWYTPGEVKGIGITMLEE-----IKVPSIKLVITLTPBA	280
Qy	321	ARNDTGYTCSKK-----HPSOSALVTIIVKGCFINATNSSDEYE-IDQVEBFCFSVREK	374
Db	281	TVKDSGDEYCAARQATREVEMKVTISVHKEGFIEIKPTFSQLEAVNLHVKGHFVVR	340
Qy	375	AYPOIRCTWTFSRKSPCEBQKGLDNGVSIIS-----KFCNHQHQ-POEYIP	418
Db	341	AYPPRISWLKNLTL-----IENLTEITTDVEKIOEIRYSKLLIRAKEEDSGHYTI	394
Qy	419	HAENDDAQFTMTFNTIRKPOVL-----ASASASQACSPSDGVPPLPSWTWKKCSDKS	471
Db	395	VAQMEDAVKSYTFELLTQVPSISLDLVDHHDHSGTGGQTVRCRTAEGTFLPDIEHMI	453
Qy	472	PNCTEETITEGVNRRKANRKVFGQWVS-----STLNMSAIIKGLVVKCCAY	517
Db	454	KCKNNETS-----WTLANN-----VSMIITEHSRRDSTVEGRVTFAKVEETIANRCLAK	504
Qy	518	NSLGTSETILLNSPGFPPTQDNISFYATIGVCLLFIIVVLTLLICHKYKQPRYESOLQ	577
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Db	561	VIESISPDGHEYIYVDPWQLPDSRWEPFRDGLVGLRVLGSGAFGKVVEGTAYGLSRSQP	620
Qy	638	SIQVAVKMLKEKADSSREALMSELKMTOLGSHENTVNLGACTLSGPTIYLIFEXCCYG	697
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Qy	735	SSMPGSRVQIHPDSDQISGLHGN---SFHSEDEIEYENQKRLBEEDLNVLTPEDDLCPA	792
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Qy	853	KWMAPESIPEGIYTIKSDVMVSYGILLWEIISLGVNRPYGPIDVAFNYKLIQNGFKMDQPF	912
Db	860	KWMAPEISIFDNLVITYLSDVMVSYGILLWEIISLGGTTPYGMWVDSTFYNKIKSGIRMAKPD	919
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RESULT 12

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; Patent No. US2002010662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
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; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-90

Query Match      22.1%   Score 1166;   DB 10;   Length 1089;
Best Local Similarity 30.3%;   Pred. No. 6.8e-70;
Matches 336;   Conservative 165;   Mismatches 365;   Indels 242;   Gaps 36;

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Db 980 MRVDSDNAYIGVYKNEEDKLDWEGGL 1007

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Job time : 45.0207 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 16:54:10 Search time 14.0071 Seconds
(without alignments)
2085.875 Million cell updates/sec

Title: US-09-919-408-4

Perfect score: 5274

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Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5274	100.0	993	1	US-08-252-517-4
3	5274	100.0	993	1	US-07-906-397A-4
4	5274	100.0	993	1	US-08-601-891-4
5	5274	100.0	993	2	US-09-021-324-4
6	5274	100.0	993	5	PCT-US92-09893-4
7	5274	100.0	1160	5	PCT-US92-05401-4
8	5240	99.4	993	1	US-08-222-299-4
9	5240	99.4	993	2	US-08-434-878-4
10	5238	99.3	993	5	PCT-US95-03718-4
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12	5238	99.3	993	5	PCT-US95-00176A-2
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29 1216.5 23.1 972 3 US-08-750-141A-2 Sequence 2, Appli
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31 1166 22.1 1089 1 US-08-168-917-4 Sequence 4, Appli
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36 1166 22.1 1089 3 US-08-980-400-36 Sequence 36, Appli
37 1166 22.1 1089 3 US-08-462-728-2 Sequence 2, Appli
38 1166 22.1 1089 4 US-09-583-459A-36 Sequence 36, Appli
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43 1166 22.1 1089 5 PCT-US92-00730-4 Sequence 4, Appli
44 1166 22.1 1089 5 PCT-US92-00862-4 Sequence 4, Appli
45 1086.5 20.6 1106 1 US-08-180-195-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-07-977-451-4
; Sequence 4, Application US/07977451
; Patent No. 5270458
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 19921119
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US UNASSIGNED
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-977-451-4

Query Match 100.0%; Score 5274; DB 1; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 961 RVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 993

RESULT 2
US-08-252-517-4
; Sequence 4, Application US/08252517
; Patent No. 5548065
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,517
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,451
; FILING DATE: 19-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-517-4

Query Match 100.0%; Score 5274; DB 1; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 901 LIQNGFKNDQPPYATBEIYIIMOSWAFDSRKRPSFNLTSFLGCCOLADAEAMYNQVNDG 960
DB 901 LIQNGFKNDQPPYATBEIYIIMOSWAFDSRKRPSFNLTSFLGCCOLADAEAMYNQVNDG 960

QY 961 RVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 993
DB 961 RVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 993

RESULT 3
US-07-906-397A-4
Sequence 4, Application US/07906397A
Patent No. 5621090
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,397A
FILING DATE: 19920626
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPPPPP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-906-397A-4

Query Match 100.0%; Score 5274; DB 1; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPALARDAGTVPLLVVFSAMIFGTITNODLPVTKCVLINHKNDSSVGKSSSYPMVSESP 60
DB 1 MPALARDAGTVPLLVVFSAMIFGTITNODLPVTKCVLINHKNDSSVGKSSSYPMVSESP 60

QY 61 EDLGCALRPOSSGTVEAAAVEVDVSASITLQVLVDAPGNISCLWVPKHSLSLNCQPHFDL 120

Db 61 EDLGCALRPOSSGCTVVEAAAEVVDVSASITLQVLVDAPGNISCLWFKHSSLNCQPHFDL 120
Qy 121 QNRGVVSVMLKMTQAGEYLLFTQSEATNTYTLFTVSIIRNTLLYTLRRPYFRKMENQD 180
Db 121 QNRGVVSVMLKMTQAGEYLLFTQSEATNTYTLFTVSIIRNTLLYTLRRPYFRKMENQD 180
Qy 181 ALVCISESVPEIIVWVLCDGSCGCKESPAVVKKEKVLHFGTDIRCCARNELGRE 240
Db 181 ALVCISESVPEIIVWVLCDGSCGCKESPAVVKKEKVLHFGTDIRCCARNELGRE 240
Qy 241 CTRLFTDLNQPOTTLPOLFLKVGEPWLIRCKAVHVNHGPGLTWELNKALEEGNYFEM 300
Db 241 CTRLFTDLNQPOTTLPOLFLKVGEPWLIRCKAVHVNHGPGLTWELNKALEEGNYFEM 300
Qy 301 STYSTNRTMIRILPAFVSSVANDGYTCSSSKHPSQSALVTIIVKGINATNSSEDE 360
Db 301 STYSTNRTMIRILPAFVSSVANDGYTCSSSKHPSQSALVTIIVKGINATNSSEDE 360
Qy 361 IDQYEEFCFVRPKAYPQIRCTWTFSRKSFPCEQKGLDNGYISIKPCNKHQPGGEYIFHA 420
Db 361 IDQYEEFCFVRPKAYPQIRCTWTFSRKSFPCEQKGLDNGYISIKPCNKHQPGGEYIFHA 420
Qy 421 ENDDAQFTKMFTLIRRKQVLAESAASQSCFSDGYPLPSWTWKCSKSPNCTEEITE 480
Db 421 ENDDAQFTKMFTLIRRKQVLAESAASQSCFSDGYPLPSWTWKCSKSPNCTEEITE 480
Qy 481 GWNKKAIRKVPQGVSSSTLNKSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Db 481 GWNKKAIRKVPQGVSSSTLNKSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Qy 541 NISFYATTGVCLLFTVLTLILCHYKKQFRIESQLOQVQVGTSSDNEYFYVDREYED 600
Db 541 NISFYATTGVCLLFTVLTLILCHYKKQFRIESQLOQVQVGTSSDNEYFYVDREYED 600
Qy 601 LKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTVSIOQVAKMLKEKADSSEREALMS 660
Db 601 LKWEPPRENLEFGKVLGSGAFGKVMNATAYGISKTVSIOQVAKMLKEKADSSEREALMS 660
Qy 661 ELKMMTOLGSHENIIVNLLGACTLSGPIYLIPEYCCYGDLLNLYLSKREKPHRTWTBIFKE 720
Db 661 ELKMMTOLGSHENIIVNLLGACTLSGPIYLIPEYCCYGDLLNLYLSKREKPHRTWTBIFKE 720
Qy 721 HNFSPYPTFQSHPNSSMPCSRVQIHPDSDQISGLHNSFHSDEDEIYENOKRLEEEEDL 780
Db 721 HNFSPYPTFQSHPNSSMPCSRVQIHPDSDQISGLHNSFHSDEDEIYENOKRLEEEEDL 780
Qy 781 NVLTPEDDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHKVVKICDFGLARDIMSDS 840
Db 781 NVLTPEDDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHKVVKICDFGLARDIMSDS 840
Qy 841 NYVVRGNARLPVKNWAPESLFGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKNWAPESLFGIYTIKSDVMSYGILLWEIFSLGVNYPGIPVDANFYK 900
Qy 901 LIONGFKMDQPPYATEEIIYIMOSWAFPSRKRPSPNLTSLGCOLADAEAEAMYNQVDG 960
Db 901 LIONGFKMDQPPYATEEIIYIMOSWAFPSRKRPSPNLTSLGCOLADAEAEAMYNQVDG 960
Qy 961 RVSECPHTYQNRPRPSREMDLGLLSPQAQVEDS 993
Db 961 RVSECPHTYQNRPRPSREMDLGLLSPQAQVEDS 993

RESULT 4

US-08-601-891-4
; Sequence 4, Application US/08601891
; Patent No. 5747651
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:

ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601.891
FILING DATE: 15-FEB-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-601-891-4

Query Match 100.0%; Score 5274; DB 1; Length 993;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVKCVLINHKNDSSVGKSSSPMVSESP 60

Db 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVKCVLINHKNDSSVGKSSSPMVSESP 60

Qy 61 EDLGCALRPOSSGCTVVEAAAEVVDVSASITLQVLVDAPGNISCLWFKHSSLNCQPHFDL 120

Db 61 EDLGCALRPOSSGCTVVEAAAEVVDVSASITLQVLVDAPGNISCLWFKHSSLNCQPHFDL 120

Qy 121 QNRGVVSVMLKMTQAGEYLLFTQSEATNTYTLFTVSIIRNTLLYTLRRPYFRKMENQD 180

Db 121 QNRGVVSVMLKMTQAGEYLLFTQSEATNTYTLFTVSIIRNTLLYTLRRPYFRKMENQD 180

QY 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEEKLHFGTDIRCCARNELGRE 240
DB 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEEKLHFGTDIRCCARNELGRE 240
QY 241 CTRLFTIDLNTQPTTLPOLFLKVGPELWIRCKAVHVNHGFGTLWELNKALBEGNYFEM 300
DB 241 CTRLFTIDLNTQPTTLPOLFLKVGPELWIRCKAVHVNHGFGTLWELNKALBEGNYFEM 300
QY 301 STYSTNRTMIRILFAVSSVARNDTGYYTCSSSKHPSQSALVTIVGKGFNATNSSEDEYE 360
DB 301 STYSTNRTMIRILFAVSSVARNDTGYYTCSSSKHPSQSALVTIVGKGFNATNSSEDEYE 360
QY 361 IQOYEFCFSVRKAYPQIRCTWTFRRKSPCEQKGLDNGYSISKFNHKGHPGEVIFHA 420
DB 361 IQOYEFCFSVRKAYPQIRCTWTFRRKSPCEQKGLDNGYSISKFNHKGHPGEVIFHA 420
QY 421 ENDDAQFTKMTLNIRKPKQVLAESAASQSCFSDGYPVPSWTWKCKSDKSPNCTBEITE 480
DB 421 ENDDAQFTKMTLNIRKPKQVLAESAASQSCFSDGYPVPSWTWKCKSDKSPNCTBEITE 480
QY 481 GVNRRKANRKFQWVSSSTLANMSEAIKGLVKCCAYNSLGTSCETILLNSPGFPFIQD 540
DB 481 GVNRRKANRKFQWVSSSTLANMSEAIKGLVKCCAYNSLGTSCETILLNSPGFPFIQD 540
QY 541 NISFVATIGVCLLFIVVLTLILCHKYKOPRYESQLMQVQVGTSSDNEYFYVDFREYEYD 600
DB 541 NISFVATIGVCLLFIVVLTLILCHKYKOPRYESQLMQVQVGTSSDNEYFYVDFREYEYD 600
QY 601 LKWEFPRENLEFGKVLGSGAFKVMNATAYGISKTGVSIOQAVKMLKEKADSSEREALMS 660
DB 601 LKWEFPRENLEFGKVLGSGAFKVMNATAYGISKTGVSIOQAVKMLKEKADSSEREALMS 660
QY 661 ELKMTQLGSHENIVNLLGACTLSGPIYILIFEYCCYGDLLNLYRSKREKPHRTWTIFKE 720
DB 661 ELKMTQLGSHENIVNLLGACTLSGPIYILIFEYCCYGDLLNLYRSKREKPHRTWTIFKE 720
QY 721 HNFSPYFTQSHPNSSMPGSRVQIHPDSQIISGLHNSFHSDEIYENOKLEEEEDL 780
DB 721 HNFSPYFTQSHPNSSMPGSRVQIHPDSQIISGLHNSFHSDEIYENOKLEEEEDL 780
QY 781 NVLTFTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHGVKVICDFGLARDIMSDS 840
DB 781 NVLTFTEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHGVKVICDFGLARDIMSDS 840
QY 841 NYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIPSLGVNPPGIPVDANFYK 900
DB 841 NYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIPSLGVNPPGIPVDANFYK 900
QY 901 LIONGFKMDOPFYATEEIIYIMOSWAFDSRKRPPSNLTSLGCOLADAEAMYNQVNDG 960
DB 901 LIONGFKMDOPFYATEEIIYIMOSWAFDSRKRPPSNLTSLGCOLADAEAMYNQVNDG 960
QY 961 RVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 993
DB 961 RVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 993

RESULT 5
US-09-021-324-4
; Sequence 4, Application US/09021324
; Patent No. 5912133
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Thor R.
; TITLE OF INVENTION: TOPIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-021-324-4
Query Match 100.0%; Score 5274; DB 2; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPIVKCVLINHKNDSSVGKSSSPMWSESP 60
DB 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPIVKCVLINHKNDSSVGKSSSPMWSESP 60
QY 61 EDLGCALRPQSSGTVEAAAVEVDVSASITLOVLVDPAGNISCLWVFKHSSLCQPHFDL 120
DB 61 EDLGCALRPQSSGTVEAAAVEVDVSASITLOVLVDPAGNISCLWVFKHSSLCQPHFDL 120
QY 121 QNRGVVSWILKMTETQAGEYLLFIQSEATNYTILFTVSRINTLLYTLRPPYFRKMNQD 180
DB 121 QNRGVVSWILKMTETQAGEYLLFIQSEATNYTILFTVSRINTLLYTLRPPYFRKMNQD 180
QY 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEEKLHFGTDIRCCARNELGRE 240
DB 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEEKLHFGTDIRCCARNELGRE 240
QY 241 CTRLFTIDLNTQPTTLPOLFLKVGPELWIRCKAVHVNHGFGTLWELNKALBEGNYFEM 300

Db 241 CTRLFTIDLNTQPTTLPOLFLKVGEPILWIRCKAVHNVHGFGLTWELNKALEEGNYFEM 300
QY 301 STYSTNRMTIRILFAFVSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360
Db 301 STYSTNRMTIRILFAFVSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360
QY 361 IDQYEEFCFVSFVKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNHKHQGPGEYIFHA 420
Db 361 IDQYEEFCFVSFVKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNHKHQGPGEYIFHA 420
QY 421 ENDDAQFTQMTINIRRRKQVLAASASQSCFSDGYPLPSWTWKCKDKNCTEITE 480
Db 421 ENDDAQFTQMTINIRRRKQVLAASASQSCFSDGYPLPSWTWKCKDKNCTEITE 480
QY 481 GWNKRNKRVFGQWVSSSTLNNSAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Db 481 GWNKRNKRVFGQWVSSSTLNNSAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
QY 541 NISFYATIGVCLLFIIVLTLLICHKYKQFRYESQLQWQVGTSSDNEYFYVDFREYED 600
Db 541 NISFYATIGVCLLFIIVLTLLICHKYKQFRYESQLQWQVGTSSDNEYFYVDFREYED 600
QY 601 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLKEKADSSERREALMS 660
Db 601 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLKEKADSSERREALMS 660
QY 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIIFYCCYGDLLNLYRSKREKPHRTWTBIFKE 720
Db 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIIFYCCYGDLLNLYRSKREKPHRTWTBIFKE 720
QY 721 HNFSFYPTFQSHPNSSMPGSRVQIHPDSQISGLHNSFHSEDEIYEYENQKLEBEEDL 780
Db 721 HNFSFYPTFQSHPNSSMPGSRVQIHPDSQISGLHNSFHSEDEIYEYENQKLEBEEDL 780
QY 781 NVLTEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Db 781 NVLTEDLLCFAYQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
QY 841 NYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDANFYK 900
QY 901 LQNGFKMDQPFVATBEIYIIMQSWAFDSRKPSPNLTSLGCOLADAEAMYNQVDG 960
Db 901 LQNGFKMDQPFVATBEIYIIMQSWAFDSRKPSPNLTSLGCOLADAEAMYNQVDG 960
QY 961 RVSECPHTYQNRPPFRMDLGLLSFQAQVEDS 993
Db 961 RVSECPHTYQNRPPFRMDLGLLSFQAQVEDS 993

RESULT 6

PCT-US92-09893-4

; Sequence 4, Application PC/TUS9209893

; GENERAL INFORMATION:

; APPLICANT: Lemischka, Ihor R.

; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Imclone Systems Incorporated

; STREET: 180 Varick Street

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10014

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/09893

;

; FILING DATE: 19921116

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Feit, Irving N. 28,601

; REGISTRATION NUMBER: 28,601

; REFERENCE/DOCKET NUMBER: LEM-3-7PT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-645-1405

; TELEFAX: 212-645-2054

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 993 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; PCT-US92-09893-4

Query Match 100.0%; Score 5274; DB 5; Length 993;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPALARDAGTVPLLVVFSGAMIFGTTINQDLPVVKVLIINHKNDSVSGKSSYPMVSESP 60

Db 1 MPALARDAGTVPLLVVFSGAMIFGTTINQDLPVVKVLIINHKNDSVSGKSSYPMVSESP 60

QY 61 EDLGCALPQSSGTYVEAAAEVDVSATITLQVLVDAPGNI SCLWVFKHSSLNCQPHFDL 120

Db 61 EDLGCALPQSSGTYVEAAAEVDVSATITLQVLVDAPGNI SCLWVFKHSSLNCQPHFDL 120

QY 121 QNRGVSVVILKWTETQAGEYLLFTIQSEATNTILFTVSI RNTLLYLRPFRKMNQD 180

Db 121 QNRGVSVVILKWTETQAGEYLLFTIQSEATNTILFTVSI RNTLLYLRPFRKMNQD 180

QY 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240

Db 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGRE 240

QY 241 CTRLFTIDLNTQPTTLPOLFLKVGEPILWIRCKAVHNVHGFGLTWELNKALEEGNYFEM 300

Db 241 CTRLFTIDLNTQPTTLPOLFLKVGEPILWIRCKAVHNVHGFGLTWELNKALEEGNYFEM 300

QY 301 STYSTNRMTIRILFAFVSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360

Db 301 STYSTNRMTIRILFAFVSVARNDTGYTCSSSKHPSQSALVTIVGKGFINATNSSEDEYE 360

QY 361 IDQYEEFCFVSFVKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNHKHQGPGEYIFHA 420

Db 361 IDQYEEFCFVSFVKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNHKHQGPGEYIFHA 420

QY 421 ENDDAQFTQMTINIRRRKQVLAASASQSCFSDGYPLPSWTWKCKDKNCTEITE 480

Db 421 ENDDAQFTQMTINIRRRKQVLAASASQSCFSDGYPLPSWTWKCKDKNCTEITE 480

QY 481 GWNKRNKRVFGQWVSSSTLNNSAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540

Db 481 GWNKRNKRVFGQWVSSSTLNNSAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540

QY 541 NISFYATIGVCLLFIIVLTLLICHKYKQFRYESQLQWQVGTSSDNEYFYVDFREYED 600

Db 541 NISFYATIGVCLLFIIVLTLLICHKYKQFRYESQLQWQVGTSSDNEYFYVDFREYED 600

QY 601 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLKEKADSSERREALMS 660

Db 601 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVGSIQVAVKMLKEKADSSERREALMS 660

QY 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIIFYCCYGDLLNLYRSKREKPHRTWTBIFKE 720

Db 661 ELKMMTQLGSHENIVNLLGACTLSGPIYLIIFYCCYGDLLNLYRSKREKPHRTWTBIFKE 720

QY 721 HNFSFYPTFQSHPNSSMPGSRVQIHPDSQISGLHNSFHSEDEIYEYENQKLEBEEDL 780

Db 721 HNFSFYPTFQSHPNSSMPGSRVQIHPDSQISGLHNSFHSEDEIYEYENQKLEBEEDL 780

QY 781 NVLTFFDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDS 840
Db 781 NVLTFFDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDS 840
QY 841 NYVVRGNARLPVKWMAPESEFEGYTIKSDVWSYGILLWEIFSLGVNPPYGPVDANFYK 900
Db 841 NYVVRGNARLPVKWMAPESEFEGYTIKSDVWSYGILLWEIFSLGVNPPYGPVDANFYK 900
QY 901 LIQNGFKMDQPPFYATEEIIYIMOSCWAFDSRKRKPSFNLTSFLGCQLADAEAMYQNVDG 960
Db 901 LIQNGFKMDQPPFYATEEIIYIMOSCWAFDSRKRKPSFNLTSFLGCQLADAEAMYQNVDG 960
QY 961 RVSECPHTYQNRPPFSREMDLGLLSPPQAQVEDS 993
Db 961 RVSECPHTYQNRPPFSREMDLGLLSPPQAQVEDS 993

RESULT 7
PCT-US92-05401-4
; Sequence 4, Application PC/TUS9205401
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05401
; FILING DATE: 19920626
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPPPT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1160 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-05401-4

Query Match 100.0%; Score 5274; DB 5; Length 1160;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVTKCVLINHKNDSSVGKSSSYPMVSESP 60
Db 20 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVTKCVLINHKNDSSVGKSSSYPMVSESP 79
QY 61 EDLGCALRPQSSGTVYAAAVDVDSASITLQVLDPAGNISCLVTFKSSLNCQPHFDL 120
Db 80 EDLGCALRPQSSGTVYAAAVDVDSASITLQVLDPAGNISCLVTFKSSLNCQPHFDL 139
QY 121 QNRGVVSVMLKMTQFAGEYLLFIQSEATNYTILFTVSRINLLYTLRRPYFRKMNQD 180
Db 140 QNRGVVSVMLKMTQFAGEYLLFIQSEATNYTILFTVSRINLLYTLRRPYFRKMNQD 199
QY 181 ALVCISSEVPEFIVEVWLCDSQGESCKEESPVAVKKEKVLHELFGTDIRCCARNELGRE 240

Db 200 ALVCISSEVPEFIVEVWLCDSQGESCKEESPVAVKKEKVLHELFGTDIRCCARNELGRE 259
QY 241 CTRLFITDINQTPOTTLPOLFLKVGEPWLIRCKAVHVNHGFGLTWELENKALEBGNFYEM 300
Db 260 CTRLFITDINQTPOTTLPOLFLKVGEPWLIRCKAVHVNHGFGLTWELENKALEBGNFYEM 319
QY 301 STYSTNRTMIRILFAFVSSVARNDTGYTTCSSSKHPSQSALVTIVGKGFINATNSSDEYE 360
Db 320 STYSTNRTMIRILFAFVSSVARNDTGYTTCSSSKHPSQSALVTIVGKGFINATNSSDEYE 379
QY 361 IDOYEEFCFSVRKAYPOIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQHPGEYIFHA 420
Db 380 IDOYEEFCFSVRKAYPOIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQHPGEYIFHA 439
QY 421 ENDDAQFTKMTFLNIRKPOVLAEASASQSCFSDGYPFLPSWTKKCSKSPNCTEITE 480
Db 440 ENDDAQFTKMTFLNIRKPOVLAEASASQSCFSDGYPFLPSWTKKCSKSPNCTEITE 499
QY 481 GWNRRKANRVFGOWYSSSTLNNSEAIKGLVKCCAYNSLGTSCETILLNSPGFPFIQD 540
Db 500 GWNRRKANRVFGOWYSSSTLNNSEAIKGLVKCCAYNSLGTSCETILLNSPGFPFIQD 559
QY 541 NISFYATIGVCLLFIVLTLILCHIKYKQFYESQLOMQVQVTGSSDNEYFYVDFREYEYD 600
Db 560 NISFYATIGVCLLFIVLTLILCHIKYKQFYESQLOMQVQVTGSSDNEYFYVDFREYEYD 619
QY 601 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGISTGVSIOAVVMKLEKADSSREALMS 660
Db 620 LKWEFPRENLEFGKVLGSGAFGKVMNATAYGISTGVSIOAVVMKLEKADSSREALMS 679
QY 661 ELKMMTQLGSHENIVNLGACTLSGPIYILFEYCCYGDLLNLYRSKREKFRHTWTEIFKE 720
Db 680 ELKMMTQLGSHENIVNLGACTLSGPIYILFEYCCYGDLLNLYRSKREKFRHTWTEIFKE 739
QY 721 HNFSEFTTQSHENSMPSGSRREVQIHPDSQIISGLHNSFHSDEIEIYENQKLEEBEDL 780
Db 740 HNFSEFTTQSHENSMPSGSRREVQIHPDSQIISGLHNSFHSDEIEIYENQKLEEBEDL 799
QY 781 NVLTFFDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDS 840
Db 800 NVLTFFDLCCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSDS 859
QY 841 NYVVRGNARLPVKWMAPESEFEGYTIKSDVWSYGILLWEIFSLGVNPPYGPVDANFYK 900
Db 860 NYVVRGNARLPVKWMAPESEFEGYTIKSDVWSYGILLWEIFSLGVNPPYGPVDANFYK 919
QY 901 LIQNGFKMDQPPFYATEEIIYIMOSCWAFDSRKRKPSFNLTSFLGCQLADAEAMYQNVDG 960
Db 920 LIQNGFKMDQPPFYATEEIIYIMOSCWAFDSRKRKPSFNLTSFLGCQLADAEAMYQNVDG 979
QY 961 RVSECPHTYQNRPPFSREMDLGLLSPPQAQVEDS 993
Db 980 RVSECPHTYQNRPPFSREMDLGLLSPPQAQVEDS 1012

RESULT 8
US-08-222-299-4
; Sequence 4, Application US/08222299
; Patent No. 5635388
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Broz, Suean D.
; APPLICANT: Matthews, William
; APPLICANT: Zeigler, Francis C.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

Query Match 99.4%; Score 5240; DB 1; Length 993;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 987; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVLLVFSAMIFGTINQDLPLVKVILNHKNDSSVSGSSYPNISEP 60
Db 1 MPALARDAGTVLLVFSAMIFGTINQDLPLVKVILNHKNDSSVSGSSYPNISEP 60

Qy 61 EDLGCALRQSSGTVEAAAEVDVDSASITLQVLDAPGNISCLWVFKSSLNQCQPHDL 120
Db 61 EDLGCALRQSSGTVEAAAEVDVDSASITLQVLDAPGNISCLWVFKSSLNQCQPHDL 120

Qy 121 QNRGVVSMVILKMTQAGEYLLFIQSEATNYTLFTVSRINLLYLRPFYKRMENQD 180
Db 121 QNRGVVSMVILKMTQAGEYLLFIQSEATNYTLFTVSRINLLYLRPFYKRMENQD 180

Qy 181 ALVCISESVPEIPEVWVLCDSQGESCKESPAVVKKEKVLHFLGTDTRCCARNELGRE 240
Db 181 ALVCISESVPEIPEVWVLCDSQGESCKESPAVVKKEKVLHFLGTDTRCCARNELGRE 240

Qy 241 CTRLTIDNQTPTTLPOLFLKVGSPMLRCKAVHNVHGFGLTWELNKALEEGNYFEM 300
Db 241 CTRLTIDNQTPTTLPOLFLKVGSPMLRCKAVHNVHGFGLTWELNKALEEGNYFEM 300

Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTSCSSKHPQSALVTIVGKGFNATNSSEDEYE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTSCSSKHPQSALVTIVGKGFNATNSSEDEYE 360

Qy 361 IQYBEFCFSVRKAPQIRCTWTFRRKPPCQKGLDNGYSISKFCNKHQGEYIFHA 420
Db 361 IQYBEFCFSVRKAPQIRCTWTFRRKPPCQKGLDNGYSISKFCNKHQGEYIFHA 420

Qy 421 ENDDAQFTKMTNIRKQVLAESAQSCFSDGVPLPSWTWKCKSDKSPNCTEITE 480
Db 421 ENDDAQFTKMTNIRKQVLAESAQSCFSDGVPLPSWTWKCKSDKSPNCTEITE 480

Qy 481 GVMNRKANRKFQGWSSSTLNMSAIEKGLVKCCAYNSLGTSCETILLNSPGFFFIQD 540
Db 481 GVMNRKANRKFQGWSSSTLNMSAIEKGLVKCCAYNSLGTSCETILLNSPGFFFIQD 540

Qy 541 NISFYATIGVCLLFIIVLLILLCHKYKQFRYESQLQMVQVGTSSDNEYVDFREYED 600
Db 541 NISFYATIGVCLLFIIVLLILLCHKYKQFRYESQLQMVQVGTSSDNEYVDFREYED 600

Qy 601 LKWEFFRENLEFGKVLGSGAFGKVMNATAYGISTGVSIOQVAVKMLKADSSEREALMS 660

Db 601 LKWEFFRENLEFGKVLGSGAFGKVMNATAYGISTGVSIOQVAVKMLKADSSEREALMS 660
Qy 661 ELKMMTOLGSHENIVNLLGACTLSGPIYLIFFEYCCYGDLLNLYRSKREKPHRTWTIEFKE 720
Db 661 ELKMMTOLGSHENIVNLLGACTLSGPIYLIFFEYCCYGDLLNLYRSKREKPHRTWTIEFKE 720
Qy 721 HNFSPYPTFQSHPNSSMPGSRREVQIHPDSQISGLHNSFHSSEDEIYENQKLEBEEDL 780
Db 721 HNFSPYPTFQSHPNSSMPGSRREVQIHPDSQISGLHNSFHSSEDEIYENQKLEBEEDL 780
Qy 781 NVLTEDLLCFAYQVAKGMFELEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Db 781 NVLTEDLLCFAYQVAKGMFELEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDS 840
Qy 841 NYVVRGNARLPVKWAPESLFEIGIYTIKSDVMSYGILLWEIISLGVNPPYGPVDANFYK 900
Db 841 NYVVRGNARLPVKWAPESLFEIGIYTIKSDVMSYGILLWEIISLGVNPPYGPVDANFYK 900
Qy 901 LIQNGFKMDQPFYATEEIYIIMQSCWAFDSRKRPSPPNLTSLFGCOLADAEEAMYQNVDG 960
Db 901 LIQNGFKMDQPFYATEEIYIIMQSCWAFDSRKRPSPPNLTSLFGCOLADAEEAMYQNVDG 960
Qy 961 RVSECPHTYQNRPPSREMDLGLLSPQAQVEDS 993
Db 961 RVSECPHTYQNRPPSREMDLGLLSPQAQVEDS 993

RESULT 9
US-08-434-878-4
; Sequence 4, Application US/08434878
; Patent No. 5997865
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Broz, Susan D.
; APPLICANT: Matthews, William C.
; APPLICANT: Zeigler, Francis C.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES 1
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,878
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 879
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-434-878-4

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Query Match      99.4%; Score 5240; DB 2; Length 993;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 987; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPALARDAGTVLLVVFSAI FGTITNQDLPVIKCVLINHKNDSSVGKSSSPMWSESP 60
Db 1 MPALARDGQGLPLLVVFSAMI FGTITNQDLPVIKCVLINHKNDSSVGKSSSPMWSESP 60

Qy 61 EDLGCALRQSSGTVYAAAVEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQPHFDL 120
Db 61 EDLGCALRQSSGTVYAAAVEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQPHFDL 120

Qy 121 QNRGVVSWILKWTQAGEYLLFQSEATNYTILFTVSIRNTLLYLTPRYPKRMENQD 180
Db 121 QNRGVVSWILKWTQAGEYLLFQSEATNYTILFTVSIRNTLLYLTPRYPKRMENQD 180

Qy 181 ALVCISSEVPEPIVWVLCDSQESCKEESPAVVKKEKVLHFGDTRCCARNELGRE 240
Db 181 ALVCISSEVPEPIVWVLCDSQESCKEESPAVVKKEKVLHFGDTRCCARNELGRE 240

Qy 241 CTRLETFIDLNQTPQTTLPOLFLKVGEPMLIRCKAVHVNHGFGLTWELENKALBEGNYFEM 300
Db 241 CTRLETFIDLNQTPQTTLPOLFLKVGEPMLIRCKAVHVNHGFGLTWELENKALBEGNYFEM 300

Qy 301 STYSTNRMTIRILFAFVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFNATNSSDEYE 360
Db 301 STYSTNRMTIRILFAFVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFNATNSSDEYE 360

Qy 361 IDQYEEFCFSVRFKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFNHKGQGEYIFHA 420
Db 361 IDQYEEFCFSVRFKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFNHKGQGEYIFHA 420

Qy 421 ENDDAQFTKMTNIRRKQVLAESAASQSCFSDGYPSPMTWKCKSDKSPNCTEEITE 480
Db 421 ENDDAQFTKMTNIRRKQVLAESAASQSCFSDGYPSPMTWKCKSDKSPNCTEEITE 480

Qy 481 GWNKANKRVFGQWSSSTLANMSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Db 481 GWNKANKRVFGQWSSSTLANMSEAIKGLVKCCAYNSLGTSCETILLNSPGPPFIQD 540

Qy 541 NISFYATIGVCLLFIWVLTLLCHKYKQFRYESQIQVAVMLKEKADSSEREAALMS 600
Db 541 NISFYATIGVCLLFIWVLTLLCHKYKQFRYESQIQVAVMLKEKADSSEREAALMS 600

Qy 601 LKWEPPRENLEFGKVLGSGAFGKVMNATAYGSKTGVSIOQVAVMLKEKADSSEREAALMS 660
Db 601 LKWEPPRENLEFGKVLGSGAFGKVMNATAYGSKTGVSIOQVAVMLKEKADSSEREAALMS 660

Qy 661 ELKMMTQLGSHENI VNLGACTLSGPIYLI FEYCCYGDLLNLYLSKREKFRHTWTBIFKE 720
Db 661 ELKMMTQLGSHENI VNLGACTLSGPIYLI FEYCCYGDLLNLYLSKREKFRHTWTBIFKE 720

Qy 721 HNFSPYPTQSHNSMPGSRVQIHPDSDQISGLHNSFHSDEIEYENQKLEBEEDL 780
Db 721 HNFSPYPTQSHNSMPGSRVQIHPDSDQISGLHNSFHSDEIEYENQKLEBEEDL 780

Qy 781 NVLTPEDLCCFAYQVAKGMFELEFKSCVHRDLAARNVLVTHGKVVKICDPGLARDIMSDS 840
Db 781 NVLTPEDLCCFAYQVAKGMFELEFKSCVHRDLAARNVLVTHGKVVKICDPGLARDIMSDS 840

Qy 841 NYVVRGNARLPVKWMAPELFGIYTIKSDVMSYIGILLWEIFSLGVNYPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWMAPELFGIYTIKSDVMSYIGILLWEIFSLGVNYPGIPVDANFYK 900

Qy 901 LIQNGFKMDQPPYATEEIIYIMQSWAFDSRKRPPFNLTSLFGCOLADAEAMYNQVDG 960
Db 901 LIQNGFKMDQPPYATEEIIYIMQSWAFDSRKRPPFNLTSLFGCOLADAEAMYNQVDG 960

Qy 961 RVSECPHTYQNRPPFSREMDLGLSPQAQVEDS 993
Db 961 PVSECPHTYQNRPPFSREMDLGLSPQAQVEDS 993
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RESULT 10
PCT-US95-03718-4
; Sequence 4, Application PC/TUS9503718
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03718
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 879PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-03718-4
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Query Match 99.4%; Score 5240; DB 5; Length 993;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 987; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Db 1 MPALARDGQGLPLLVVFSAMI FGTITNQDLPVIKCVLINHKNDSSVGKSSSPMWSESP 60

Qy 61 EDLGCALRQSSGTVYAAAVEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQPHFDL 120
Db 61 EDLGCALRQSSGTVYAAAVEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQPHFDL 120

Qy 121 QNRGVVSWILKWTQAGEYLLFQSEATNYTILFTVSIRNTLLYLTPRYPKRMENQD 180
Db 121 QNRGVVSWILKWTQAGEYLLFQSEATNYTILFTVSIRNTLLYLTPRYPKRMENQD 180

Qy 181 ALVCISSEVPEPIVWVLCDSQESCKEESPAVVKKEKVLHFGDTRCCARNELGRE 240
Db 181 ALVCISSEVPEPIVWVLCDSQESCKEESPAVVKKEKVLHFGDTRCCARNELGRE 240

Qy 241 CTRLETFIDLNQTPQTTLPOLFLKVGEPMLIRCKAVHVNHGFGLTWELENKALBEGNYFEM 300
Db 241 CTRLETFIDLNQTPQTTLPOLFLKVGEPMLIRCKAVHVNHGFGLTWELENKALBEGNYFEM 300

Qy 301 STYSTNRMTIRILFAFVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFNATNSSDEYE 360
Db 301 STYSTNRMTIRILFAFVSSVARNDTGYTCSSSKHPSQSALVTIVGKGFNATNSSDEYE 360

Qy 361 IDQYEEFCFSVRFKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFNHKGQGEYIFHA 420
Db 361 IDQYEEFCFSVRFKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFNHKGQGEYIFHA 420
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Qy 421 ENDDAQFTKMTLNIRRKQVLAASASQSCFSDGYPLPSWTWKCDKSPNCTEEITE 480
Db 421 ENDDAQFTKMTLNIRRKQVLAASASQSCFSDGYPLPSWTWKCDKSPNCTEEITE 480
Qy 481 GWNKANKRVFGQWVSSTLNMSBAIKFLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Db 481 GWNKANKRVFGQWVSSTLNMSBAIKFLVKCCAYNSLGTSCETILLNSPGPPFIQD 540
Qy 541 NISFYATIGVCLLFIVLTLCHKYKQFRYESQLOMVOVGTSSDNEYFYVDREYED 600
Db 541 NISFYATIGVCLLFIVLTLCHKYKQFRYESQLOMVOVGTSSDNEYFYVDREYED 600
Qy 601 LKWEPPRENLEFGKVLGSGAFKVMNATAYGKGTGVSQVAVKMLKEKADSSEREALMS 660
Db 601 LKWEPPRENLEFGKVLGSGAFKVMNATAYGKGTGVSQVAVKMLKEKADSSEREALMS 660
Qy 661 ELKMTQLGSHENIVNLGACTLSGPYILIFPCYCCYGLLNLVLRKREKFRHTWTEIPKE 720
Db 661 ELKMTQLGSHENIVNLGACTLSGPYILIFPCYCCYGLLNLVLRKREKFRHTWTEIPKE 720
Qy 721 HNFSEYPTFQSHPNSSMPCSRREVQIHPDSQISGLHNSFHSDEIEYENQKLEEEEDL 780
Db 721 HNFSEYPTFQSHPNSSMPCSRREVQIHPDSQISGLHNSFHSDEIEYENQKLEEEEDL 780
Qy 781 NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKWKICDFGLARDIMSDS 840
Db 781 NVLTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKWKICDFGLARDIMSDS 840
Qy 841 NYVVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIFSLGVNPPGIPVDANFYK 900
Db 841 NYVVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIFSLGVNPPGIPVDANFYK 900
Qy 901 LIQNGFKMDQFPYATEEYIIMQSCWAFDSRKRPFNLTSLFGQLADAEAMYNQVNDG 960
Db 901 LIQNGFKMDQFPYATEEYIIMQSCWAFDSRKRPFNLTSLFGQLADAEAMYNQVNDG 960
Qy 961 RVSECPHTYQNRPPESREMDLGLLSPQAQVEDS 993
Db 961 RVSECPHTYQNRPPESREMDLGLLSPQAQVEDS 993

RESULT 11

US-08-183-211-2
; Sequence 2, Application US/08183211
; Patent No. 5618709
; GENERAL INFORMATION:
; APPLICANT: Alan M. Gewirtz, Donald Small, Curt I. Civin.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEO- TIDES
; TITLE OF INVENTION: SPECIFIC FOR STK-1 AND METHOD FOR
; TITLE OF INVENTION: INHIBITING EXPRESSION OF THE STK-1 PROTEIN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL GONDA LAVORGNA & MONACO
; STREET: Suite 1800, Penn Center Plaza
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/183.211
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 3957-15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5618709e
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-183-211-2

Query Match 99.3%; Score 5238; DB 1; Length 993;

Best Local Similarity 99.7%; Pred No. 0;

Matches 991; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVVKVLIHKNKNDSSVGKSSYPMYSESP 60

Db 1 MPALARDAGTVPLLVVFSAMIFGTITNQDLPVVKVLIHKNKNDSSVGKSSYPMYSESP 60

Qy 61 EDLGCALRPOSSGTYEAAADEVDSASITLQVLVDAPGNI SCLWVFKHSSLNCQPHFDL 120

Db 61 EDLGCALRPOSSGTYEAAADEVDSASITLQVLVDAPGNI SCLWVFKHSSLNCQPHFDL 120

Qy 121 QNRGVSVVILKMTETOAGEYLLFIQSEATNTYITLFTVSI RNTLLYTLRRPYFRKXENOD 180

Db 121 QNRGVSVVILKMTETOAGEYLLFIQSEATNTYITLFTVSI RNTLLYTLRRPYFRKXENOD 180

Qy 181 ALVCISESVPEPIVSWVLCDSSQESCKEESPAVVKKEKVLHLELFGTDIRCCARNELGRE 240

Db 181 ALVCISESVPEPIVSWVLCDSSQESCKEESPAVVKKEKVLHLELFGTDIRCCARNELGRE 240

Qy 241 CTRLTIDNLQTPQTTLPOLFLKVGEPDWIRCKAVVNHGFGLTWELNKALEEGNYFEM 300

Db 241 CTRLTIDNLQTPQTTLPOLFLKVGEPDWIRCKAVVNHGFGLTWELNKALEEGNYFEM 300

Qy 301 STYSTNRTMIRILFAFVSVSVAENDTGYVTCSSSKHPSQSALVTI VCKGFINATNSSDEYE 360

Db 301 STYSTNRTMIRILFAFVSVSVAENDTGYVTCSSSKHPSQSALVTI VCKGFINATNSSDEYE 360

Qy 361 IDQYEEFCFSVRFKAYPQIRCTWTSPRSKSPCEQKGLDNGYSISKFCNHKHQPGEYIFH- 419

Db 361 IDQYEEFCFSVRFKAYPQIRCTWTSPRSKSPCEQKGLDNGYSISKFCNHKHQPGEYIFH- 420

Qy 420 AENDDAQFTKMTLNIRRKQVLAASASQSCFSDGYPLPSWTWKCDKSPNCTEEIT 479

Db 420 AENDDAQFTKMTLNIRRKQVLAASASQSCFSDGYPLPSWTWKCDKSPNCTEEIT 479

Qy 480 EGVWNRKANRVFGQWVSSTLNMSBAIKFLVKCCAYNSLGTSCETILLNSPGPPFIQ 539

Db 480 EGVWNRKANRVFGQWVSSTLNMSBAIKFLVKCCAYNSLGTSCETILLNSPGPPFIQ 539

Qy 540 DNISFYATIGVCLLFIVLTLCHKYKQFRYESQLOMVOVGTSSDNEYFYVDREY 599

Db 540 DNISFYATIGVCLLFIVLTLCHKYKQFRYESQLOMVOVGTSSDNEYFYVDREY 599

Qy 600 DLKWEPPRENLEFGKVLGSGAFKVMNATAYGKGTGVSQVAVKMLKEKADSSEREALM 659

Db 600 DLKWEPPRENLEFGKVLGSGAFKVMNATAYGKGTGVSQVAVKMLKEKADSSEREALM 659

Qy 660 SELKMTQLGSHENIVNLGACTLSGPYILIFPCYCCYGLLNLVLRKREKFRHTWTEIPK 719

Db 660 SELKMTQLGSHENIVNLGACTLSGPYILIFPCYCCYGLLNLVLRKREKFRHTWTEIPK 719

Qy 720 EHNFSFYPTFQSHPNSSMPCSRREVQIHPDSQISGLHNSFHSDEIEYENQKLEEEED 779

Db 720 EHNFSFYPTFQSHPNSSMPCSRREVQIHPDSQISGLHNSFHSDEIEYENQKLEEEED 779

Qy 780 LNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKWKICDFGLARDIMSD 839

Db 780 LNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKWKICDFGLARDIMSD 839

Qy 840 SNYVVRGNARLPVKWMAPESLFEGYITIKSDVMSYGILLWEIFSLGVNPPGIPVDANFY 899

Db 840 SNVVRGNARLPVKWMAPELFGIYTIKSDVMSYGILLWEIFSLGWNYPGIPVDANFY 899
Qy 900 KLQNGFKMDQPPYATEEYIIMQSCWAFDSRKRPFPPNLTSLGCOLADAEAMYNQVND 959
Db 900 KLQNGFKMDQPPYATEEYIIMQSCWAFDSRKRPFPPNLTSLGCOLADAEAMYNQVND 959
Qy 960 GRVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 993
Db 960 GRVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 993

RESULT 12
PCT-US95-00176A-2
; Sequence 2, Application PC/TUS9500176A
; GENERAL INFORMATION:
; APPLICANT: Alan M. Gewirtz, Donald Small, Curt I. Civin.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
; TITLE OF INVENTION: SPECIFIC FOR STK-1 AND METHOD FOR INHIBITING EXPRESSION OF THE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SEIDEL GONDA LAVORNA & MONACO
; STREET: Suite 1800, Penn Center Plaza
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00176A
; FILING DATE: 6 January 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,211
; FILING DATE: 14 January 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 3957-14 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: None
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
PCT-US95-00176A-2

Query Match 99.3%; Score 5238; DB 5; Length 993;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 991; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 1 MPALARDAGTVLLVVFSAWIFGTITNQLPVIKCVLINHKNDSSVGKSSSYPWVSESP 60
Db 1 MPALARDAGTVLLVVFSAWIFGTITNQLPVIKCVLINHKNDSSVGKSSSYPWVSESP 60
Qy 61 EDLGCALRPQSGTGYEAAAEVDVSASITLQVLVDAPGNISCLWVFKHSSLNQCPHFDL 120
Db 61 EDLGCALRPQSGTGYEAAAEVDVSASITLQVLVDAPGNISCLWVFKHSSLNQCPHFDL 120
Qy 121 QNRGVSVMLKMTQAGEYLLFIQSEATNTYLTFTVSRNTLLYTLRRPYFRKMENQD 180
Db 121 QNRGVSVMLKMTQAGEYLLFIQSEATNTYLTFTVSRNTLLYTLRRPYFRKMENQD 180
Qy 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHFGTDIRCCARNELGRE 240

Db 181 ALVCISESVPEPIVWVLCDSQGESCKEESPAVVKKEKVLHFGTDIRCCARNELGRE 240
Qy 241 CTLEFTIDLNOTPOTTLPOLFLKVGELPLWIRCKAVHVNHGFLTWELNKALESGNYFEM 300
Db 241 CTLEFTIDLNOTPOTTLPOLFLKVGELPLWIRCKAVHVNHGFLTWELNKALESGNYFEM 300
Qy 301 STYSTNRTMIRILFAFVSSVARNDTGYTCTSSSKHPSQSALVTIVGKGFINATNSSDEYE 360
Db 301 STYSTNRTMIRILFAFVSSVARNDTGYTCTSSSKHPSQSALVTIVGKGFINATNSSDEYE 360
Qy 361 IDOYEEFCFSVRFKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQHPGEYIFH- 419
Db 361 IDOYEEFCFSVRFKAYPQIRCTWTFSRKSPCEQKGLDNGYSISKFCNKHQHPGEYIFH 420
Qy 420 AENDDAQFTKMTLNIRRRKQVLAELASASQSCFSDGYPLPSWTWKKCSDKSPNCTEIT 479
Db 421 AENDDAQFTKMTLNIRRRKQVLAELASASQSCFSDGYPL-SMTWKKCSDKSPNCTEIT 479
Qy 480 EGVNNEKANRKVFQGWVSSSTLNNSAIGFLVKCCAYNSLGTSCETILLNSPGFPFPIQ 539
Db 480 EGVNNEKANRKVFQGWVSSSTLNNSAIGFLVKCCAYNSLGTSCETILLNSPGFPFPIQ 539
Qy 540 DNISFYATIGVCLLFIVLTLICHKYKKOFRYESQLQMVQVGTGSSDNEYFYVDFREY 599
Db 540 DNISFYATIGVCLLFIVLTLICHKYKKOFRYESQLQMVQVGTGSSDNEYFYVDFREY 599
Qy 600 DLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVSIOQAVKMLKEKADSSERELM 659
Db 600 DLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTVSIOQAVKMLKEKADSSERELM 659
Qy 660 SELKMTOLGSHENIVNLLGACTLSGPIYLIPEYCCVGDLLNLYRSKREKPHRTWTIFK 719
Db 660 SELKMTOLGSHENIVNLLGACTLSGPIYLIPEYCCVGDLLNLYRSKREKPHRTWTIFK 719
Qy 720 EHNFSFYPTFQSHPNSSMPGSRREVQHPDSQDQISGLHNSFHSSEDEIYEENQKLESEED 779
Db 720 EHNFSFYPTFQSHPNSSMPGSRREVQHPDSQDQISGLHNSFHSSEDEIYEENQKLESEED 779
Qy 780 LNVLTPEDLCLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSD 839
Db 780 LNVLTPEDLCLCFAYQVAKGMEFLFKSCVHRDLAARNVLVTHGKVKICDFGLARDIMSD 839
Qy 840 SNVVRGNARLPVKWMAPELFGIYTIKSDVMSYGILLWEIFSLGWNYPGIPVDANFY 899
Db 840 SNVVRGNARLPVKWMAPELFGIYTIKSDVMSYGILLWEIFSLGWNYPGIPVDANFY 899
Qy 900 KLQNGFKMDQPPYATEEYIIMQSCWAFDSRKRPFPPNLTSLGCOLADAEAMYNQVND 959
Db 900 KLQNGFKMDQPPYATEEYIIMQSCWAFDSRKRPFPPNLTSLGCOLADAEAMYNQVND 959
Qy 960 GRVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 993
Db 960 GRVSECPHTYQNRPPFSREMDLGLLSPOAQVEDS 993

RESULT 13
US-08-222-299-2
; Sequence 2, Application US/08222299
; Patent No. 5635388
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Broz, Susan D.
; APPLICANT: Matthews, William
; APPLICANT: Zeigler, Francis C.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,299
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELEPHONE: 415/952-9881
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1000 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-222-299-2

Query Match 86.0%; Score 4533.5; DB 1; Length 1000;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 851; Conservative 56; Mismatches 84; Indels 3; Gaps 2;

QY 1 MPALA-RDAGTVPLAVFAMIFGITNODLPVIRKVLINHNKNDSSVGKSSYPNVMS 59
DB 1 MRALQSRDRLLLVLSWILETVTNDLPVIRKVLISHENNGSSAGKPSRYMRVGS 60
QY 60 PEDLCALRPOSQSGTYEAAAEVDDVSATITLQVLVDAPGNTSCLWVFKHSSLNCPHPD 119
DB 61 PEDLOCTPRQSEGTYEAAATVEAESGITLQVLATFGDLSCLWVFKHSSLGCPHPD 120
QY 120 LQNRGVGVMILKMTQTAGEYLLFTQSBATNYTLFTVSIRNTLYTLRRPYFRKQENQ 179
DB 121 LQNRGIVSMALNVTQTAGEYLLHQSEAAANYTLFTVNRDTQLYVLRPYFRKQENQ 180
QY 180 DALVCISVSPEPIVEVWLCDSQGESCKEESPAVVKKEKVLHELFGTDIRCCARNELGR 239
DB 181 DALLCISEGPEPTVEWVLCSSHRESCKEEGPAVVRKEKVLHELFGTDIRCCARNALGR 240
QY 240 ECTRLFTIDLNOTPOTTLPOLFLKVGEPILWIRCKAVHNVHGLTWELNKALEEGNYFE 299
DB 241 ESTKLTIDLNAPOSTLPOLFLKVGEPILWIRCKAVHNVHGLTWELNKALEEGSYFE 300
QY 300 MSTYSTNRTMIRILFAPVSSVARNDTGYITCSSSKHPSQSALVTIYVKGFINATNSSEY 359
DB 301 MSTYSTNRTMIRILAFVSSVGRNDTGYITCSSSKHPSQSALVTILEKGFINATSSQEEY 360
QY 360 EIDQVEEPCFSVRKAYPOIRCTWTSRKSFPCEQKGLONGYSISKFCNHKQOPGEYIFH 419
DB 361 EIDPYEKFCSVRKAYPIRCTWTSRKSFPCEQKGLONGYSISKFCDHKNKPGYIIFY 420
QY 420 AENDDAQFTKMTLNRKRPQVLAEASQSCFSDGYPLPSMTWKCKSDKSPNCTEIT 479
DB 421 AENDDAQFTKMTLNRKRPQVLANASQSCSDGYPLPSMTWKCKSDKSPNCTEITP 480
QY 480 EGVWNRKANRVKFGQWVSSTLNMSEAIKGLVKCCAYNSLGTSCETILLNSGPPFFIQ 539
DB 481 EGVWNRKANRVKFGQWVSSTLNMSEAGKGLLVKCCAYNSMGTSCTIFLNSGPPFFIQ 540
QY 540 DNISFYATIGVCLLFLVTLTLLCHYKQPRYESQLQVQVVTGSSDNEYFYVDREY 599
DB 541 DNISFYATIGLCLPFTLVILVILCHYKQPRYESQLQVQVVTGTPLDNEYFYVDREY 600
QY 600 DLKWEFPRENLEFGKLGSAFGKVNATAYGISKGTGVSIOAVKMLKEKADSSREALM 659

DB 601 DLKWEFPRENLEFGKLGSAFGKVNATAYGISKGTGVSIOAVKMLKEKADSSREALM 660
QY 660 SELKXMTOLGSHENIVNLLGACTLSGPIYLIEYCCYGDLLNVLRSKRKFKRTWTTEIFK 719
DB 661 SELKXMTLGHHDNIVNLLGACTLSGPVYLIEYCCYGDLLNVLRSKRKFKRTWTTEIFK 720
QY 720 EHNFSFYPTFQSHPNSSMPGSRREVQIHDPDSQISGLHGNPSHSEDEIEYENQKRL--EEE 777
DB 721 EHNFSFYPTFQAHNSNSMPGSRREVQLHPPLDQLSGFNGNSIHSEDEIEYENQKRLAEEEE 780
QY 778 EDNLVLTTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHKVVKICDFGLARDIM 837
DB 781 EDNLVLTTFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHKVVKICDFGLARDIL 840
QY 838 SDSNYVVRGNARLPVKWMAPELSLFGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDAN 897
DB 841 SDSNYVVRGNARLPVKWMAPELSLFGIYTIKSDVWSYGILLWEIFSLGVNYPGIPVDAN 900
QY 898 FYKLQNGFMDQPFYATEEIIYIMQSWAFDSRKRSPFNLTSLFLGCOLADAEAMYNQ 957
DB 901 FYKLQSGFKMEQPFYATEGIIYVMQSWAFDSRKRSPFNLTSLFLGCOLADAEAMYNQ 960
QY 958 VDRVSECPHTYQNRPPSRREMDLGLLSPQAQVE 991
DB 961 MCGNVPEHPSIYQNRRLPSREAGSEPPSPQAQVK 994

RESULT 14

US-08-434-878-2
Sequence 2, Application US/08434878
Patent No. 5997865
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Broz, Susan D.
APPLICANT: Matthews, William C.
APPLICANT: Zeigler, Francis C.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES 1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,878
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1000 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-434-878-2

Query Match 86.0%; Score 4533.5; DB 2; Length 1000;

Best local Similarity 85.6%; Pred. No. 0; Matches 851; Conservative 56; Mismatches 84; Indels 3; Gaps			
Qy	1	MPALA-RDAGTVPLLLVPSAMIFGTTNQDLPVVKCVLIHNKNDSSVGKSSSSPYMVSES 59	
Db	1	MRALAQRSDRRLLLLVLSVILETVTNQDLPVVKCVLI SHENNGSSAGRPSSVPMVRGS 60	
Qy	60	PEDLGCCALRPSSGTVYEAAAVEVDVSASITLQVLVDAPGNISCLWPKHSSLNCQPHFD 119	
Db	61	PEDLQCTPRRQSEGTVEAAVEVAESGISTLQVLQATPGDLSCLWPKHSSLGCPHFD 120	
Qy	120	LONRGVSMVTLKMTETCAGGYLLFIQSEATNYTLFTVYSIRNTLLTYLRRPYFRKMENQ 179	
Db	121	LONRGVSMALNTETQAGGYLLHIQSEAAANYTLFTVNVYRDQLYVLRPYFRKMENQ 180	
Qy	180	DALVCISSEVPEPIVEWVLCDSQGESCKEESPAVVKKEKVLHLEFGTDIRCCARNELGR 239	
Db	181	DALLCISGVPEPTVEWVLCSSHRESCKEESPAVVKKEKVLHLEFGTDIRCCARNALGR 240	
Qy	240	ECTRLFTIDLNQTTQTLPLQFLKVGBLEPLWTRKXAVHNVHGFGLTWBLENKALBEGNYFE 299	
Db	241	ESTKLTFTDLNQAPQSTLPQLFLKVGBLEPLWTRCKAIHNVHGFGLTWLEDKALEEGSYFE 300	
Qy	300	MSTYSTNTMTIRILLPAFVSSVARNDGTGYTCCSSKHPSSQSALVTIVCKGFNATNSEDY 359	
Db	301	MSTYSTNTMTIRILLAFVSSVGRNDGTGYTCCSSKHPSSQSALVTILEBGFNATSSQEEY 360	
Qy	360	EIDYEEFCFSVRFKAYPOIRCTWTFRKSPPCBQKGLDNGYSISKFNHKKHOPGEYIFH 419	
Db	361	EIDPYEFCFSVRFKAYPIRCTWIFQASPPCBQGLEGDGYSISKFDHKNKPEYIFY 420	
Qy	420	AENDDAQTKMFTLINRRKPOVLAAEASQASCPSDGYPPLPSWTWKKCSKSPNCTBEIT 479	
Db	421	AENDDAQTKMFTLINRRKPOVLANASQASQSSDGYPLPSWTWKKCSKSPNCTEIP 480	
Qy	480	BGVNVRKANRKFQGWSSSTFLANSEAIKGPLVKCCAYNSLGTSCETILLNSCPQPFPIQ 539	
Db	481	BGVNWKANRKFQGWSSSTFLANSEAGLULVKCCAYNSMGTSCTETILLNSGPPFPFIQ 540	
Qy	540	DNISFYATIGVCLLFIIVLTLLICHYKKQFPRYESQLQWQVVTGSSDNEYFYVDFPREY 599	
Db	541	DNISFYATIGCLFPIVVLIVLICHYKKQFPRYESQLQIQTGTPLDNEYFYVDFRDY 600	
Qy	600	DLKWEFFRENLERKVLGSGAFGKVMNATAYIGTKTVGSQVAVVMKKEKADSSERALM 659	
Db	601	DLKWEFFRENLEFGKVLGSGAFGRVMNATAYIGTKTVGSQVAVVMKKEKADSCKEALM 660	
Qy	660	SELKMTQLGSHENIVNLGACTLSGPTLYLIFEYCCYGDLLNLYRSKREKPHRTWTIEFK 719	
Db	661	SELKMTHLGHNDINVLGACTLSGPPVYLIFEYCCYGDLLNLYRSKREKPHRTWTIEFK 720	
Qy	720	EHNFSFYPTFQSHNSNMPGSRREVQIHPDSDQISGLHGNFSHSEDEIYENQKRL--EEE 777	
Db	721	EHNFSFYPTFOAHNSNMPGSRREVQLHPDLDLSGFNGNSIHSEDEIYENQKRLAEEEE 780	
Qy	778	EDLNVLPFEDLLCFAYQVAKMEFLPKSCVHRDLAARNVLVTHGKVVKICDFGLARDIM 837	
Db	781	EDLNVLPFEDLLCFAYQVAKMEFLPKSCVHRDLAARNVLVTHGKVVKICDFGLARDIL 840	
Qy	838	SDSNVVRGNARLPVKWMAPESLPEGIYTIKSDVWSYGILLWEIFSLGVNPPYGPVPDAN 897	
Db	841	SDSSVVRGNARLPVKWMAPESLPEGIYTIKSDVWSYGILLWEIFSLGVNPPYGPVPDAN 900	
Qy	898	FYKLIQNGFKMDQPFYATEEIIYIMQSCWAFDSKRKPSFPNLTSLFLGCOLADAEAMYQN 957	
Db	901	FYKLIQSGFKMQEPFATEGIYFVQWCMWAFDSKRKPSFPNLTSLFLGCOLADAEAMYQN 960	
Qy	958	VDGVSCEPHTYQNRNRPFSREMDLGLLSPOAQVE 991	
Db	961	MGNVNPBHPHPIYQNRRLSREAGSEPPSQAQVK 994	

RESULT 15

PCT-US95-03718-2
; Sequence 2, Application PC/TUS9503718
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03718
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 879PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US95-03718-2

Query Match	86.0%;	Score	4533.5;	DB	5;	Length	1000;
Best Local Similarity	85.6%;	Pred.	No. 0;				
Matches	851;	Conservative	56;	Mismatches	84;	Indels	3;
Gaps							
Qy	1	MPALA-RDAGTVP	LLLVFVSAMIFGTITNODLPV	KVLINHKNDSSVCKSSYPMVSES	59		
Db		:	:	:	:	:	:
Qy	60	PEDLGCA	LRPQSSGTVEAAAEVVDVS	AITLQVLVDAPGNISCLWVFKHSSLNCPHED	119		
Db		:	:	:	:	:	:
Qy	61	PEDLQCT	PRQSGTVEAATVEA	SSGITTLLQVQLATPDLISCLWVFKHSSLCQPHED	120		
Db		:	:	:	:	:	:
Qy	120	LQNRGV	SVMLKWTQTQAGEYLLF	QSEATNVYTLFTVSI	RNTLLYTLRRPYFRKQENQ	179	
Db		:	:	:	:	:	:
Qy	121	LQNRGI	VSMAILNVTQTQAGEYLLH	IQSEAAVYTLFTVNVN	RDQLYLRPYFRKQENQ	180	
Db		:	:	:	:	:	:
Qy	180	DALVCIS	ESYPEPIVEVWLCD	SQGESCKEESPAVVKKEKVLHELFGTD	IRCCARNELGR	239	
Db		:	:	:	:	:	:
Qy	181	DALLCIS	EGPEPTVEVWLCS	SHRECKEEGPAVVRKEKVLHELFGTD	IRCCARNALGR	240	
Db		:	:	:	:	:	:
Qy	240	ECTRL	ETIDLNQPTTLLPOLFK	VCEPLWIRCKAIVHNVHG	LGLTWELKNKALERNYPE	299	
Db		:	:	:	:	:	:
Qy	241	ESTKL	FTIDLNQAPQSTLLPOLFK	VCEPLWIRCKAIVHNVHG	LGLTWELDEKDALESGSYPE	300	
Db		:	:	:	:	:	:
Qy	300	MSTYSTNR	TMRIRLIFAVSSVARN	DTGYTCSSSKHPSQSALVT	IVGKGFINATSSSEY	359	
Db		:	:	:	:	:	:
Qy	301	MSTYSTNR	TMRIRLLAFVSSVGR	NDTGYTCSSSKHPSQSALVT	ILEKGFINATSSQEEY	360	
Db		:	:	:	:	:	:
Qy	360	EIDQY	EEPCFSVRFKAYPOIR	CTWTFPSRKSFCPEQKGLD	NGYSISKFCNHKHOPEYIFH	419	
Db		:	:	:	:	:	:
Qy	361	EIDPY	EKPCFSVRFKAYPR	IRCTWTFPSQRFCEQRL	EGDYSISKFDHKNKPEYIFY	420	
Db		:	:	:	:	:	:
Qy	420	AENDDAQ	FTMFTLNIRLRKPQ	VLAAASQASQSCFSDGYPLPS	WTWKKCSDKSPNCTEIT	479	

Db 421 AENDDAQTKFTLNIRKQVLANASASQASCSGDPPLPSWTWKCSKSPNCTEIP 480
Qy 480 EGVNKRKANRVFGQWVSSTLNMSAIGFLVKCAVNSLCTSCETILLNSPGPPFIQ 539
Db 481 EGVNKRKANRVFGQWVSSTLNMSAIGFLVKCAVNSLCTSCETILLNSPGPPFIQ 540
Qy 540 DNISFYATIGVCLLFIIVLTLIICHYKQKQFYESQLOQWVOTGSSDNEYFYVDFREY 599
Db 541 DNISFYATIGVCLLFIIVLTLIICHYKQKQFYESQLOQWVOTGSSDNEYFYVDFREY 600
Qy 600 DLKWEFFRENLEFGVLGSGAFGKVMATAYGISKTGVSIOVAVNMLKEKADSSREALM 659
Db 601 DLKWEFFRENLEFGVLGSGAFGKVMATAYGISKTGVSIOVAVNMLKEKADSSREALM 660
Qy 660 SELKXMTQLGSHENTVNLGACTLSGPVYLIIFEYCCYGLLNLRSKREKPHRTWTEIFK 719
Db 661 SELKXMTQLGSHENTVNLGACTLSGPVYLIIFEYCCYGLLNLRSKREKPHRTWTEIFK 720
Qy 720 EHNFSFYPTFQSHPNSSMPGSRVQIHPDSQISGLHGNSFHSEDEIEYENQKRL--EEE 777
Db 721 EHNFSFYPTFQSHPNSSMPGSRVQIHPDSQISGLHGNSFHSEDEIEYENQKRLAE 780
Qy 778 EDLNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHKVVKICDFGLARDIM 837
Db 781 EDLNVLTFFEDLLCFAYQVAKGMEFLFKSCVHRDLAARNVLTGHKVVKICDFGLARDIL 840
Qy 838 SDSNYVVRGNARLPVKWMAPESLFEGITYIKSDVMSYGILLWEIFSLGVNYPYGPVVDAN 897
Db 841 SDSNYVVRGNARLPVKWMAPESLFEGITYIKSDVMSYGILLWEIFSLGVNYPYGPVVDAN 900
Qy 898 FYKLIQNGFKMDQPYATEEYIIWQSWAFDSRKRPSFPNLTSLGCOLADAEAMYNQ 957
Db 901 FYKLIQSGFKMEQPFYATEGIYFVNQSWAFDSRKRPSFPNLTSLGCOLADAEAMYNQ 960
Qy 958 VDGRVSECPHTYQNRPPESREMDLGLLSPQAQVE 991
Db 961 MGNVPEHPSIYQNRRLPSREAGSEPPSPQAQVK 994

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